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21 – 24 de Octubre · 2025
Bogotá, Colombia



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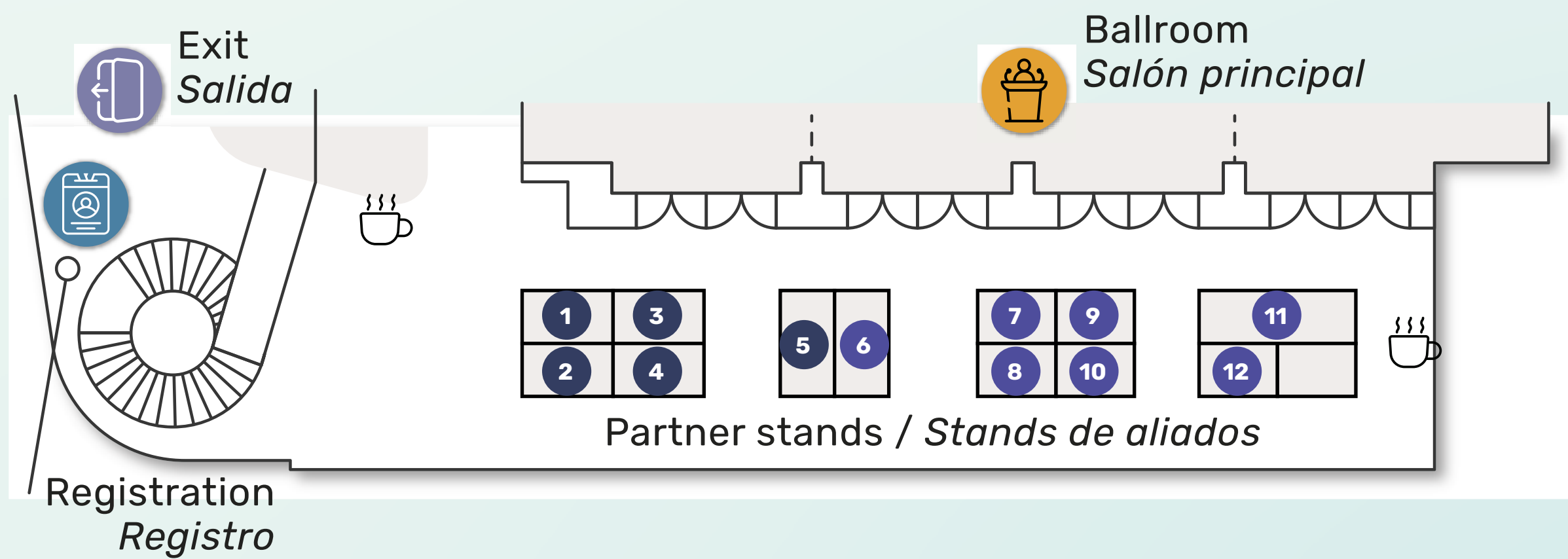
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Keynote & Plenary Speakers

*Conferencistas
Magistrales y Plenarios*

Session: **EVT-PLENARY-TUE****7001427**

21/10/25 | 09:00

Room: Ballroom

ORAL • EN

What data do we need, and what data do we have for monitoring global biodiversity?

Presenter

Alice Hughes

Authors

Alice Hughes (University of Hong Kong • Hong Kong)

Abstract

Globally we are beginning to realise the need for environmental policies to be built on evidence. For example, the recent Global Biodiversity Framework (GBF) is underpinned by a monitoring framework built on a selection of indicators designed to track progress towards GBF targets. Yet, any indicator is only as good as the data used to develop it, thus understanding the limitations and assumptions in environmental data which provides the basis for indicators is crucial.

The exponential growth in the availability of diverse types of ecological data has seemingly changed the problem for many ecologists trying to understand the natural world from having insufficient data to approach many ecological questions, to one of how to usefully analyse ever growing volumes of data. Yet despite this huge volume of data, biases within the data require caution to ensure their sensible use, as biases may shape the outcomes of analysis and potentially misrepresent true ecological patterns. These shortcomings have fundamental implications for the use of this data to identify trends and patterns in biodiversity, and thus for our ability to provide what is needed for science-driven policy. Here I discuss data needs, and limitations, then provide recommendations to guide sensible and effective use and interpretation of data. I discuss frameworks and standard pipelines to enable more effective use of data, and better approaches for the generation of further data to aid the development of effective conservation, policy and management. I also discuss examples of science-driven indicators currently used within policy, such as ecological conservation redlines to provide case-studies of how science can directly and effectively be used within spatial prioritisation and management. Finally, I highlight priorities ahead for both research, and biodiversity targets, as well as discussing short and longterm solutions as we fill knowledge gaps and develop more accurate model approaches.

Dr. Alice Hughes**Associate Professor**

Professor, Biosciences, Faculty of Science, University of Melbourne, Australia

Keynote Speaker

Session: **EVT-PLenary-TUE**

5074617

21/10/25 | 09:45

Room: Ballroom

ORAL • EN

From Land and Waters to Code and Cloud: Indigenous Data Sovereignty for Biodiversity and Rights-Based Governance

Presenter
Lydia Jennings

Authors
Lydia Jennings (Dartmouth College • United States)

Abstract
Indigenous Peoples continue to steward the world’s most biodiverse ecosystems, while are also asserting their sovereign rights within rapidly expanding digital environments. This talk explores how Indigenous Data Sovereignty serves as a critical tool for advancing rights-based approaches to biodiversity governance—from the tangible realms of land and water to the intangible, yet powerful, domains of code and cloud. Drawing from community-based examples, policy frameworks, and Indigenous-led data infrastructures, the presentation will highlight how Indigenous Nations are protecting knowledge systems, asserting governance over ecological and digital territories, and challenging extractive models of conservation and data use. In an era when environmental decision-making is increasingly driven by algorithms, remote sensing, and big data, ensuring Indigenous Peoples’ control over their data is inseparable from their rights to land, life, and future-making. This keynote invites us to reimagine digital ecosystems not as abstract or detached, but as deeply connected to sovereignty, relationality, and the ethical care for all forms of life.

Dr. Lydia Jennings
Assistant Professor
Department of Environmental Studies, Dartmouth College, USA
Keynote Speaker



Session: **EVT-PLENARY-WED**

7004420

22/10/25 | 09:00

Room: Ballroom

ORAL • EN

The Future of Biodiversity Data Sharing: Absence, AI and Human-Powered Interoperability

Presenter
Sabina Leonelli

Authors
Sabina Leonelli (Technical University of Munich • Germany)

Abstract
This talk reflects on three challenges of biodiversity data sharing and analysis, and their interrelations. The first challenge is data absence, with massive gaps in biodiversity surveys despite the enormous efforts invested in data gathering. The second challenge is the integration of AI into data collection, management and analysis. The third challenge is the development of interoperable and sustainable data ecosystems at a moment of great digital fragility. I argue that these three challenges can be confronted not by attempting to remove human agency and judgement from data analysis, but rather by articulating the role of human agency more clearly and placing it at the centre of data management, integration and mining activities. I exemplify this argument through examples from bio-ontologies and other forms of data semantics, data sharing strategies and infrastructures, and novel forms of AI-enabled data mining such as data visitations.

Dr. Sabina Leonelli

Professor, Philosophy and History of Science and Technology

School of Social Sciences and Technology, Technical University of Munich, Germany
Keynote Speaker



Session: **EVT-PLENARY-THU****5074618**

23/10/25 | 09:15

Room: Ballroom

ORAL • EN

Digitally Native Species Discovery: Tackling Insect Diversity with Robots, Megabarcoding, and Artificial Intelligence

Presenter

Rudolf Meier

Authors

Rudolf Meier (Museum für Naturkunde and Humboldt University • Germany)

Donat Agosti (Plazi • Switzerland)

Amrita Srivathsan (Museum für Naturkunde • Germany)

Abstract

Most of Earth's biodiversity remains unknown: only about 20% of species are formally described, while the remaining 80% remain undescribed. Over the past 250 years, biodiversity research has generated an enormous “analog backlog” of publications and collections, but creating more analog data in an era of machine learning and digital infrastructures is counterproductive. This talk presents a vision for digitally native species discovery and description that integrates hyperdiverse insect research with innovative technologies including high-throughput DNA barcoding on nanopore sequencers, robotic specimen handling and imaging, and artificial intelligence for data extraction and species description. Preliminary species hypotheses generated with cost-effective megabarcoding are validated with targeted morphological research, then translated into species descriptions using AI-assisted tools. In the process, each specimen that is processed becomes the anchor for structured digital records on Zenodo containing sequences, images, metadata, and traits. This ensures that data are FAIR-compliant—interlinked, transparent, reproducible, and immediately reusable for conservation and ecological monitoring. By prioritizing scalability and interoperability, the approach accelerates biodiversity discovery while producing species descriptions that are both human- and machine-readable. In doing so, the vast “dark taxa” of insects can become visible and tractable, enabling biodiversity research, monitoring, and conservation in a truly digital age.

Dr. Rudolf Meier**Professor, Integrative Biodiversity Discovery***Museum für Naturkunde, Berlin, Germany**Keynote Speaker*

Session: **EVT-PLENARY-TUE****7108573**

22/10/25 | 08:30

Room: Ballroom

ORAL • ES

Biodiversity Information Standards (TDWG): social and conceptual infrastructure for integrating biodiversity information

Presenter

María Cecilia Londoño Murcia

Authors

María Cecilia Londoño Murcia (Instituto Humboldt, GEO BON • Colombia)

Abstract

The International Working Group on Taxonomic Databases (TDWG) was established in 1985 to promote biodiversity data sharing and collaboration among organizations, projects, and people who manage biodiversity information. To achieve these goals TDWG develops standards for publishing biodiversity data and provides a forum for advancing biodiversity informatics.

This presentation will explore how TDWG provides critical elements for developing biodiversity information standards. In particular, we will detail three core facets of the TDWG organization and our on-going partnership with the Global Biodiversity Information Facility (GBIF).

TDWG's organizational structure includes an Executive Committee, a suite of standing committees for on-going operational concerns, a Technical Architecture Group (TAG) and an array of interest, task and maintenance groups that develop and maintain standards. These groups and committees provide TDWG's administration, maintain existing standards and best practices, and support the efforts of the community to create, expand and implement data standards using current methodologies of computer and information science.

One of TDWG's responsibilities is the ratification and revision of standards. Ratification entails both expert and public review to ensure best practice consistent with open science. TDWG's maintenance groups use a similar processes to add, change, or deprecate elements of ratified standards. TDWG's communications infrastructure provides the community with documentation about standards and encourages contributions and collaborations to make these standards more effective.

TDWG has been engaged in a partnership with GBIF since its inception in 2001. TDWG provides the openness that offers access and input from members of the global biodiversity science community, while GBIF enables governments to cooperate and develop the infrastructure needed to make primary biodiversity data accessible and useful.

Session: **EVT-PLENARY-WED****7020847**

22/10/25 | 08:45

Room: Ballroom

ORAL • EN

Biodiversity Information Standards (TDWG): social and conceptual infrastructure for integrating biodiversity information

Presenter

Stanley Blum

Authors

Stanley Blum (Biodiversity Information Standards (TDWG) • United States)

David Bloom (Biodiversity Information Standards (TDWG) • United States)

Abstract

The International Working Group on Taxonomic Databases (TDWG) was established in 1985 to promote biodiversity data sharing and collaboration among organizations, projects, and people who manage biodiversity information. To achieve these goals TDWG develops standards for publishing biodiversity data and provides a forum for advancing biodiversity informatics.

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Session: **EVT-PLENARY-THU****7014670**

23/10/25 | 08:45

Room: Ballroom

ORAL • EN

Empowering the Mesoamerican Region to Support Biodiversity Conservation through Data Science and Open Access

Presenter

Patricia Koleff

Authors

Patricia Koleff (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO) • Mexico)

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Tania Urquiza-Haas (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)

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Hersson Ramírez Molina (CONAGEBIO • Costa Rica)

Gandhi Gandhi Ponce Juárez (Consejo Nacional de Áreas Protegidas (CONAP) • Guatemala)

Melisa Ojeda (Bióloga y Consultora independiente • Guatemala)

Abstract

The lack of high-quality biodiversity data and limited regional capacity in data science are barriers to effective conservation decision-making in Mesoamerica. To address these challenges, the Costa Rica Institute of Technology (ITCR), in collaboration with leading biodiversity- focused institutions across Mesoamerica, including the National Commission for the Knowledge and Use of Biodiversity (CONABIO, Mexico), the National Commission for Biodiversity Management (CONAGEBIO, Costa Rica), the National Council for Protected Areas (CONAP, Guatemala), and the Entomological Museum of León (Nicaragua), has created the Data Science Network for the Conservation of Mesoamerican Biodiversity (redbioma.org) consortium. This initiative aims to establish a robust network of biodiversity institutions, observers, and researchers across Central America and Mexico using data science to address conservation challenges with a strong emphasis on scientific collaboration, capacity building, open science, and the empowerment of communities to adopt innovative approaches for conservation.

In its initial phase, Redbioma successfully engaged with over 500 stakeholders including practitioners, researchers, and policymakers, to identify critical conservation needs and capacity gaps. Many of these participants have taken part in a training program focused on data science to support biodiversity conservation and empowering local learning communities. The training offerings include courses such as Machine Learning Applied to Biodiversity Data, Statistics for Data Science, Geospatial Biodiversity Data Processing Using Python, Introduction to Ecological Niche Modeling, Systematic Conservation Planning, and Ecological Connectivity, among others.

A fundamental component of Redbioma is its biodiversity data portal, hosted by GBIF, which provides free and open access to more than 94 million occurrence records from over 1,100 datasets contributed by nearly 200 institutions.

As it moves forward with the support of the CSUCA-IDRC Project and GBIF, Redbioma remains committed to expanding its training programs, promoting collaborative research and data-driven solutions, and fostering inclusive community engagement in sustainable conservation efforts.

Session: **EVT-PLenary-THU****7108544**

23/10/25 | 09:00

Room: Ballroom

ORAL • EN

OBIS: Globally Trusted Data for Ocean Conservation, Management and Biodiversity Action

Presenter

Katherine Tattersall

Authors

Ward Appeltans (OBIS • Belgium)

Laurent Chmiel (OBIS • Finland)

Dan Lear (Marine Biological Association • UK)

Katherine Tattersall (CSIRO • Australia)

Abstract

The Ocean Biodiversity Information System (OBIS) is the key biodiversity component of UNESCO-IOC and stands at the forefront of global efforts to monitor marine life. Powered by a community of over 6,000 scientists worldwide, OBIS is the world's largest open-access platform for marine life data. Its datasets are FAIR (Findable, Accessible, Interoperable, Reusable), standardized, and quality-controlled. OBIS delivers high-quality, trustworthy, ready-to-use biodiversity data that supports evidence-based decision-making and conservation, advances research, guides marine management, and enables the sustainable use of marine resources.

OBIS participates in transforming local data holders into global contributors, ensuring local input visibility and impact on the global stage while maintaining data ownership and providing recognition. Through its 29 regional and 7 thematic Nodes spread across the world and its active community, OBIS acts as an inclusive global platform, strengthening local expertise and amplifying diverse regional voices.

To maximize impact, OBIS mobilizes cutting-edge technologies, including environmental DNA (eDNA), animal tagging & tracking, and AI-powered image analysis to accelerate the rate of availability and accessibility of marine biodiversity observations. OBIS also leverages advanced models to turn complex data into high-resolution decision-support tools, making information directly actionable for conservation efforts and evidence-driven management.

Data delivered by OBIS supports critical global conservation goals, such as the 30x30 Target of the Kunming-Montreal Global Biodiversity Framework (KMGBF). As the Ocean component of a Global Biodiversity Observing System, OBIS is recognized for helping to inform and report on the progress to reach the goals and objectives outlined in international agreements. Through strong partnerships, such as with the Global Ocean Observing System (GOOS), and the development of standardized methods for data collection and sharing, OBIS is an essential component for achieving sustainable management of marine ecosystems and building shared Ocean knowledge for the benefit of all.



Day 1 – Tuesday, October 21
Día 1 – Martes 21 de octubre

Symposia & Panel Sessions

*Sesiones de
Simposios y Paneles*

Session

6803272

Symposium

21/10/25 | 11:15

Room: Ballroom A

Data Integration for Conservation: Earth Observations for Biodiversity Monitoring in Colombia

Organizers

Elkin Noguera-Urbano

Victor Gutierrez-Velez

Mary Blair

Daniel Lopez-Lozano

Angela Mejia

Description

Colombia has significantly advanced its use of Earth Observation products for biodiversity decisions, with support from NASA's GEO BON program. NASA has funded projects in collaboration with Colombian institutions like the von Humboldt Institute and the National Natural Parks of Colombia, as well as US institutions like Temple University and the American Museum of Natural History, among others.

This symposium will showcase these projects and their impact on biodiversity monitoring. Examples include BioTablero, a biodiversity analysis system; enhancements to BioModelos, a species distribution mapping tool; and the development of Essential Biodiversity Variables using GEDI and Landsat data. A current project supports the National Parks System in monitoring and producing conservation indicators.

These NASA projects are vital for conservation, providing data for environmental monitoring and climate change understanding. They inform effective conservation strategies globally. This event will highlight the outcomes of NASA's initiatives with GEO BON and Colombia BON, demonstrating their contribution to biodiversity and ecosystem health monitoring.

The symposium invites contributions and discussions on all aspects of environmental issues related to NASA's projects from a diverse range of disciplines, including ecology, geology, biodiversity informatics, and more. Speakers will discuss how NASA's projects contribute to conservation and align with GEO BON's goals.

Session: 6803272**7013733**

21/10/25 | 11:20

Room: Ballroom A

ORAL • EN

Downscaling the area of habitat mapping approach to assist in species range map refinement for Colombia

Presenter

Wenxin Yang

Authors

Wenxin Yang (University of California, Santa Barbara • United States)

Amy Frazier (University of California, Santa Barbara • United States)

Lei Song (University of California, Santa Barbara • United States)

Patrick Roehrdanz (Conservation International • United States)

Nick McManus (Conservation International • United States)

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Joana Krieger (Conservation International • Brazil)

Elkin Noguera Urbano (Colombia)

Susana Rodriguez Buriticá (Colombia)

Abstract

Area of habitats (AOH) are available areas within species ranges to sustain species movement and survival that considers factors like land cover and elevation. AOH maps have been widely used in various tasks from estimating species richness to setting restoration priorities. They are usually created by masking broader species ranges with elevation and habitat types based on habitat through land cover type translation matrices. However, most data-driven AOH workflows have been developed at a continental to global scale, which can be affected by local uncertainties in the input data, and may not be equally applicable across regions.

Therefore, we propose a revised AOH workflow that incorporates local contexts to be applied at a national level. We test this workflow in Colombia, a megadiverse country with various ongoing conservation efforts. It has high species endemism for flora and fauna with unique and diverse land cover types, where global data products can be more uncertain and less representative. We use a national land cover dataset produced by IDEAM to match with species occurrences of different habitat preferences, and run bootstraps of logistic regressions to address subsampling bias. Instead of retaining habitat (i.e., land cover pairs with the highest odds ratios), we remove those with consistently low odds ratios and enhance results with expert opinions. Finally, we refine species distribution range maps produced from BioModelos using the translation matrix and compare results with outputs from the global workflow. The proposed workflow is reproducible and replicable across regions and can capture local contexts.

Session: 6803272**7015878**

21/10/25 | 11:30

Room: Ballroom A

ORAL • EN

Integrating Remote Sensing and Biological Records to assess Ecological Integrity in a Colombian Tropical Rainforest

Presenter

Luis Hernando Romero Jimenez

Authors

Luis Hernando Romero Jimenez (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Susana Rodriguez Buritica** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Jose Camilo Fagua Gonzalez** (Universidad Nacional de Colombia • Colombia)

Abstract

Comprehensive biodiversity assessment for decision makers is increasingly essential for guiding conservation and management strategies. This task remains elusive, especially in low-income countries, due to information gaps and analytical challenges regarding uncertainty and suboptimal data quality. Assessing ecological integrity using remote sensing data offers a valuable approximation. However, although cost-effective, these indicators may not fully capture forest ecosystem complexity, as they often ignore some key functional and compositional components. Addressing this challenge, especially for applications in low-income countries, we propose integrating remote sensing data with field-based biological records to develop a forest integrity indicator that explicitly absorbs some uncertainty, promoting transparent communication between scientists and decision-makers. Using the Structural Condition Index (SCI) as a proxy for forest structure, we applied machine learning models to relate it to recent biological records (composition) and satellite-based primary productivity indicators (function). This approach combines the quality of habitat assessments with uncertainty given by incongruent information between records and remote sensing information to identify areas of high integrity and low uncertainty, suitable for conservation efforts, and areas of lower integrity or high uncertainty, which may reflect human impact or data gaps—highlighting them as priorities for further study. The model that best integrates the variables was the Gradient Boosting Machine algorithm (Accuracy= 0.724 and Kappa= 0.493). By integrating diverse data sources, this indicator helps overcome taxonomic and data biases, offering a flexible, updatable tool for long-term biodiversity monitoring.

Session: 6803272**7023203**

21/10/25 | 11:40

Room: Ballroom A

ORAL • EN

Integrating Expert Knowledge, Land Cover Data, and Post-Processing Workflows to Enhance Ecosystem Change Detection in Colombia's Protected Areas

Presenter

Victor Gutierrez-Velez

Authors

Victor Gutierrez-Velez (Temple University • United States)**Angela Mejía** (Temple University • United States)**Equipo de Profesionales Parques Nacionales Naturales de Colombia** (Parques Nacionales Naturales de Colombia • Colombia)**Jeronimo Rodriguez** (Temple University • United States)**Victoria Sarmiento** (Temple University • United States)**Mary E. Blair** (American Museum of Natural History • United States)

Abstract

As a to global top biodiversity country, Colombia is central to address the global biodiversity crisis. Protected areas are key to achieve national biodiversity conservation goals. Therefore, timely ecosystem change detection is critical for informing conservation efforts in protected areas. This study synthesizes existing ecosystem monitoring capacity by the National Park System in Colombia (NPS) with advances in land cover and vegetation transformation mapping using satellite data to advance ecosystem change monitoring in Colombian protected areas.

First, we integrate national and global datasets to develop methods for automated land cover change mapping. We used standardized methods by NPS to extract reliable training samples for 15 key land cover classes across four protected areas representing a variety of environmental conditions and generated class probability layers using automated classification techniques. Validation data, collected through expert workshops demonstrated an overall accuracy of between 65 and 72% among study sites, and revealed an improvement in overall classification performance that is 11 to 23% higher than the official national land cover product for selected classes.

Second, we evaluated the utility of OPERA-DIST-ALERT, a satellite-based vegetation transformation alert system, for informing early warning alerts produced by NPS. We developed a workflow combining OPERA-DIST-ALERT metrics with other ancillary datasets to identify locations representing NPS alerts, using machine learning algorithms. The application resulted in an 80% overall accuracy in tested sites. False alert detections were prominent and mostly related to natural disturbances, anthropogenic perturbances in previously transformed areas, and frequent in mountainous areas, and during high pluviosity seasons.

Together, these approaches demonstrate that combining legacy knowledge, global products, and streamlined workflows can inform ecosystem monitoring efforts. An assessment of the performance of the land cover mapping workflow to evaluate multiannual change and the reduction of false alert detection are essential for institutional operationalization of these tools.

Session: 6803272**7020109**

21/10/25 | 11:50

Room: Ballroom A

ORAL VIRTUAL • EN

Software co-design between end users and developers to enhance utility for biodiversity conservation: a use case with Colombia BON

Presenter

Mary Blair

Authors

Mary Blair (American Museum of Natural History • United States)

Elkin A. Noguera-Urbano (Colombia)

Jose Manuel Ochoa-Quintero (Colombia)

Andrea Paz (Canada)

Cristina Lopez-Gallego (Colombia)

Maria Ángela Echeverry-Galvis (Colombia)

Juan Zuloaga (Canada)

Pilar Rodríguez (Mexico)

Leonardo Lemus-Mejia (Colombia)

Daniel López-Lozano (United States)

Abstract

Creating software tools for biodiversity conservation requires more than technical expertise, it demands the inclusion of a range of differing perspectives throughout the development process, especially decision-makers. Software tools for biodiversity conservation often fall short in this regard, partly because broad decision-maker needs may exceed the toolkits of single research groups or even institutions. We show that participatory, collaborative co-design enhances the utility of software tools for better decision-making in biodiversity conservation planning, as demonstrated by our experiences developing a set of integrated tools for the Colombia Biodiversity Observation Network (BON Colombia). Specifically, we undertook an interdisciplinary, multi-institutional collaboration of ecological modelers, software engineers, and a diverse profile of potential end users, including decision makers, conservation practitioners, and biodiversity experts. We leveraged and modified common paradigms of software production, including co-design and agile development, to facilitate collaboration through all stages to ensure the accessibility and applicability of the new tools to inform decision-making for biodiversity conservation planning. By fostering interoperability, integrating diverse data sources, and centering user needs, our work contributes to broader efforts to monitor and conserve biodiversity more effectively.

Session: 6803272**7020992**

21/10/25 | 12:00

Room: Ballroom A

LIGHTNING TALK • ES

Alas Seguras: una herramienta para orientar decisiones de conservación de aves migratorias en Colombia

Presenter

Valentina Grisales Betancur

Authors

Valentina Grisales Betancur (Audubon Americas • Colombia)

Jorge Velásquez-Tibatá (Audubon Americas • Colombia)

Jill Deppe (National Audubon Society • United States)

Abstract

La pérdida de aves migratorias en las Américas exige decisiones estratégicas basadas en evidencia para maximizar los beneficios de conservación. En este contexto, el proyecto *Alas Seguras* —liderado por la National Audubon Society en colaboración con BirdLife International, Calidris, el Instituto Humboldt y el NASA Goddard Space Flight Center— desarrolló un sistema de apoyo a decisiones (DSS) que identifica paisajes prioritarios para la conservación de aves migratorias en Colombia.

Esta herramienta, gratuita y en línea, permite a los usuarios generar mapas personalizados que integran modelos de distribución de aves migratorias, datos satelitales (GEDI, Landsat), información sobre cobertura terrestre, estructura forestal, disponibilidad hídrica y límites sociales y políticos. Co-diseñada con actores de iniciativas como Conserva Aves y BirdLife International, la herramienta fue pensada para adaptarse a distintos niveles de toma de decisión, desde la planificación estratégica hemisférica hasta intervenciones locales.

Alas Seguras organiza su análisis en torno a cuatro módulos de acción: agricultura y ganadería amigables con las aves, fortalecimiento de comunidades locales y gestión de áreas protegidas. Cada módulo permite combinar capas, establecer umbrales y asignar pesos para priorizar sitios de intervención donde las inversiones puedan tener mayor impacto ecológico y social. Por ejemplo, ha sido utilizada para identificar zonas donde los créditos de carbono podrían vincularse con prácticas ganaderas sostenibles y conservación de aves.

Financiado por el programa Ecological Conservation de la NASA, *Alas Seguras* no solo mejora el acceso a datos científicos para tomadores de decisiones, sino que también representa una innovación replicable en América Latina. Su desarrollo demuestra cómo integrar observaciones de la Tierra, datos de biodiversidad y procesos participativos puede transformar la conservación de aves migratorias, los ecosistemas y las comunidades que dependen de ellos.

Session: 6803272**7021024**

21/10/25 | 12:05

Room: Ballroom A

LIGHTNING TALK VIRTUAL • EN

GEDI Viz App: Vegetation structure visualization and analysis tool for Colombian ecosystems

Presenter

Ivan Gonzalez

Authors**Ivan Gonzalez** (Northern Arizona University • United States)**Jant Patrick** (Northern Arizona University • United States)**Abstract**

Forest structure is an Essential Biodiversity Variable (EBVs). It provides a better understanding of structural ecosystem traits such as habitat heterogeneity and carbon stocks, among others. Forest structure had been studied through field campaigns and direct measurement on individuals, on the recognized 0.1 Ha plots. Field campaigns are an accurate method that demands personal and financial investment, and provides low spatial resolution, making it challenging to analyze larger extents. The NASA GEDI instrument, launched in 2019, has been collecting measurements and generating a new dataset that describes vegetation vertical profiles. Colombia, a megadiverse country, has a high number of ecosystems and multiple combinations of climate and topography. These conditions also imply a challenge for a more extensive inventory and assessment of each ecological unit. This work collected and aggregated 70 million points, representing 15 ecoregions and 20 cover types. We aggregated the GEDI information of vegetation height, plant area index, and vegetation coverage, and presented statistics for each unique combination of the ecological units. We also provided a graphical user interface (GUI) with several utilities to allow dynamic queries on the dataset, given the extensive unique combinations of the response variables and analyzed units. The GUI modules include visualizations for: GEDI individual shots, ecological units statistics, spatial filter, a multi-dimensional aggregation, and a GEDI comparison with wall-to-wall vegetation predictions.

Session: 6803272**7023194**

21/10/25 | 12:10

Room: Ballroom A

ORAL • EN

Evaluating the impact of NASA-Supported Biodiversity products for biodiversity decision-making in Colombia

Presenter

Victor H Gutierrez-Velez

Authors

Victor H Gutierrez-Velez (Temple University • United States)**Viviana Ceballos** (Temple University • United States)**Maria Helena Olaya Rodriguez** (Instituto Humboldt • Colombia)**Camila Parra** (Instituto Humboldt • Colombia)**Patrick Jantz** (Northern Arizona University • United States)**Mary E Blair** (American Museum of Natural History • United States)

Abstract

Colombia is the world's second most biodiverse country. It is home of a great number of endemic and threatened species and some of the world's rarest and most threatened ecosystems. Rapid biodiversity loss urges to better understand biodiversity change and to integrate this biodiversity knowledge into decision-making. We present the impact of four NASA-supported projects on biodiversity decision-making in Colombia. Evaluated projects include the development and expansion of the BioTablero and BioModelos information platforms, the production of datasets characterizing forest structure and diversity, and the development of a protocol for community-based biodiversity monitoring. All projects were implemented through partnerships between U.S. institutions and the Alexander von Humboldt Institute.

Using policy reviews, project documentation, and extensive consultations with end-users, the evaluation assessed how project outputs influenced protected area designation and management across national, regional, and local scales. We further illustrate impacts through the production of three workflows at these three scales, explicitly connecting data products to decisions. Results show that NASA-supported products are relevant to 27 biodiversity policy indicators. The projects yielded knowledge gains represented by 10 publications, 3 software tools, and multiple datasets. They also provided standard methods and improved capacity and efficiency for species distribution modeling and biodiversity monitoring. Their integration into national and international information platforms facilitate their use for conservation planning and reporting, the identification of priorities sites for conservation, and to promote sustainable practices through community engagement.

NASA's support has thus improved access to biodiversity information in Colombia, with project outputs being incorporated into official conservation decision-making workflows. Ongoing collaboration between the Humboldt Institute and end-users along with continued platform and data development suggest that the full scope of impact is still emerging, with greater long-term benefits anticipated.

Session

6803154

Symposium

21/10/25 | 11:15

Room: Ballroom B1

A Global Ocean Biodiversity Observing System supporting governance framework implementation

Organizers

Ward Appeltans

Andrew Rodrigues

Emma Heslop

Audrey Darnaude

Frank Muller-Karger

Description

Effective monitoring is crucial for advancing our understanding of marine biodiversity and ecosystem trends, assessing progress towards global conservation goals, and informing adaptive management strategies. In support of international governance frameworks—most notably the Kunming-Montreal Global Biodiversity Framework (GBF) and the UN Convention on the Law of the Sea's Biodiversity Beyond National Jurisdiction (BBNJ) agreement—this session will explore how data, observation systems, and international collaboration can underpin robust and inclusive biodiversity monitoring efforts across all ocean domains, including areas beyond national jurisdiction (ABNJ).

This session will demonstrate how ocean observing initiatives contribute to a comprehensive and connected Global Biodiversity Observing System for the ocean. In particular, it will have presentations that show how to:

- (i) Implement and utilise the Global Ocean Observing System's Essential Ocean Variables (EOVs) to detect biodiversity change and identify its drivers;
- (ii) Enhance observing technologies, methodologies, and data workflows to address the biodiversity data needs of the BBNJ agreement and the GBF;
- (iii) Strengthen data standardisation, quality control, integration, and accessibility ensuring data is FAIR and data products are applicable for effective management and decision making.

By showcasing advances in marine biodiversity monitoring and data management, this session aims to foster communities of practice that can support effective science-policy interfaces and accelerate implementation of global ocean governance frameworks.

Session: 6803154**7020191**

21/10/25 | 11:15

Room: Ballroom B1

ORAL • EN

From Observation to Impact: Co-created tools emphasize the role of data management in global biodiversity observing systems

Presenter

Elizabeth Lawrence

Authors

Elizabeth Lawrence (UNESCO | IOC Project Office for IODE Ocean Biodiversity Information System • Canada)

Lina Mtwana Nordlund (Uppsala University • Sweden)

Abstract

Biological and ecosystem observations are essential for tracking biodiversity, monitoring ecosystem health, and informing ecosystem-based management. Yet they remain less coordinated compared to physical and biogeochemical observations, limiting their application in addressing global challenges. The Horizon Europe project, BioEcoOcean, is developing a Blueprint for Integrated Ocean Science, a transformative, co-creative initiative to strengthen collaboration and innovation within the ocean observation community.

Designed as a question-driven, flexible resource, the Blueprint encourages users to critically reflect on aspects of the ocean observation system, from planning and data collection to application in policy, management, and societal benefit. It aims to encourage cross-disciplinary dialogue, bridge gaps across sectors, disciplines, and stakeholder groups, and alignment with frameworks such as the Global Ocean Observing System's Essential Ocean Variables (GOOS EOVs). The Blueprint is being designed not as a rigid manual, but a dynamic tool informed by future thinking, design thinking, and possibility mapping.

This presentation will introduce the Blueprint, demonstrating its utility with OBIS data as a use case, tracing how data relates to and 'flows' through each Blueprint component, and emphasizing the critical role of data management. As the Blueprint is a co-creative process, we invite global collaboration to provide feedback and contribute to refining its structure and content. This presentation will also highlight how the Blueprint aligns with global biodiversity goals, and its potential to support a comprehensive and connected Global Biodiversity Observing System.

Session: 6803154

7011394

21/10/25 | 11:25

Room: Ballroom B1

ORAL • EN

Collective science to inform global ocean protections

Presenter

William Oestreich

Authors

William Oestreich (Monterey Bay Aquarium Research Institute • United States)

Max Czapanskiy (Bren School of Environmental Science & Management and the College of Creative Studies, University of California Santa Barbara • United States)

Kakani Katija (Monterey Bay Aquarium Research Institute • United States)

Nicholas Record (Tandy Center for Ocean Forecasting, Bigelow Laboratory for Ocean Sciences • United States)

Melissa Chapman (Department of Environmental Systems Science • Switzerland)

Abstract

In June 2023, the United Nations adopted the High Seas Treaty. Two years later, signatories are poised to ratify this treaty and create a legal instrument to implement marine protected areas (MPAs) in our greatest global commons, ocean areas beyond national jurisdiction. Protection of the open and deep ocean is timely: we stand at the precipice of an industrial revolution in Earth’s largest remaining wilderness. Deciding where to strategically implement high seas MPAs under this treaty requires robust biodiversity information, yet publicly accessible data is sparse, particularly at depth. There is now an opportunity for collective science action to support this collective policy action. Realizing this opportunity necessitates swift solutions to 1) support and incentivize standardized public sharing of existing biodiversity data; 2) broaden the scope of participatory science to process ocean observations into biodiversity data; and 3) equitably implement new data collection with research partners across our global community. Here, we first perform rigorous analysis of geographic and socioeconomic biases in publicly accessible oceanic biodiversity data. We then explore and propose collective actions under the 3 aforementioned solution spaces which to provide make biodiversity data across our global ocean more accessible and robust. These collective and coordinated science actions are critical to maximizing the potential efficacy of conservation decisions under the protection mechanism afforded by the High Seas Treaty.

Session: 6803154**7020627**

21/10/25 | 11:35

Room: Ballroom B1

ORAL VIRTUAL • EN

SPACEWHALE: Using satellite imagery to survey whales in remote areas and thus to enhance conservation efforts

Presenter

Julika Voß

Authors

Julika Voß (Bioconsult SH • Germany)

Caroline Hoeschle (BioConsult SH • Germany)

Recep Can (BioConsult SH • Germany)

Amel Ben Majoub (BioConsult SH • Germany)

Vlad Kosarev (BioConsult SH • Germany)

Kelly McLeod (HiDef Aerial Surveying Limited • United Kingdom)

Abstract

There is an ambitious global goal to protect 30% of the ocean by 2030 and since COP15, a goal to halt biodiversity loss. However, only 8.1% of the ocean is protected and over 80% are still unexplored. But mapping these areas and key indicator species like whales using ship-based and aerial surveys tend to be limited in scale/scope, time-consuming, expensive and pose safety risks to surveyors; while acoustic monitoring is difficult to convert into counts of individuals for most species. For overcoming these challenges, BioConsult SH and HiDef Aerial Surveying Ltd developed the service SPACEWHALE: By monitoring whales from space using satellite imagery, their minimum number and distribution can be determined quickly and over wide cross-border areas, yet at similar costs to traditional survey methods.

SPACEWHALE uses very high-resolution satellite imagery with a resolution of 0.31 m per pixel. It takes a “snapshot” of the ocean area of interest and can capture very large and remote areas almost instantaneously. We teamed up a semi-automatic process to evaluate satellite images combining state-of-the-art artificial intelligence and marine mammal experts’ quality assurance. Using whales as indicators for a high biodiversity, we can study previously completely unexplored areas and help accelerating the designation of Important Marine Mammal Areas and Marine Protected Areas, provide environmental impact assessments for offshore wind farm operators and offer an efficient tool for mandatory baseline monitoring of whale populations. SPACEWHALE can collect the data we need in years instead of decades. We have already successfully monitored about 10,000 km² and are at a step where satellite-based data informs applied conservation and provides useful guidance to find solutions that balance species conservation with human use of the seas; it has the potential to elevate conservation efforts to appropriate spatial scales for wide ranging species.

Session: 6803154**7018632**

21/10/25 | 11:45

Room: Ballroom B1

ORAL • EN

Opening new frontiers with near-real time biological ocean data

Presenter

Jonathan Pye

Authors

Jonathan Pye (Ocean Tracking Network • Canada)**Ian Jonsen** (StochasticQC • Canada)**Clive McMahon** (Sydney Institute of Marine Science • Australia)**Ward Appeltans** (Intergovernmental Oceanographic Commission of UNESCO|Ocean Biodiversity Information System • Belgium)**Elizabeth Lawrence** (Intergovernmental Oceanographic Commission of UNESCO|Ocean Biodiversity Information System • Canada)**Ana Lara-Lopez** (Intergovernmental Oceanographic Commission of UNESCO|Global Ocean Observing System • Australia)**Audrey Darnaude** (CNRS, (MARBEC) • France)

Abstract

A globally coordinated and sustained ocean observing system is essential to assess the state of the ocean and its biological resources at national, regional, and global scales. The Global Ocean Observing System (GOOS), coordinated by the Intergovernmental Oceanographic Commission of UNESCO, is a worldwide network of observing systems collecting ocean physics, biogeochemistry, biodiversity and ecosystems data.

One of these networks, AniBOS (Animal Borne Ocean Sensors), provides freely available oceanographic measurements from remote and under-sampled regions in the ocean. AniBOS uses biologging, deploying sensors on marine animals, to collect physical and ecological data at the scale and resolution of animal movements.

For the past 21 years, the Integrated Marine Observing System (IMOS) – a major contributor to AniBOS – has delivered near-real-time physical oceanographic data to the Global Telecommunication System (GTS) for weather forecasting. This same technology can be used to deliver biological and ecological information about the tagged animals. A collaborative pilot project between GOOS, IMOS, the Ocean Biodiversity Information System (OBIS), and the Ocean Tracking Network (OTN) is developing automated workflows to quality-control AniBOS biological data converting into Darwin Core (DwC) format for near-real-time publication to OBIS.

The project uses IMOS southern elephant seal data from miniaturized conductivity-temperature-depth tags, quality-controls the location data automatically and translates these locations and metadata into DwC for OBIS publication. This will be expanded to include quality-controlled data from other tracking devices, with future capabilities to summarise and publish additional biological variables (e.g. diving and surface behavior), and integrate with physical parameters.

This innovation will enable impactful applications such as:

- Real-time information on protected species location to mitigate vessel strikes and inform dynamic fishing closures;
- Improved identification of ecological hotspots to inform conservation;
- Demonstration of integrated, multidisciplinary data delivery systems;
- A blueprint for building real-time, cross-disciplinary data delivery systems to inform science, management, policy.

Session: 6803154

7020127

21/10/25 | 11:55

Room: Ballroom B1

ORAL • EN

Leveraging Animal Movement Data for Global Marine Biodiversity Monitoring

Presenter

Authors

- Autumn-Lynn Harrison (Smithsonian National Zoo and Conservation Biology Institute • United States)
- Lacey Hughey (Smithsonian National Zoo and Conservation Biology Institute • United States)
- Talia Speaker (WILDLABS at WWF • United States)
- Sarah Davidson (Max Planck Institute for Animal Behavior • Germany)
- Antonio Ferraz (United States)
- Aidin Niamir (Senckenberg • Germany)
- Matt Ogburn (Smithsonian Environmental Research Center • United States)
- Ximena Velez-Zuazo (Smithsonian National Zoo and Conservation Biology Institute • Peru)

Abstract

Effective monitoring of marine biodiversity must reflect not only patterns in species presence and abundance, but also the processes that sustain connectivity and ecosystem functions. Animal movement data provide detailed insights into these processes. Existing infrastructures for animal tracking and bio-logging connect experts and host data going back decades and being collected in near-real time. These have demonstrated their usefulness to marine biodiversity monitoring, but opportunities to improve the data integration for global efforts remain. The newly launched Animal Movement Biodiversity Observation Network (Move BON) aims to elevate animal movement as a critical dimension of biodiversity observation. By convening researchers, data holders, and institutions across marine, freshwater, aerial, and terrestrial systems, Move BON is guided by four overall goals: (1) enhancing science-policy integration by promoting a shared understanding of the movement data pipeline; (2) coordinating with existing initiatives to identify and close critical information gaps; (3) deriving actionable insights by linking movement changes to biodiversity outcomes; and (4) operationalizing solutions through national partnerships, capacity building, and case studies. As the initiative takes shape, Move BON is exploring opportunities to align with the Global Ocean Observing System’s Essential Ocean Variables (EOVs) framework and contribute to a more connected, process-informed Global Biodiversity Observing System for the ocean.

Session: 6803154**7020675**

21/10/25 | 12:05

Room: Ballroom B1

ORAL VIRTUAL • EN

Ocean data application for biodiversity inclusive Marine Spatial Planning

Presenter

Silas Principe

Authors

Silas Principe (OBIS (IODE|IOC|UNESCO) • Belgium)

Pieter Provoost (OBIS (IODE|IOC|UNESCO) • Belgium)

Ward Appeltans (OBIS (IODE|IOC|UNESCO) • Belgium)

Anna M. Addamo (Nord University • Norway)

Mark John Costello (Nord University • Norway)

Abstract

Countries have committed to protecting at least 30% of the ocean by 2030, with European countries further committing to a minimum of 10% under strict protection. This will be achieved through the establishment of marine protected areas (MPAs) and other effective area- based conservation measures (OECMs). A key challenge is determining where to locate these areas to maximize biodiversity conservation while ensuring climate resilience as ecosystems shift under climate change. The Horizon Europe project MPA Europe uses the systematic conservation planning approach to map a network of MPAs across Europe that represent the widest range of species, habitats, and ecosystems—while also maximizing blue carbon potential. To support this effort, the Ocean Biodiversity Information System (OBIS) has developed species distribution models (SDMs) for over 12,000 marine species. SDMs analyze the relationship between species occurrences and environmental conditions to predict potential distributions across large areas, helping overcome data gaps. Our modelling framework combines species occurrence data from OBIS and GBIF (Global Biodiversity Information Facility) with environmental layers from Bio-ORACLE. Models were fitted at high resolution (~5 km) and projected into the future using five CMIP6 Shared Socioeconomic Pathway (SSP) scenarios for 2050 and 2100. The framework is fully open-source, enabling adaptation and use in other regions. Importantly, the project is being co-developed with stakeholders to ensure relevance and usability. As a next step, we aim to expand the modelling framework to additional species globally, offering a valuable tool for marine biodiversity conservation. In parallel, the project is working on the final spatial prioritization. Results will be compiled into an atlas to support countries in meeting their conservation goals.

Session: 6803154**7020909**

21/10/25 | 12:15

Room: Ballroom B1

ORAL • EN

eDNA Expeditions -- Scaling Biodiversity Monitoring Globally Through Community Science

Presenter

Saara Suominen

Authors

Saara Suominen (Ocean Biodiversity Information System • Belgium)**Pieter Provoost** (Ocean Biodiversity Information System • Belgium)**Silas Principe** (Ocean Biodiversity Information System • Belgium)**Ward Appeltans** (Ocean Biodiversity Information System • Belgium)

Abstract

The eDNA Expeditions at UNESCO World Heritage sites project (2022-2024) demonstrated the power of eDNA metabarcoding as a cost-effective biomonitoring tool with global reach. In just under 3 years, the project engaged over 250 citizen scientists and successfully collected and sequenced nearly 400 samples, resulting in over 600 million sequences. As a result, over 4,400 marine species were identified across 20 UNESCO World Heritage Marine sites. This experience shows the power of environmental DNA (eDNA) and community engagement to scale biodiversity monitoring in an inclusive way. By equipping citizen scientists with easy-to-use eDNA sampling tools and protocols, the project enabled local communities around the world to contribute to global biodiversity datasets—many for the first time. This talk will present the vision, methodology, and outcomes of eDNA Expeditions, showcasing the supporting data management strategies and the resulting eDNA dashboard, that allows for the effective discovery of the eDNA datasets by citizens and site managers.

Session: 6803154**7019772**

21/10/25 | 12:25

Room: Ballroom B1

ORAL VIRTUAL • EN

Dotting the connections: using agent-based models to link habitats and biodiversity

Presenter

Lars O. Mortensen

Authors

Lars O. Mortensen (DHI A S • Denmark)

Verena Schrameyer (DHI A S • Denmark)

Ole Bjørn Brodnicke (DHI A S • Denmark)

Jonas Brandi Mortensen (DHI A S • Denmark)

Abstract

Connectivity of habitats plays a significant role in maintaining healthy marine ecosystems by providing a key mechanism for the dispersal and recruitment of species. Furthermore, the biodiversity of an ecosystem has often been linked to the number of connections the ecosystem has to the broader regional area. But with the current extended development ongoing in the world's oceans, there is an increased risk that habitat connectivity will be disrupted, which in turn can lead to cascading effects of biodiversity degradation in either the disrupted ecosystems or connected ecosystems.

To support the decisionmakers and managers in managing their biodiversity footprint, we have developed an approach using agent-based modelling coupled with ecological modelling together with local and regional developed hydrodynamic model (Hansen et al. 2015) to assess the connectivity of local and regional areas. This approach enables us to model how entities (such as species), proxies (such functional traits), or concepts (such as biodiversity), of a local area is linked to other areas both locally and regionally through hydrodynamic interactions. Furthermore, by coupling observational data on biodiversity with hydrodynamic and static information through general additive models and machine learning algorithms we also map the spatial distribution of biodiversity.

The coupling of the two approaches allows for predicting the spatio-temporal distribution of biodiversity and enables quantitative assessments on how biodiversity will change in time and space as a consequence of anthropogenic disturbances. The approach allows stakeholders, developers and managers to move from qualitative assessments to quantitative assessments of biodiversity footprints.

Session

6798855

Symposium

21/10/25 | 11:15

Room: Ballroom B2

Advancing biodiversity goals from local to global scales using iNaturalist

Organizers

Carrie Seltzer

Tony Iwane

Alison Young

Description

iNaturalist is a citizen science platform for crowdsourcing biodiversity records. The mobile app and website are used around the globe to both build community and generate data. Collectively, millions of people have contributed photos and identifications of more than 500,000 unique taxa. For more than 100,000 species, this information enables the development of predictive models for geographic distribution and visual similarity.

Learn how iNaturalist helps other organizations advance specific biodiversity goals or objectives at various scales from local to global. Lightning talks will address the objectives, outcomes or impacts, what did & didn't work, and transferable lessons for others with similar goals and/or challenges.

Examples of goals or objectives could include monitoring the success of site restoration, improving regional invasive species management, a specific policy outcome, national biodiversity targets, identifying conservation priorities, improving awareness or education, etc. We especially welcome examples of Indigenous groups using iNaturalist.

Session: 6798855**7020775****21/10/25** | 11:15**Room:** Ballroom B2**ORAL • EN**

Using iNaturalist to restore habitat for biodiversity: a vision

Presenter

Carrie Seltzer

Authors

Carrie Seltzer (iNaturalist • United States)**Scott Loarie** (iNaturalist • United States)

Abstract

Now that iNaturalist has enough data to model the ranges of more than 100,000 species across all taxa, new tools can be developed to allow people to not only record species, but also help them identify high-priority species that they could aim to attract through changing management practices.

Imagine you have a project on iNaturalist for a park. Using the modeled ranges for 100,000 species, we can predict which species are most likely to be found there. By focusing on the subset of species that are most “charismatic”, we can predict a set of species present and absent from the site. From this list and respective species sensitivities we can compute the health of the site based on the characteristics of species present and absent from the site. All of this can be distilled to a biodiversity score for a given area. By improving habitat to attract more of the target species (or even just rallying people to help find more of the species that already exist), the score can improve.

Degrading the habitat and losing species will reduce the score over time.

This feature idea is in the concept stage and we are eager to learn from the presenters and attendees if and how this might be used in practice.

Session: 6798855**7009778**

21/10/25 | 11:30

Room: Ballroom B2**ORAL • EN**

A systematic review of how iNaturalist is contributing to local and global peer-reviewed research

Presenter

Corey Callaghan

Authors

Corey Callaghan (University of Florida • United States)

Brittany Mason (University of Florida • United States)

Abstract

Participatory science has grown in popularity, with iNaturalist standing out as one of the most widely used platforms worldwide, with

>100,000 observations uploaded daily. To better understand the current usage of iNaturalist data in biodiversity research, we conducted a systematic literature review, performing a comprehensive bibliometric analysis to quantify geographic and taxonomic coverage of iNaturalist data in the literature and identify research topics. We manually searched for, and then categorized, articles based on the geographic range, study taxa, species information, article topic, analyses conducted, iNaturalist data type, data role, and project data usage. We found that the use of iNaturalist data in scientific literature is rapidly growing, with over a 10-fold increase in the last five years. At least 683 taxonomic families were represented in iNaturalist literature. Some taxonomic classes, such as Mammalia, Reptilia, and Amphibia, were overrepresented compared to the proportion of iNaturalist observations, whereas Aves, Insecta, and Magnoliopsida were underrepresented. Geographically, the scientific literature used iNaturalist data from 240 countries. Countries with lower development indices were significantly more likely to have an overrepresentation of iNaturalist literature compared to the proportion of iNaturalist observations. Research topics included species distribution modeling, population trends, behavior, species discovery, and data quality. Certain taxa (e.g., mammals and reptiles) were overrepresented, while others (e.g., birds, insects, and flowering plants) were underrepresented relative to iNaturalist's overall dataset. By democratizing biodiversity data collection, iNaturalist is increasingly being used to monitor species, inform conservation priorities, and fill taxonomic and geographic knowledge gaps—contributing directly to local and global biodiversity research. Our review highlights the platform's current scientific value and future potential of iNaturalist to shape the future of biodiversity research.

Session: 6798855**7015783**

21/10/25 | 11:40

Room: Ballroom B2**LIGHTNING TALK VIRTUAL • EN**

From Pixels to Policy: Piloting iNaturalist as a Scalable Tool for Biodiversity Monitoring in Rapidly Urbanizing Environments

Presenter**Pasindu Dilshan Abegunawardhana****Authors****Pasindu Dilshan Abegunawardhana** (Foundation for Ecology & Research on Nature • Sri Lanka)**Salindra Kasun Dayananda** (Foundation for Ecology & Research on Nature • Sri Lanka)**Zahra Farook** (Université Paris Cité • France)**Abstract**

Urban expansion poses increasing threats to biodiversity, particularly in fragmented green spaces such as institutional grounds, roadside habitats and remnant ecological patches. In this pilot project, we explored the use of iNaturalist for rapid biodiversity monitoring within a highly disturbed suburban site in Sri Lanka. Using a hybrid methodology that combined visual encounter surveys, structured sampling (pitfall and light traps), and opportunistic data collection, we documented 188 fauna species over a three-day period, including 155 species directly uploaded to iNaturalist. This approach enabled real-time data collection, community validation, and expert engagement, while providing an accessible interface for longitudinal monitoring. iNaturalist facilitated not only species identification but also metadata standardization and automated georeferencing, allowing for downstream use in conservation planning and ecological assessments. Our objectives included (1) assessing the feasibility of citizen-led biodiversity baselining in urbanized spaces, (2) evaluating the spatial distribution of faunal diversity across microhabitats and (3) piloting a replicable monitoring framework aligned with national biodiversity targets. Our study led to increased public awareness, an open-access dataset and the establishment of a reference point for future site comparisons useful for urban ecological restoration, invasive species alerts or land-use impact assessment. Challenges identified included intermittent observer effort, limited taxonomic certainty in less-photographable taxa (e.g., cryptic invertebrates) and poor media quality compromising dataset integrity. To improve future efforts, we recommend comprehensive training modules on proper documentation techniques and implementing regular bioblitzes to maintain consistency. Sustained engagement strategies will be essential to maintain data collection standards over time. This project underscores the potential of iNaturalist as a low-cost, scalable tool to support biodiversity policy, urban planning, and community education. Its integration into schools, municipalities or local conservation initiatives offers an adaptable model that can bridge data gaps and promote ecological resilience in rapidly changing environments.

Session: 6798855

7020991

21/10/25 | 11:45

Room: Ballroom B2

LIGHTNING TALK • EN

Harnessing iNaturalist to Test Eyespot Mimicry in South American Moths

Presenter

Chandra Earl

Authors

Chelsea Skojec (Florida Museum of Natural History • United States)

Chandra Earl (NEON (National Ecological Observatory Network) • United States)

Angela McTammany (University of Central Florida • United States)

Vaughn Shirey (Florida Museum of Natural History • United States)

Abstract

As biodiversity science increasingly relies on large-scale, data-driven approaches, community science platforms like iNaturalist play a critical role in expanding research capacity, especially for underrepresented taxa and regions. In this project, we leveraged iNaturalist imagery to support ecological and evolutionary analyses of *Automeris*, a genus of moths primarily found in South America. These species exhibit elaborate hindwing eyespots that may function as visual mimicry of owl eyes, a widely cited anecdotal explanation for their function, but testing this hypothesis at scale has historically been limited by data availability (particularly images) and geographic coverage in traditional specimen datasets.

To address these gaps, we combined iNaturalist photographs with digitized museum specimens and species occurrence records from GBIF and SCAN. iNaturalist images were used to train neural networks to assess visual similarity between moth eyespots and owl faces. The platform's geographic and taxonomic breadth enabled us to access a much broader range of in-situ moth imagery than would be possible through collections alone. This imagery was also used in quality-controlled pipelines to evaluate perceptual confusability, a key step in testing mimicry hypotheses.

In parallel, we used cleaned and harmonized occurrence records from GBIF and SCAN to build species distribution models for *Automeris* moths, and combined these with expert-derived owl range maps from Birds of the World to assess geographic overlap between likely mimics and models across the Americas. Together, these analyses revealed trait and range patterns suggestive of mimicry, while also highlighting the value of iNaturalist for supporting hypothesis-driven research rooted in visual signaling and perception across biodiversity- rich, but relatively data-poor regions.

Session: 6798855**7016226**

21/10/25 | 11:50

Room: Ballroom B2

ORAL VIRTUAL • ES

iNaturalist como herramienta de ciencia participativa para el conocimiento de la biodiversidad de lepidópteros diurnos urbanos en Colombia.

Presenter

Beatriz Helena Mojica Figueroa

Authors

Beatriz Helena Mojica Figueroa (UTS • Colombia)

Fabian Andres Sierra Galvis (UIS • Colombia)

Abstract

La ciencia participativa es una herramienta útil que en los últimos años ha permitido el conocimiento de la biodiversidad urbana gracias a plataformas tecnológicas a través de la participación cada vez mayor de ciudadanos que de manera voluntaria aportan datos a través de sus aplicativos móviles. Se realizó una revisión del SiB (red nacional de datos abiertos sobre biodiversidad) donde de un total de 133270 registros correspondientes a 5746 especies se verifica que iNaturalist está aportando el 27% (33650) de los datos de Lepidópteros con 2493 especies, correspondientes a las familias Nymphalidae(1193), Lycaenidae(416), Hesperidae(524), Pieridae(156), Riodinidae(110) y Papilionidae(94). De igual manera se revisaron datos desde la web de iNaturalist que actualmente cuenta con más de 1.900.000 observaciones de las cuales más de 298 mil corresponden a Lepidópteros, siendo esto posible gracias a una comunidad de más de

53.000 Naturalistas, incentivando la integración de grupos de trabajo y redes colaborativas que favorecen el intercambio de conocimientos. iNaturalist se posiciona como uno de los medios más eficientes para compartir datos alrededor de proyectos que se generan en la plataforma. El City nature challenge es uno de los más destacados, es un reto que ha generado en sus cinco versiones consecutivas desde el año 2021 cerca de 123 mil observaciones y 4000 especies, de las cuales, los lepidópteros corresponden a cerca de 3000 observaciones y 366 especies, cifra importante a nivel urbano, donde gracias al apoyo del instituto Humboldt y la participación de ciudades y áreas metropolitanas, se destacan con la generación de datos de lepidópteros en su orden, Medellín, Bucaramanga, Pereira, Cali y Bogotá, insumo para tomadores de decisiones respecto a conservación de especies nativas, control de aquellas con potencial invasor, y en general gestión y apropiación de la biodiversidad urbana.

Session: 6798855**7019960**

21/10/25 | 12:00

Room: Ballroom B2**LIGHTNING TALK VIRTUAL • EN**

Phenology at a Native Plant Nursery: Phenology as one tool to identify success & obstacles to seed production for restoration

Presenter

Gail Baker

Authors

Gail Baker (Friends of Buford Park Native Plant Nursery • United States)

Abstract

Native plant nurseries are not “black boxes”. Wild collected seeds are grown and harvested within an agricultural model before they are directed to a natural setting for habitat restoration. Our 5-year study presents baseline plant phenology data from a native plant nursery to inform nursery management and improve seed production for habitat restoration success. And inspire research about how nursery location influences surrounding native and urban ecosystems as a source or sink for pollinators, seed dispersers, seed predators, herbivores and pathogens.

From 2020 through 2025 weekly photographs of 60 native plant species grown in a native plant nursery were posted on iNaturalist. Species diversity was represented by plant habit, ecosystem of origin and a spectrum of taxonomic groups. For every observation, each phenophase was photographed and annotated: vegetative (no fruits or flowers); flower buds, flowers, fruits or seeds. Percent estimates of each phenophase were included in the Notes for all observation. Over 8000 observations have been posted, and on-site weather data recorded since 2021. Three parallel projects within the nursery boundary record fungi and wildlife that interact with the nursery plant community and phenophases of wild relatives of the nursery species within 2 km of the nursery. Nursery annual seed harvest weights for each species are matched with phenology observations. Team members are community volunteers.

Results show yearly durations and variations of phenophases within species and overlaps between species. We are matching these data with weather and annual seed harvest to determine if there are indicators to predict viable seed set and harvest times. Flowering and fruiting duration and peak overlap data need to be partnered with community ecologists to determine herbivore and pollinator impact on plant reproductive success.

Native plant nurseries should be recognized as influential plant community within an ecosystem and valuable research sites

Session: 6798855**7020239**

21/10/25 | 12:05

Room: Ballroom B2**LIGHTNING TALK • EN**

Wiki loves iNaturalist: how Wikimedians integrate iNaturalist content on Wikipedia, Wikidata, and Wikimedia Commons

Presenter

Tiago Lubiana

Authors**Tiago Lubiana** (Biodiversity Heritage Library • Brazil)**Siobhan Leachman** (Wikimedia Aotearoa New Zealand, Wellington, New Zealand • New Zealand)**Richard Littauer** (Te Herenga Waka Victoria University of Wellington • New Zealand)**Abstract**

iNaturalist and Wikipedia have a lot in common: collaborative, large-scale, open infrastructures made by volunteer communities with long- reaching impact on human knowledge flows. Naturally, there is a large overlap between both communities, a set of nature- and open knowledge-loving people that work for better integration between both platforms.

In this talk, we will explain how Wikimedians can incorporate iNaturalist into their editing workflows. We will showcase the software tools for integrating content from iNaturalist into Wikimedia Commons and Wikidata (such as inat2wiki.toolforge.org). We will also share the tales of the WikiProject Biodiversity on Wikidata, and our different types of engagement activities, from WikiContests, to WikiBioBlitzes, to outreach activities about Creative Commons licenses, their use in iNaturalist, and their Wiki compatibility.

Finally, we will present how to keep track of iNaturalist content on Wikimedia projects. With over 200,000 images on Wikimedia Commons used in over 30,000 Wikipedia pages, which receive around ~20 million views per month, we celebrate the immense contribution iNaturalist has brought to the open knowledge ecosystem.

We hope that this talk will serve as a conversation starter to further strengthen the collaboration between both communities for mutual benefit.

Session: 6798855**7020066**

21/10/25 | 12:10

Room: Ballroom B2

LIGHTNING TALK VIRTUAL • EN

Fifteen years of BioDiversity4All - building a national citizen science network with iNaturalist

Presenter

Patrícia Tiago

Authors

Patrícia Tiago (BioDiversity4All • Portugal)

Abstract

Launched in 2010, BioDiversity4All began as a national biodiversity platform connected to the Dutch “Observado” system, where it remained until 2018. In its first eight years, the platform focused on creating bridges between the scientific community and diverse societal groups – including schools, municipalities, NGOs, farmers, divers, birdwatchers, and nature-based tourism agents – with the goal of making biodiversity data collection a truly participatory process.

In 2018, BioDiversity4All became the official Portuguese node of iNaturalist, the first in Europe. This shift brought a turning point: only through iNaturalist’s intuitive and user-friendly interface was it truly possible to grow and sustain a national biodiversity community. The platform’s design lowered participation barriers and allowed for real-time feedback, species identification, and global collaboration, unlocking new potential for engagement and scientific relevance. This move opened new opportunities for international collaboration and allowed BioDiversity4All to scale up its reach and impact while maintaining a strong national identity and user community.

Today, BioDiversity4All is deeply embedded in national biodiversity initiatives. It is used in environmental education programs, school curricula, municipal biodiversity planning, invasive species monitoring, and large-scale participatory events such as BioBlitzes. Its open data is increasingly valued by researchers and institutions, bridging the gap between grassroots observation and academic science.

This presentation reflects on the 15-year journey of BioDiversity4All, from its early days with Observado to the dynamic, community-driven platform it has become within the iNaturalist network. It shares lessons learned in creating inclusive, scientifically useful citizen science infrastructure, and explores opportunities for strengthening biodiversity engagement through collaborative approaches in the Ibero- American region.

Session

6798929

Symposium

21/10/25 | 11:15

Room: Tolima

Integrating DNA Reference Databases and Molecular Taxon Concepts in Biodiversity Databases

Organizers

Urmas Kõljalg

Emilie Boulanger

Tobias Frøslev

Rutger Vos

Pieter Provoost

Description

Reference databases and molecular species concepts are foundational for DNA-based biodiversity research and essential for extending detection and monitoring to neglected branches of the tree of life. Challenges remain in ensuring their effective use and integration into biodiversity data infrastructures. This session will showcase advancements in DNA reference databases, efforts to connect molecular and taxonomic species concepts, enhanced integration of molecular taxa into biodiversity data systems, and strategies for crediting reference data providers.

We invite contributions that address:

- Significant developments in DNA reference databases.
- Challenges and solutions in curating and standardizing DNA reference databases.
- Strategies for integrating and operationalizing reference databases in data platforms.
- Incentives for sharing up-to-date DNA reference data, including usage tracking and contributor recognition.

By connecting researchers, managers and curators of databases and datasets, and infrastructure developers, this session aims to drive improvements in the management and integration of DNA reference data in biodiversity data systems.

Session: **6798929****7018520**

21/10/25 | 11:20

Room: Tolima

LIGHTNING TALK VIRTUAL • EN

Towards building a national genetic reference library for species identification in support of biodiversity research and public policies in France

Presenter

Liliana Ballesteros-Mejia

Authors**Liliana Ballesteros-Mejia** (Direction de l'Expertise - DGD-REVE. Muséum national d'Histoire naturelle. • France)**Nirmala Seon-Massin** (Direction de l'Expertise - DGD-REVE. Muséum national d'Histoire naturelle. • France)**Aurélié Lacoëuilhe** (PatriNat (OFB, MNHN, CNRS, IRD), 75005 • France)**Olivier Gargominy** (PatriNat (OFB, MNHN, CNRS, IRD), 75005 • France)**Rodolphe Rougerie** (Institut de Systématique, Évolution, Biodiversité (ISYEB) - UMR 7205 Muséum national d'Histoire naturelle, CNRS, Sorbonne Univer • France)**Abstract**

Biological diversity is being strongly affected by the rapid environmental changes of the Anthropocene, and our ability to identify species presents a major challenge for monitoring the impacts of these changes and designing sound response policies. Molecular methods, - such as DNA barcoding, metabarcoding, and eDNA - offer promising solutions, however, their power depends on the completeness and reliability of DNA reference libraries.

As part of France's national biodiversity strategy for 2030, the National Museum of Natural History in Paris (MNHN) and the French Biodiversity Agency (OFB) are developing GenRef - a national referential of genetic sequences. This public and open-access tool will provide access to high-quality DNA sequences linked to reliable taxonomic identifications of eukaryotic species present in mainland France and its overseas territories.

GenRef will centralise, structure and validate genetic reference sequences and their associated metadata using semi-automated workflows and expert review. Closely integrated with the national nomenclatural and taxonomic registry (TaxRef), it will be interoperable with the major international databases housing the sequences such as GenBank, ENA, Unite, and BOLD, while also working closely with French research institutions and natural history collections to incorporate their data and expertise.

We present here a first prototype to demonstrate the general design of GenRef and the structure of its workflow, including: (i) automatic query of genomic databases via API, (ii) record quality scoring based on multiple criteria, (iii) record categorisation.

By addressing the critical need to improve accessibility to high-quality genetic/genomic data linked to verified reliable taxonomic identifications, GenRef will support national efforts in biodiversity monitoring, research, conservation and policy making.

Session: 6798929**7028498**

21/10/25 | 11:25

Room: Tolima

LIGHTNING TALK • EN

Who's Who? Identifying “species” for regional biodiversity

Presenter

Regina Wetzer

Authors

Regina Wetzer

Abstract

Traditionally, species descriptions have relied solely on morphology, providing the foundation for understanding marine diversity. And as critically important biodiversity surveys are undertaken, creating accurate regional species lists is important for gathering accurate baseline data of where organisms are at a specific point in time. But many original descriptions are inadequate, lacking detailed images, drawings, and identification keys, making even common species difficult to identify. Additionally, species names are often misapplied to specimens far from their type localities, despite many organisms having limited dispersal capabilities.

Molecular data can reveal cryptic diversity and refine species boundaries, but integrating it with morphology and the names we use is not always straightforward. Using intertidal idoteid isopods from the Northeastern Pacific and their mitochondrial COI and 16S sequences, we highlight key considerations for refining genetic databases and improving species lists. This effort enhances taxonomic accuracy and provides essential resources for improving biodiversity monitoring and our abilities to utilize environmental DNA and related techniques in our conservation efforts

Session: 6798929**7018712**

21/10/25 | 11:30

Room: Tolima

ORAL VIRTUAL • EN

Implementing FAIR Digital Objects for Molecular and Traditional Taxonomy Integration

Presenter

Sharif Islam

Authors

Sharif Islam (Naturalis Biodiversity Center • Netherlands)

Abstract

Molecular biodiversity data often exists as unclassified groupings (e.g., ASVs, OTUs, BINs) that pose integration challenges with traditional taxonomic systems. These data elements (often lacking formal Linnaean assignments) need to be interoperable and reusable across biodiversity infrastructures.

This talk proposes treating such data elements as FAIR Digital Objects (FDOs), enabling persistent linking, machine-actionable metadata, and cross-platform integration. Building on existing frameworks such as Taxonomic Data Objects (Upham & Poelen), the UNITE Taxon Hypothesis paradigm, and TDWG TCS version 2 discussions, this approach applies content-derived identifiers, versioned provenance metadata, and lightweight JSON-LD serialisation aligned with RO-Crate standards.

The method transforms provisional groupings into citable, modular objects while preserving their hypothetical nature. A preliminary JSON-LD implementation demonstrates how barcode clusters with multiple, conflicting species names can be expressed as self-contained, semantically rich digital objects. Relationship properties such as `interpretedAs` and `isIncludedIn` support mapping these groupings to multiple taxonomic viewpoints while maintaining their original structure and metadata.

This framework supports FAIR-compliant workflows, promotes recognition for reference data providers through explicit attribution metadata, and provides a framework to track, compare, and cite evolving species hypotheses. It is particularly valuable where classifications remain unresolved, under debate, or not yet integrated into reference databases and taxonomic backbones such as the Catalogue of Life.

By treating such early-stage data elements as first-class digital objects, this approach enhances integration between molecular and traditional taxonomic approaches while maintaining scientific rigor around provisional assignments.

Session: 6798929**7003826**

21/10/25 | 11:45

Room: Tolima

ORAL • EN

A BOLD view of DNA barcodes: vectors, trees, and context

Presenter

Roderic Page

Authors

Roderic Page (University of Glasgow • United Kingdom)

Abstract

The use of short, standardised sequences of DNA (“barcodes”) to identify biological specimens has had a major impact on our ability to characterise the biodiversity on the planet. The majority of DNA barcode data is hosted by BOLD (<https://boldsystems.org>). In this talk I present an alternative interface to DNA barcode data, one that emphasises interactive exploration of barcodes and their relationships. BOLD View (<https://bold-view-bf2dfe9b0db3.herokuapp.com>) takes a recent data package from BOLD and indexes the DNA using k -mer vectors. Using vectors enables fast searching for similar barcodes, which in turn enables the interactive display of phylogenetic trees for barcodes. This tree puts the barcodes into a broader context so users can see how they relates to other barcodes, and see whether clusters of barcodes (“BINs”) make phylogenetic sense. Additional visualisations include summaries of competing taxonomies for barcodes, and the edit history for a barcode. The BOLD database aggregates millions of DNA barcodes, but does not link to the original publications of these barcodes, thus losing the scientific context for these sequences. BOLD View attempts to restore this by including links to papers, enabling users to discover why the barcodes were collected and what was learnt from them. The talk will outline how the different visualisations used in BOLD View were constructed, as well as the technical challenges of processing BOLD data packages in their current form.

Session: 6798929**7011476**

21/10/25 | 12:00

Room: Tolima

ORAL • EN

UNITE: Managing and communicating eukaryotic biodiversity through DNA-based species hypotheses

Presenter

Kessy Abarenkov

Authors

Kessy Abarenkov (Natural History Museum, University of Tartu • Estonia)

R. Henrik Nilsson (Department of Biological and Environmental Sciences, University of Gothenburg • Sweden)

Kadri Põldmaa (Natural History Museum, University of Tartu • Estonia)

Vladimir Mikryukov (Institute of Ecology and Earth Sciences, University of Tartu • Estonia)

Urmas Kõljalg (Institute of Ecology and Earth Sciences, University of Tartu • Estonia)

Abstract

UNITE (<https://unite.ut.ee>) offers a web-based sequence management environment and analytical services for the molecular identification of fungi and other eukaryotes. It comprises over 3.8 million sequences derived from Sanger sequencing and metabarcoding, sourced either from International Nucleotide Sequence Databases Collaboration or contributed directly by UNITE users. These sequences, complemented by source metadata and trait information, are clustered into approximately 1.9 million species hypotheses (SHs) at six interspecific distance thresholds. Each SH is assigned a unique digital object identifier (DOI) to enable unambiguous referencing across studies. Each SH comprises a distinct dataset of DNA sequences and associated metadata, visualised on the UNITE website.

Out of the total 226,479 fungal SHs defined at a 1.0% gap (distance) between sister species, 31% have been assigned a formal species name, and 7% include sequences from type specimens. For comparison, the Catalogue of Life database contained 155,869 formally described and currently accepted fungal species names as of May 2025.

A distinctive feature of the UNITE SH system is its capacity to facilitate communication of both formally described and undescribed species, including those known only from environmental DNA (eDNA). UNITE supports the following activities:

1. Identification and communication of previously unidentified eDNA sequences across studies and datasets over time.
2. Contribution of representative sequences along with their source metadata for the creation of novel SHs.
3. Publication of eDNA datasets to the Global Biodiversity Information Facility (GBIF; as DNA-derived taxon occurrences linked to UNITE SHs within the GBIF taxonomic backbone.

Session: 6798929**7020329**

21/10/25 | 12:15

Room: Tolima

ORAL • EN

Integrating DNA Reference Data and Molecular Taxon Concepts in GBIF

Presenter

Tobias Frøslev

Authors

Tobias Frøslev (Global Biodiversity Information Facility • Denmark)

Thomas Stjernegaard (Global Biodiversity Information Facility • Denmark)

Dmitry Schigel (Global Biodiversity Information Facility • Denmark)

Tim Robertson (Global Biodiversity Information Facility • Denmark)

Abstract

Despite rapid advances in DNA-based biodiversity assessment, integrating sequence-based data into mainstream biodiversity infrastructures remains a global challenge. GBIF addresses this gap by improving integration and operationalization of environmental DNA (eDNA) data within its data platform. This work aims to create infrastructure that enables sequence-based search, dynamic taxonomic reinterpretation, and scalable integration of reference libraries – core components necessary for turning DNA data into usable biodiversity knowledge.

This initiative will prototype a DNA reference catalogue, where creators of DNA reference libraries can publish their products and make them available for users. The catalogue will also serve a taxonomic reinterpretation engine that utilizes steadily improving reference data to keep taxonomic inference standardized and updated across DNA-derived occurrences in GBIF. The aim is to support FAIR-compliant publication pipelines and reward data contributors through improved citation tracking and metrics.

By ensuring that taxonomic interpretations remain current and that database publishers receive clear credit and citation, GBIF strengthens the reliability and scientific value of DNA-derived biodiversity data, and facilitates improved biodiversity monitoring. The initiative underscores the importance of sustained recognition for the work of DNA reference data creators and curators. This talk invites collaboration to shape these tools and workflows, making molecular biodiversity data and reference databases more impactful and acknowledged components of the global biodiversity knowledge base.

Session: 6798929**7020914**

21/10/25 | 12:30

Room: Tolima

ORAL • EN

The eDNAqua-Plan proposal towards a future of federated, curated and reliable reference libraries

Presenter

Emilie Boulanger

Authors

Emilie Boulanger (OBIS • France)

Frédéric Rimet (INRAE • France)

Filipe Costa (University of Minho • Portugal)

Saara Suominen (OBIS • Belgium)

Ian Probert (Sorbonne University • France)

Peter Woollard (EMBL-EBI • United Kingdom)

Abstract

DNA barcode reference libraries are the critical backbone for identifying species from molecular sequence data. As environmental DNA (eDNA) and metabarcoding are increasingly adopted for biodiversity assessments, monitoring frameworks, and environmental decision-making, the accessibility and reliability of reference sequences become ever more important. This reliability depends on the availability of taxonomically curated reference sequences that are findable, accessible, and whose curation processes are transparent, verifiable, and updatable. Currently, reference libraries vary widely in their standards and implementation of curation and annotation procedures. Some focus on specific organism groups and employ rigorous curation workflows, while others are large-scale repositories aggregating sequences from diverse taxa and sources—often with inconsistent levels of quality and curation.

The eDNAqua-Plan project, funded by the EU Horizon programme, aims to harmonise the eDNA data landscape towards a federated system of FAIR and reliable reference libraries. Building on an assessment of the current status and landscape of DNA barcode reference libraries for aquatic organisms in Europe, the project sets out to propose a plan for the future system of federated libraries. A federation of reference libraries provides advantages over a single centralised repository, including sustainability, resilience and the ability to leverage the distributed expertise of existing reference libraries. These would need to adhere to shared standards for essential metadata, taxonomic curation procedures, and interoperable data exchange—paving the way for more consistent and trustworthy biodiversity data.

This presentation will outline the current recommendations developed by the eDNAqua-Plan consortium and invite feedback from the DNA (meta)barcoding community to support the development of robust and operational standards.

Session

6797423

Symposium

21/10/25 | 11:15

Room: Caldas

Forensic Applications in Biodiversity Research: EUDR case studies and beyond

Organizers

Christophe Van Neste
Pierre Bonnet

Description

With climate change and global biodiversity decline, lawmakers have been implementing legislation to curtail the negative impact of human actors on further decline. A few noteworthy pieces of legislation are the European Union Deforestation Regulation (EUDR) and the updated European Environmental Crime Directive (ECD) in 2024. To serve enforcement of these new legislation frameworks, forensic scientific services will be required (e.g. scientific methods used to investigate and analyze evidence). This session aims to explore the broader applications of forensic methods in biodiversity monitoring, with a focus on EUDR and ECD, but also inviting abstracts with a broader international context. We are particularly seeking contributions on uncertainty and bias characterizations of biodiversity studies. By highlighting diverse forensic techniques, this session will also encourage submissions on other topics including ecocide cases, integrating open data, and community participation in capacity building. The organizers, dr. ir. Christophe Van Neste and dr Pierre Bonnet, will facilitate a dynamic discussion on how forensic science contributes to policy-making and the documentation of biodiversity and deforestation. Join us to delve into the interdisciplinary approaches that drive forward our understanding of the natural world and foster a collaborative environment for knowledge exchange.

Session: 6797423**7018497**

21/10/25 | 11:15

Room: Caldas

ORAL • EN

The clock is ticking for registering biodiversity [meta]data for forensic applications

Presenter

Christophe Van Neste

Authors

Christophe Van Neste (Meise Botanic Garden • Belgium)

Quentin Groom (Meise Botanic Garden • Belgium)

Oldoni Damiano (INBO • Belgium)

Lissa Breugelmans (Meise Botanic Garden • Belgium)

Bollen Robrecht (Meise Botanic Garden • Belgium)

Piet Stoffelen (Meise Botanic Garden • Belgium)

Frederik Leliaert (Meise Botanic Garden • Belgium)

Filip Vandelook (Meise Botanic Garden • Belgium)

Steven Dessenin (Meise Botanic Garden • Belgium)

Victor Deklerck (World Forest ID • Belgium)

Abstract

The European Union Deforestation Regulation (EUDR) obliges companies placing Forest Risk Commodities (FRCs), such as timber, coffee, cocoa, and soy, on the EU market to conduct due diligence to ensure these products are not linked to deforestation or forest degradation. Member states are responsible for enforcing the regulation through checks, including scientific proofs, and penalties. In response, Meise Botanic Garden has established an atomic laboratory to analyze the elemental composition of FRCs, supporting the creation of global reference databases in collaboration with World Forest ID. The objective is to have it operate as a fully forensic laboratory. This presentation will share the insights of operationalising the lab: 1) establishing a set of Standard Operating Procedures (SOPs) tailored to specific FRCs, 2) building a software platform allowing for full traceability and auditing, 3) first results of a project on coffee trees growing in Yangambi, DR Congo. The platform uses Infrastructure as Code (automated provisioning of compute and data resources), based on a template for the B-Cubed European Horizon Europe project (<https://b-cubed.eu/>). This allows other laboratories or enforcement agencies to deploy their own instance of the platform. Even more, it would allow importing/exporting companies to set up their own system, if they want to level up on their due diligence, a key requirement for the EUDR. The open source platform, available at <https://github.com/AgentschapPlantentuinMeise/MeiseCSI>, logs all user actions and modifications to the data. Future work includes integrating with the World Forest ID evaluation platform and submitting regularly verified observations to the Global Biodiversity Information Facility (GBIF).

Session: **6797423****7020361**

21/10/25 | 11:30

Room: Caldas

ORAL VIRTUAL • EN

So beautiful yet highly poached: The European goldfinch (*Carduelis carduelis*) in the southern Levant.

Presenter

Gila Kahila BarGal

Authors

Gila Kahila BarGal (The Hebrew University • Israel)

Abstract

Bird trapping, trade, and destruction of the European goldfinch (*Carduelis carduelis*) natural habitats are driving the species to extinction. In Israel, the species is currently classified as “Near Threatened,” with these anthropogenic pressures intensifying significantly over the past two decades. In particular, illegal smuggling and hybridization with the domesticated common canary (*Serinus canaria*) have become growing concerns for both conservation and wildlife law enforcement. Our study aimed to assess the taxonomy and genetic variability of *C. carduelis* populations in Israel, tracing their origins to support forensic investigations and conservation efforts. A total of 150 specimens were analyzed, comprising both contemporary and historical (museum) samples of *C. carduelis*, *S. canaria*, and their hybrids (commonly referred to as “Banduc”). Each specimen was morphologically and genetically characterized to determine species identity and population origin. The genetic dataset included mitochondrial gene regions and nuclear short tandem repeats (STRs), providing a robust framework for identifying individuals, populations, and assessing genetic diversity. The obtained database was used to resolve forensic cases and determine the characteristics of the contemporary population in the southern Levant. The findings underscore the need to expand genetic reference databases to include populations across Europe, given the detection of individuals with genetic signatures inconsistent with native Levantine populations. This expansion is crucial for accurately tracing the origins of trafficked birds and evaluating the full extent of the illegal trade. Overall, the study demonstrates the value of integrating genetic tools into wildlife conservation and enforcement strategies.

Session: 6797423**7012767**

21/10/25 | 11:45

Room: Caldas

ORAL VIRTUAL • EN

A metric-agnostic framework for multispecies presence-absence thresholding

Presenter

Sébastien Gigot--Léandri

Authors

Sébastien Gigot--Léandri (France)

Pierre Bonet (AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD • France)

Joly Alexis (Inria • France)

Servajean Maximilien (LIRMM, Université de Montpellier • France)

Munoz François (Université Lyon 1 • France)

Mouillot David (MARBEC, Université de Montpellier • France)

Botella Christophe (Inria • France)

Abstract

Biodiversity is declining globally, and while protected areas remain a vital tool to mitigate this loss, their effectiveness is influenced by multiple underlying factors. Understanding the complex dynamics of biodiversity is therefore essential for both conservation assessment and regulatory planning. In this context, species distribution models (SDMs) have significantly improved our ability to characterize ecological niches and elucidate the relationships between biotic and abiotic factors.

Although modern SDMs can address complex multispecies prediction tasks using a wide range of covariates, many practical

ecological applications still require binary decisions, i.e. determining whether a species is present or absent at a given site. Such decisions are critical for estimating biodiversity ranges, predicting species assemblages, or mapping protected species. As a result, even with highly accurate models, binarizing outputs remains necessary, inevitably introducing uncertainty due to the loss of information inherent in this decision-making process.

To assess the similarity between two binary species sets, and thereby evaluate not only the model's output but also the decision quality, numerous evaluation metrics are available, each emphasizing different aspects of predictive performance. For example, some metrics may favor overestimating species ranges, while others adopt a more conservative approach relative to presence prediction. Identifying a general method that adapts effectively to any metric thus remains a challenging task.

The literature often circumvents this problem using data-driven approaches, which come at the cost of increased risk of overfitting, inherent biases, and significant computational burden, especially as the number of species increases.

We introduce a new framework that optimizes the binarization process by theoretically maximizing the expected score. Our method does not require additional calibration data, is agnostic to the choice of evaluation metric, and achieves equivalent or better results than state-of-the-art performance across three distinct case studies, demonstrating its robustness and practical relevance for ecological decision-making.

Session: 6797423**7019965**

21/10/25 | 11:55

Room: Caldas

ORAL • EN

A High-Resolution Biodiversity Mapping Platform for Environmental Forensics

Presenter

Rémi Palard

Authors

Rémi Palard (AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD • France)**Lukas Picek** (INRIA • France)**César Leblanc** (INRIA • France)**Benjamin Deneu** (Eidg. Forschungsanstalt WSL • Switzerland)**Pierre Bonnet** (AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD • France)**Maximilien Servajean** (LIRMM, AMIS, Université Paul-Valéry • France)**Thomas Paillot** (INRIA • France)**Mathias Chouet** (AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD • France)**Antoine Affouard** (INRIA • France)**Alexis Joly** (INRIA • France)

Abstract

The increasing frequency of environmental crimes, ranging from illegal deforestation to habitat destruction and biopiracy, requires new tools for evidence collection, monitoring, and legal enforcement. Biodiversity data, when appropriately spatialized and contextualized, can serve as crucial forensic evidence. In this context, the GeoPl@ntNet platform emerges as a novel solution for exploring, visualizing, and extracting plant biodiversity information at high spatial resolution.

GeoPl@ntNet is an open-source, web-based platform developed within European projects. It leverages data collected by scientists and citizen science observatories, which have generated millions of geotagged plant observations worldwide. These records are used to train advanced deep learning models that produce predictive, high-resolution distribution maps for thousands of plant species.

The platform enables users to explore species occurrences and biodiversity indices across spatial scales, from local sites to national coverage.

While primarily designed for ecological research and conservation planning, GeoPl@ntNet also presents significant potential for environmental forensic applications. Investigators can detect non-native species at specific locations or identify biodiversity anomalies linked to anthropogenic disturbance. These tools are valuable for verifying habitat destruction in protected areas, assessing compliance with conservation laws, or tracing the origin of plant material in cases of illegal trade.

The platform integrates several technical innovations, including spatially explicit species modeling, real-time filtering, and comparison layers with official biodiversity datasets. Its transparent architecture and reproducibility make it suitable for producing legally admissible evidence, especially when combined with standardized sampling protocols and remote sensing inputs.

GeoPl@ntNet is being developed in collaboration with actors involved in managing and protecting natural and human-made environments, as well as policy-makers, to adapt its features to operational needs. By supporting rapid, cost-effective, and legally robust biodiversity assessments, it bridges the gap between citizen science and environmental governance, and positions itself as a key enabler of forensic biodiversity intelligence.

Session: 6797423**7018658**

21/10/25 | 12:10

Room: Caldas

ORAL VIRTUAL • EN

Individual-Based Value Assessment of Biodiversity in Policy Implementation: A Best-Worst Scaling Survey on Gravity Criteria

Presenter

Sandra Rousseau

Authors

Axelle Francx (KU Leuven • Belgium)

Sandra Rousseau (KU Leuven • Belgium)

Abstract

Environmental legislation aimed at conserving biodiversity often lacks quantifiable tools to assess the severity of harm at the level of individual specimens and ecotopes. To fill this gap, we developed an interdisciplinary framework that integrates ecological, remediation, ethical, and social criteria.

We conducted a Best–Worst Scaling (BWS) survey of policymakers, experts and practitioners, asking them to rank potential gravity criteria for the assessment of biodiversity harm in permitting and sanctioning decisions. Grounded in random utility theory, BWS captures individual preferences by repeatedly asking respondents to identify the most and least preferred options among a small set of gravity criteria. The sample is collected via snowballing and includes experts with different disciplinary backgrounds, functions and European nationalities.

The results are based on the current sample of 116 participants since the data collection is not yet complete. The set of ecological criteria received the highest weight in the gravity assessment (approx. 50%), followed by remediation feasibility (25%) and the social (13%) and ethical (12%) criteria, when considering individual plants, plants and ecotopes. Specifically, for individual plants and animals, the gravity criteria with the highest impact on the scoring are the species extinction risks at the global, regional and local level, the total and relative impact on the local population, the ecological role of the species and its protected status in binding legal texts. For ecotopes, the most impactful criteria are the rarity, quality and connectivity of the habitat, habitat provision, total and relative size of the damaged area, and the protected status.

Based on these results, we can propose a weighted scoring system to guide permitting and sanctioning decisions, ensuring penalties and remediation measures proportionally reflect actual biodiversity harm. By offering clear, evidence-based criteria, the proposed framework enhances legal certainty, improves policy implementation, and fosters greater consensus in assessing biodiversity impacts.

Session: 6797423**7017424**

21/10/25 | 12:20

Room: Caldas

ORAL • EN

PlantCLEF 2025: advancing AI-based multi-Species plant identification in vegetation quadrats for supporting environmental law and biodiversity monitoring.

Presenter

Giulio Martellucci

Authors

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Bonnet Pierre (France)

Vinatier Fabrice (France)

Abstract

Developments in European environmental regulations, such as Directive (EU) 2024/1203 on environmental protection through criminal law and Regulation (EU) 2023/1115 on imported deforestation, require scalable methods for inventorying and monitoring plant communities.

The 2025 edition of the PlantCLEF challenge introduces a task addressing this need and is highly relevant to the forensic science of biodiversity: the automatic identification of all plant species in high-resolution images of vegetation quadrats – rectangular plots used in standardized ecological inventories. By framing the challenge as a multi-label classification problem, PlantCLEF 2025 pushes the frontier of AI-based biodiversity assessment to meet forensic needs.

Vegetation plot inventories are essential for monitoring ecosystems, assessing habitat quality, and tracking environmental stressors. In forensic contexts, they can provide evidence for cases of habitat degradation or support ecological restoration efforts. However, traditional field studies are time-consuming and require expert knowledge, making large-scale deployment challenging.

PlantCLEF 2025 overcomes these limitations by evaluating AI models trained on single plant images for their ability to identify multiple co-occurring species in complex quadrat scenes. The difficulty of this task – due in part to domain shift, occlusion and high species diversity – reflects the complexity of forensic scenarios, where samples may be incomplete or degraded, and accurate species-level identification is crucial for enforcing regulations.

The challenge offers a benchmark for AI approaches that can be used in forensic science, promoting robust and transparent solutions for digital evidence pipelines to support environmental law enforcement. Hosted on Kaggle and presented at the CVPR-FGVC workshop and CLEF conference, PlantCLEF encourages collaboration among biodiversity monitoring authorities, forensic botanists, and computer scientists.

The results will be shared to foster dialogue and explore this challenge as a testbed for innovation at the intersection of AI, ecology, and environmental law enforcement.

Session: 6797423**7014491**

21/10/25 | 12:30

Room: Caldas

ORAL • EN

Challenges in using AI-based citizen-generated plant observations as forensic evidence in biodiversity investigations

Presenter

Pierre Bonnet

Authors

Pierre Bonnet (CIRAD • France)

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Mathias Chouet (CIRAD • France)

Jean-Christophe Lombardo (Inria • France)

Hugo Gresse (Inria • France)

Thomas Paillot (Inria • France)

Vanessa Hequet (IRD • France)

Hervé Goëau (CIRAD • France)

Alexis Joly (Inria • France)

Abstract

The development of citizen science platforms such as Pl@ntNet, iNaturalist or Flora Incognita, which facilitate the production of field observations by the general public, has enabled tens of millions of plant occurrences to be generated worldwide over the last 10 years. These observations, a large proportion of which are available through GBIF, can be used in a multitude of scientific, educational and even forensic contexts.

Because of the high volume and speed with which these observations are produced, the data may prove relevant for new uses, including providing useful evidence in investigations into crimes against the environment and biodiversity. The aim of this presentation is to present a number of potential and proven uses of these data and services in support of the authorities gathering evidence of interest during their investigations. The use of image-based services to help identify species supports, for example, the work of customs authorities at airports to detect species that are banned from trade, or entry (because of the environmental risks they may pose). The use of occurrences of species in protected areas where farming is prohibited, or involved in the production of drugs, may prove relevant in dating the conduct of illegal activities.

Various examples will be presented and discussed, with particular reference to the scientific, ethical and societal issues involved. The current state of thinking on the reliability of participatory services and data (biases, uncertainties, quality controls) and their evidential value in a legislative context will be shared. An important point will be the contribution of AI models and collaborative annotation protocols to the reliability of species identifications.

The overall aim of this presentation will be to encourage dialogue between researchers in data science, life science and human and social science, in order to identify the relevant directions for such developments.

Session

6799243

Symposium

21/10/25 | 11:15

Room: Valle

Global Infrastructure: Current state, sustainability, and paths forward through data partnerships

Organizers

Rebecca Snyder

Holly Little

Sharon Grant

Reem AlMealla

Nicholas Pyenson

Juan Sebastián Gonzalez Sanabria

Daniel Fernando Piraquive Piraquive

Javier Antonio Ballesteros Ricaurte

Description

The global biodiversity data infrastructure is a diffuse network of individually developed systems and platforms at critical points in their funding models, host organization support, and technological evolution. Many are undergoing transformation while developing new approaches to data integration and modeling. Understanding the current status and associated risks is crucial as we work toward the long-term sustainability of this shared global infrastructure through coordinated community action.

Addressing these challenges requires fostering peer-to-peer diplomacy that builds trust, shares knowledge, and strategizes common goals across geopolitical boundaries. By developing partnerships between institutions with complementary biodiversity datasets, we strengthen data institutions while accelerating scientific insights and policy impact. These collaborative efforts help overcome impediments to interoperability, dark data challenges, and discoverability limitations.

Open data and infrastructures are essential for transparency in governance and scientific policies while enabling cross-regional cooperation on biodiversity monitoring and conservation. This session will showcase ongoing initiatives that promote open biodiversity data availability, examine the current state of platforms and tools, and explore collaborative approaches to establishing joint infrastructures. Together, we will identify pathways toward sustainable global data systems that transcend institutional boundaries and help communities access the resources needed to address biodiversity challenges in their regions.

Session: 6799243**7020681**

21/10/25 | 11:20

Room: Valle

ORAL • EN

Mapping the Future: Examining 25 Years of U.S. Engagement in GBIF

Presenter

Stephen Formel

Authors

Stephen Formel (Formel Data Services • United States)

JJ Dearborn (Smithsonian Institution | Biodiversity Heritage Library • United States)

Sharon Grant (Field Museum of Natural History • United States)

David Bloom (TDWG | VertNet • United States)

Carole Sinou (Canadensys, Université de Montréal • Canada)

Katie Pearson (United States)

Martin Kalfatovic (International Image Interoperability Framework Consortium • United States)

Kent McFarland (Vermont Center for Ecostudies-Vermont Atlas of Life • United States)

Teresa J. Mayfield-Meyer (United States)

Abstract

In 1999, the OECD Megascience Forum called for a global, interoperable biodiversity data infrastructure—leading to the formation of the Global Biodiversity Information Facility (GBIF) in 2001. As GBIF approaches its 25th anniversary, this milestone invites reflection on progress toward that vision and the evolving role of the United States as a founding participant. The original OECD blueprint laid out seven work plan components which include:

- Interoperability, standards and linking of distributed data systems;
- An electronic catalogue of names of known organisms;
- Digitization of natural history collections;
- A “Species Bank” to integrate species-level knowledge;
- Digital biodiversity literature resources;
- Training and capacity building; and
- Public and institutional outreach.

To assess U.S. contributions across these dimensions, we are conducting a national survey of biodiversity data infrastructures. The survey inventories technical platforms, identifies persistent gaps, and examines the risks that political and economic dynamics pose to funding and infrastructure strategies.

Our hypothesis is that many GBIF-US participants depend on a small number of technical staff, many of whom are not connected to GBIF directly and perform underrecognized and often uncompensated roles in enabling global biodiversity data exchange. While this may seem intuitively true, empirical evidence is lacking. We seek to understand what organizations and mechanisms are responsible for success, where the community and model are fragile, and how progress might be constrained by the current GBIF voting structure.

The findings will inform strategic coordination and potential recommendations to enhance GBIF’s governance and funding model, with the goal of strengthening data mobilization across the region. They will also highlight the need for renewed U.S. engagement and leadership to address emerging biodiversity data priorities, such as AI-assisted validation and Indigenous data governance. The presentation will explore how today’s imperatives might shape the next 25 years.

Session: **6799243****7010550**

21/10/25 | 11:30

Room: Valle

ORAL • EN

A New Future for the Biodiversity Heritage Library: from institutional reliance to global resilience

Presenter

Nicole Kearney

Authors

Nicole Kearney (Biodiversity Heritage Library • Australia)

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Colleen Funkhouser (Smithsonian Institution. Biodiversity Heritage Library (BHL) • United States)

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JJ Dearborn (Biodiversity Heritage Library (BHL) • United States)

Joseph deVeer (Ernst Mayr Library, Harvard University • United States)

Elisa Herrmann (Museum für Naturkunde • Germany)

David Iggulden (Royal Botanic Gardens Kew • United Kingdom)

Abstract

In April 2025, the Biodiversity Heritage Library (BHL) released a public statement titled *A New Future for the Biodiversity Heritage Library*, announcing that the Smithsonian Institution, BHL's administrative host since 2006, will cease to host BHL on January 1, 2026. This decision, delivered to the BHL community only weeks prior, places one of the world's largest and longest-running open biodiversity data infrastructures at a critical inflection point.

BHL is a global consortium of libraries, museums, and herbaria, working collaboratively to digitize and openly share biodiversity literature. It provides over 63 million freely accessible pages spanning more than 500 years, connecting taxonomic data, historical context, and linked research infrastructures. The sudden withdrawal of institutional hosting not only disrupts this deeply networked digital platform, but highlights the precarity of even mature, community-led initiatives when reliant on a single institutional anchor.

This presentation will explore BHL's transition response, from the immediate operational challenges and rapid community mobilization, to its exploration of new administrative models, including fiscal sponsorship, distributed operational services, and in-kind institutional partnerships. It will highlight how BHL's global stewardship, shared governance, and deep culture of collaboration enabled the global consortium to secure key functions and begin envisioning a more resilient future.

As pressures on funding, policy, and host institution support grow worldwide, BHL's experience serves as a cautionary tale, emphasizing the need for distributed leadership, sustainable funding models, and cross-institutional collaboration across geopolitical boundaries. At the time of writing (May 2025), BHL's future is uncertain. Our hope is that by the Living Data Conference (October 2025), we can present a case study in how established data infrastructures can pivot toward more agile, collaborative, and robust systems, while continuing to deliver open, interoperable data for global biodiversity science. At the very least, we'll have news to share...

Session: 6799243**7014370**

21/10/25 | 11:40

Room: Valle

ORAL • EN

Power and Policy: Simulating GBiOS and the impacts of data sharing and investment on global trend detection

Presenter

Andrew Gonzalez

Authors

Andrew Gonzalez (McGill University • Canada)

Abstract

Global efforts to halt biodiversity loss via the Kunming–Montreal Global Biodiversity Framework, critically depend on our ability to accurately detect and understand biodiversity trends across scales. A Global Biodiversity Observing System (GBiOS) aims to

unite national monitoring efforts, but its effectiveness is influenced by various factors, including national monitoring capacity and data sharing infrastructure. This presentation introduces a simulation model designed to explore the statistical power of a GBiOS to detect regional biodiversity trends under varying conditions.

The simulation models many countries, each with changing biodiversity levels and national Biodiversity Observation Networks (BONs) of varying observation site densities. We incorporate realistic challenges like observation error and, crucially, disparities in national capacities to share data with a global data center. This allows us to quantify how incomplete data reporting impacts statistical power for trend detection – our ability to discern true regional and global changes.

Furthermore, the model investigates strategies to enhance GBiOS performance. We simulate scenarios where targeted investments are made to improve data infrastructure and sharing capabilities in countries with initially modest capacities. By comparing trend detection power under “Baseline” versus “Investment” scenarios, we assess the potential return on investment for strengthening global data pipelines.

Key parameters explored include the number of participating countries, the density of BON sites per country, observation error rates, the magnitude and consistency of true biodiversity change, and varying national data sharing probabilities. Results, highlight the interplay between these factors. This simulation provides a quantitative tool to inform strategic decisions for optimizing GBiOS design, prioritizing investments, and ultimately strengthening our collective ability to monitor and assess progress to biodiversity targets. The findings are particularly relevant for discussions on capacity building and international cooperation centered on building GBiOS.

Session: 6799243

7020125

21/10/25 | 11:50

Room: Valle

ORAL • EN

It Takes a Network: Building Biodiversity Knowledge Through Collaboration

Presenter
Sandra Emry

Authors
Sandra Emry (University of British Columbia • Canada)

Abstract
Biodiversity is declining at an alarming rate, and there is an urgent need to synthesize data across time and space to understand the scope and drivers of these changes. While technological advances have vastly expanded our access to environmental data, a full understanding of biodiversity trends also requires looking to the past. The Living Data Project brings together historical and contemporary data—including paper maps, digital reports, images, articles, and community science records—to build curated datasets that inform regional and national biodiversity assessments. Central to this work is collaboration. Addressing complex biodiversity questions requires diverse partnerships that span institutions, disciplines, and skill sets. This talk explores how collaborative pathways can improve data accessibility, interoperability, and the real-world application of biodiversity science. Using case studies from the Living Data Project, developed in partnership with government agencies and environmental NGOs, I will illustrate the workflow from rescuing legacy datasets to generating biodiversity estimates and delivering outputs ranging from academic publications to policy white papers and interactive web-based tools.

Session: 6799243**7020042**

21/10/25 | 12:00

Room: Valle

ORAL VIRTUAL • EN

Planning for community-driven enhancement of information ecosystems to facilitate the discovery and use of paleontological specimen data

Presenter

Erica Krimmel

Authors

Erica Krimmel (United States)

Talía Karim (University of Colorado Boulder • United States)

Holly Little (Smithsonian National Museum of Natural History • United States)

Lindsay Walker (University of Kansas • United States)

Alex Lawrence (Smithsonian National Museum of Natural History • United States)

Adam Mansur (Smithsonian National Museum of Natural History • United States)

Amanda Millhouse (Smithsonian National Museum of Natural History • United States)

Edward Gilbert (University of Kansas • United States)

Nico Franz (University of Kansas • United States)

Carl Simpson (University of Colorado Boulder • United States)

Abstract

Globally, the paleontology collections community has invested heavily in digitization of primary specimen data over the past decade, including over \$10 million funded through competitive awards in the United States alone. These data provide an important deep time complement to extant biodiversity data, but are disproportionately less discoverable. For the past two years, an Open Science Ecosystem project has explored why this is the case, and in this talk, we present our process and key findings. Using a community-based approach that centers the role of humans in open science cyberinfrastructure, we gathered feedback from a diffuse network of stakeholders and audiences—including everyone from researchers to developers. Feedback was then layered onto a high-level assessment of gaps in shared global data infrastructure, in order to make tailored recommendations for addressing them. Our recommendations are designed to be specific, actionable, and scalable as they lay the foundation for building out a network of FAIR (Findable, Accessible, Interoperable, Reusable), CARE (Collective benefit, Authority to control, Responsibility, Ethics), and research-ready data. The results also include resources to help improve data at its source and to provide a mechanism for increasing data mobilization from paleontology collections.

Critically, we present these recommendations as a result of coordinated community action, both through the project at hand and the longer-term perspective of the Paleo Data Working Group (<https://paleo-data.github.io>).

Session: 6799243**7018607**

21/10/25 | 12:10

Room: Valle

ORAL • EN

Strengthening Biodiversity Data Infrastructure with ObservIA: An AI-Assisted Modular Approach

Presenter

Simon Beauvillier

Authors

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Rodriguez-Cuicas Maria-Émilie (St Lawrence Global Observatory • Canada)

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Kutos Omnain (St Lawrence Global Observatory • Canada)

Couturier Mathilde (St Lawrence Global Observatory • Canada)

Abstract

The global biodiversity data infrastructure consists of numerous independently managed systems, presenting substantial challenges regarding interoperability, sustainability, and data discoverability. These issues must be effectively addressed to support biodiversity monitoring, research, and policy-making. Canada's ocean and biodiversity data landscape is built on a foundation of collaboration, interoperability, and open access. The Canadian Integrated Ocean Observing System (CIOOS) is a national initiative that unites regional and sectoral expertise to share high-quality ocean data through a user-friendly platform that adheres to international best practices.

Within this national framework, the St. Lawrence Global Observatory (SLGO)—the CIOOS Regional Association for the St. Lawrence River and Gulf—has developed ObservIA, a modular, automated, and AI-assisted data-ingestion pipeline that streamlines the integration, transformation, validation, and publication of biodiversity datasets. ObservIA weaves automated microservices with AI-driven assistance to standardize formats, populate metadata, and flag anomalies in near-real time. A rigorous, continuous feedback loop monitors performance

—while human experts review and approve each AI suggestion—to ensure accuracy and adaptability as data volumes grow and standards evolve. ObservIA tackles fragmentation, reduces manual effort, and cuts time-to-publication while producing outputs fully aligned with international standards. The resulting high-quality datasets flow seamlessly into SLGO, CIOOS, OBIS, and GBIF repositories, boosting global discoverability and reuse.

This session will demonstrate ObservIA in action—showing automated metadata creation, automated transformation, and rigorous validation—and outline how its open, microservice architecture fosters collaboration, transparency, and interoperability. Participants will see how the strategic use of automation and AI is strengthening global biodiversity data infrastructure, promoting sustainable data management, and enhancing cooperation. Ultimately, ObservIA supports global biodiversity conservation by empowering researchers, policymakers, and stakeholders through findable, accessible, interoperable, and reusable data resources.

Session **6960773-2**

Symposium

21/10/25 | 11:15

Room: Cauca

Computational Methods & Tools (Contributed Oral Presentations)

Organizers
David Fichtmueller

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-2**7021039**

21/10/25 | 11:15

Room: Cauca

ORAL • EN

galaxias: An R & Python toolset for sharing biodiversity data

Presenter

Peggy Newman
Erika Suárez

Authors

Peggy Newman (CSIRO • Australia)
Martin Westgate (CSIRO • Australia)
Amanda Buyan (CSIRO • Australia)
Dax Kellie (CSIRO • Australia)
Shandiya Balasubramaniam (CSIRO • Australia)

Abstract

GBIF is the largest biodiversity database in the world, and is widely used as a data source for biodiversity research. However, in our experience in the Atlas of Living Australia, researchers make up a comparatively small proportion of our data *providers*, despite this cohort's high ecological literacy and commitment to data quality. Partly this reflects a historical bias towards larger institutions, but it is also the result of limited knowledge and tooling to convert existing datasets to Darwin Core in a software environment known to these communities. Here we present 'galaxias', a suite of software tools written in both R and Python, to ease the

process of describing, packaging and sharing biodiversity data with GBIF and its partner nodes. Our goal is to support greater volume and quality of submissions from researchers, while also growing collaboration with the research community on open science goals and improved data quality.

Session: 6960773-2**7015755**

21/10/25 | 11:25

Room: Cauca

ORAL • EN

Repeatable workflow for visualizing Global Biodiversity Information Facility species occurrences by IUCN threat status on interactive dashboards

Presenter

Ellie Linden

Authors

David Bucklin (NatureServe • United States)

Ellie Linden (Colorado Natural Heritage Program • United States)

Vinamra Mathur (Colorado Natural Heritage Program • United States)

Abstract

Increased threatened global biodiversity has generated a demand for visualizing data in an accessible manner to inform decisions related to Global Biodiversity Framework. Projects through the Biodiversity Indicators Program housed within the Colorado Natural Heritage Program at Colorado State University focus on developing dashboards that include data and indicators related to the Global Biodiversity Framework for nations and regions around the world. These dashboards are handed off to local partners for long-term management who have deep knowledge of the region and varying levels of technical capacity for data management. While decision-making is often required at the national and regional levels, robust data is not always available at those scales, thus the reliance on global datasets. Developing repeatable workflows utilizing global data can avoid “reinventing the wheel” and ensure robust processing methods can be easily applied regardless of analytical expertise.

The Biodiversity Indicators Program collaborated with NatureServe to develop an ArcGIS toolbox that robustly processes Global Environment Information Facility species occurrences and IUCN threat status data. This toolbox was incorporated into a workflow that color-codes species occurrence points by IUCN threat status to visualize as intuitive spatial layers on interactive dashboards. The workflow ensures local dashboard managers can easily process and visualize the data in a defensible manner regardless background and knowledge of “big data,” thereby increasing inclusivity. The dashboard functionality allows the user to easily explore the layers (e.g. running filters and calculating statistics), thereby proving the ability to apply fine-scale data to on-the-ground decision-making, often addressing Global Biodiversity Framework targets (e.g. protected area expansion). Continual development and evolution of repeatable workflows are crucial for expanding who can process datasets as well as who can access, explore, and apply data to decision-making.

Session: 6960773-2**7020882**

21/10/25 | 11:35

Room: Cauca

ORAL • EN

The pdindicatoR package: Spatial Phylogenetic Diversity Indicators from GBIF Datacubes

Presenter

Lissa Breugelmans

Authors

Lissa Breugelmans (Meise Botanic Garden • Belgium)

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Niels Billiet (Meise Botanic Garden • Belgium)

Maarten Trekels (Meise Botanic Garden • Belgium)

Steven B. Janssens (Meise Botanic Garden • Belgium)

Quentin Groom (Meise Botanic Garden • Belgium)

Ward Langeroot (INBO • Belgium)

Joe Miller (GBIF • Denmark)

Abstract

To achieve the GBF's ambitious 2030 targets, we need reliable spatial biodiversity indicators derived from repeatable workflows using the most current biodiversity data. The EU-funded B3 project addresses this need by leveraging the concept of 'data cubes' to improve access and aggregate the extensive species occurrence data available through the Global Biodiversity Information Facility (GBIF). These datacubes provide a structured, standardized input for modeling and indicator workflows.

An important indicator in this regard is phylogenetic diversity (PD), which accounts not only for the number of species but also for their evolutionary distinctiveness. Conserving PD helps preserving evolutionary traits across the tree of life, and will safeguard the 'option value' of biodiversity for humanity. Recognizing this, the GBF includes a PD indicator as a complementary measure under Goal A (halting extinction by 2050) and Goal B (ensuring sustainable use of biodiversity and maintaining nature's contributions to people).

Within the B3 project, a workflow was developed which combines a user-provided phylogenetic tree and a GBIF occurrence datacube to produce maps of phylogenetic diversity for any chosen taxonomic group. The functions related to this workflow are bundled in the R package pdindicatoR. The workflow output highlights biodiversity hotspots and quantifies how much PD is currently safeguarded within existing protected areas. This information can guide conservation planning by identifying priority regions for protection.

To demonstrate the utility of our workflow, we applied it to flowering plants in Belgium. Using a comprehensive angiosperm phylogeny and GBIF occurrence data, we generated spatial maps of phylogenetic diversity and overlaid them with current protected area boundaries. In addition, national red list data were used to assign extinction probabilities for all species and to calculate the 'Expected loss of PD' indicator. This case study illustrates how our tool can inform data-driven conservation strategies and support GBF implementation.

Session: 6960773-2**7021038**

21/10/25 | 11:45

Room: Cauca

ORAL • EN

Cubification of Biodiversity Data: FAIRiCUBE and the European Habitat Classification System

Presenter

Susanna Ioni

Authors

Susanna Ioni (Natural History Museum Vienna • Austria)

Heimo Rainer (Natural History Museum Vienna • Austria)

Abstract

Terrestrial Habitats are commonly characterized by dominant plant species or a combination of those. We investigated the European Habitat Classification System from EUNIS <https://eunis.eea.europa.eu/habitats.jsp> by analyzing the actual and potential geographical distribution of its indicator species. For this purpose we evaluated combined species occurrences, and vegetation analyses, i.e. plot and transect data, in combination with topographic and climatic data. The “EUNIS Habitat S22 Alpine and subalpine ericoid heath” was taken as an example and indicator species for this specific habitat were verified for their value of being representative examples for the given habitat type.

In the analysis we had to distinguish between preserved specimens (collection data) and human observations ([observation.org](https://www.observation.org); [inaturalist.org](https://www.inaturalist.org); [naturgucker.de](https://www.naturgucker.de)). Taxonomic scrutiny and geographic uncertainty values for georeferenced records were essential quality criteria as well.

The concepts of “pseudo-absences” and “gap filling procedures” were deployed prior to computation for potential species distributions applying “Random Forest Models”.

Results have shown that the concept of indicator species for a specific habitat type can be challenged on the basis of prevailing preferences of plants for (micro)climatic conditions and topographic situations as well as influences by sympatric neighboring species.

It is emphasized that properly selected machine learning methods on the basis of a carefully defined basis of plant occurrence data are providing more precise insight into the actual composition of terrestrial plant communities.

Session: 6960773-2

7005445

21/10/25 | 11:55

Room: Cauca

ORAL • EN

ukbioprepr: An R package to support reproducible preparation of environmental data for biodiversity modelling in the UK

Presenter

Charlotte Rose Rush

Authors

Charlotte Rose Rush (University of Essex • United Kingdom)

Martin Wilkes (University of Essex • United Kingdom)

Abstract

Biodiversity modelling is essential for measuring and predicting ecological responses to environmental change and assessing progress towards targets prescribed by the Global Biodiversity Framework. The United Kingdom benefits from rich biodiversity time-series data and various open-source environmental datasets. However, integrating these into modelling workflows remains challenging – especially for researchers and professionals without considerable data processing expertise. Fragmented sources, spatial and temporal discrepancies and undocumented or unreproducible processing methods often create barriers and hinder coordination.

We present **ukbioprepr**, a user-friendly R package developed to address key environmental data preparation challenges in UK biodiversity modelling. It provides functions for downloading, harmonising and extracting site-level environmental variables from open-source datasets on climate, land cover and soil properties. Original data products are processed to align spatially and temporally with UK biodiversity data, allowing consistent covariate generation for time-series modelling from 2000 onward. Substantial data engineering – including reprojection, temporal interpolation and spatial alignment – supports model-ready outputs, whilst limitations (e.g. sparse soil data in urban areas) are transparently documented.

ukbioprepr supports both point-based and grid-based survey data and includes methods for aggregating climate variables over biologically relevant time periods (e.g. seasons, custom annual windows). These features enable integration across spatial and temporal scales and support diverse biodiversity modelling approaches. We demonstrate its application in a case study modelling occupancy of the native UK wildflower *Hyacinthoides non-scripta*, using derived environmental predictors. The case study further illustrates how these data products can inform ecological predictions under future climate scenarios, showcasing **ukbioprepr**'s potential to support both current assessments and scenario-based forecasting.

By lowering technical barriers and enabling consistent environmental data integration, **ukbioprepr** supports scalable, reproducible biodiversity modelling in the UK. The package exemplifies how targeted frameworks can streamline modelling workflows and improve coordination across biodiversity research and policy – principles that can be applied globally.

Session: 6960773-2**7007075**

21/10/25 | 12:05

Room: Cauca

ORAL • EN

Introducing b3gbi: An accessible and powerful R package for calculating biodiversity indicators from standardized data cubes

Presenter

Shawn Dove

Authors

Shawn Dove (Justus Liebig University of Giessen • Germany)

Abstract

The current biodiversity crisis requires rapid, reliable, and repeatable biodiversity monitoring data for decision making. The B-Cubed (Biodiversity Building Blocks for Policy) project aims to improve the integration and accessibility of biodiversity data through standardization, automated workflows, and software tools. As part of this effort, biodiversity data cubes – a standardized data format developed within the B-Cubed framework and available from GBIF – provide a powerful resource.

The b3gbi R package, an output of the B-Cubed project, uses these biodiversity data cubes to calculate biodiversity indicators across time and space. It's designed for ease of use: a publicly hosted graphical user interface is available for those not comfortable with coding, while R functions offer more powerful features for those who are.

Users can analyse biodiversity data spatially or temporally using many common biodiversity indicators and variables (e.g., species richness, evenness, rarity, occupancy turnover), calculate uncertainty, and create publication-quality figures. The b3gbi package streamlines the entire process from importing the data cube to generating figures. Core functions run with sensible defaults, often requiring no parameters to be specified unless users want to customize their analysis.

b3gbi is open source and designed in a modular way to support ongoing development and community contributions. For instance, a new indicator can be added by coding the necessary functions and registering it within the package, without needing to modify core package code. It is also part of the B-Cubed R universe and is interoperable with other tools in this ecosystem.

While the b3gbi package focuses on applying established indicators, its key contribution is breaking new ground in making biodiversity data cube analysis accessible to all user types – from scientists and policymakers to private users – thus helping to turn complex data into understandable results.

Session: 6960773-2**7020036**

21/10/25 | 12:15

Room: Cauca

ORAL • EN

Galaxy-Ecology EBV operationalization pilot: Computational workflows with high FAIRness level can facilitate automatic report creation to support policies

Presenter

Yvan Le Bras

Authors

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Abstract

One of the main challenges in linking science and decision-making is turning heterogeneous data into clear, understandable, and useable products. For the past two years, the French BON has been running a pilot project in Antarctica to test how Essential Biodiversity Variables (EBVs) can be used as a tool for standardizing, automating, and visualizing biodiversity data.

EBVs help introduce a first level of harmonization, which makes it easier to design reproducible tools. In this context, a new Galaxy workflow has been developed. It includes a Boosted Regression Trees (BRT) model to automatically create eco-regions and display them in a way that non-specialists can understand. This process follows the “atomisation-generalisation” approach promoted by the Galaxy Ecology initiative (<https://doi.org/10.1093/gigascience/giae122>), which ensures the reproducibility and transferability of the processing steps.

Another concrete application of this method is now being used to automate the production of scientific reports for the CCAMLR on the state of Antarctic ecosystems. The system is based on a series of modular scripts developed using an innovative way of using “Jupyter” notebooks, integrated into Galaxy as interactive tools. This allows Python, R (or other) code to be run directly on the platform. Thanks to the “atomisation-generalisation” guidelines, visualizations and results can be adjusted dynamically according to the datasets and geographical areas, here using interactive Jupyter notebooks in batch mode and combined in a computational workflow.

The approach has two main goals: to improve the readability and comparability of these reports for decision-makers, and to make them easier to reuse in other governance contexts. By combining the use of EBVs, automation through Galaxy, and open scripts by Jupyter, this approach helps make biodiversity data more accessible, usable, and better integrated into decision-making at all levels.

Session

6798937-1

Symposium

21/10/25 | 14:00

Room: Ballroom A

Darwin Core Data Package: an updated model and format for exchanging biodiversity data (Part 1)

Organizers

Kate Ingenloff

John Wieczorek

Peter Desmet

Yi Ming Gan

Jörg Holetschek

Description

In this session we will present the Darwin Core Data Package (DwC-DP), a new model and format for sharing biodiversity data. DwC-DP is designed to overcome the limitations of Darwin Core Archives (such as the star schema) and introduces a semantic model for biodiversity data. This model consists of a number of related tables (e.g. Events, Occurrences, Agents, Assertions) that aim to capture the diversity of biodiversity data in a common model, while still feeling familiar to data publishers. As a format, DwC-DP builds upon the Data Package standard and expresses data as CSV files and technical information as a machine-readable metadata file (similar to Darwin Core Archives). DwC-DP is the result of an extended iterative approach supported by the Global Biodiversity Information Facility (GBIF) and based on a wide range of use cases. Some of these use cases (e.g. survey data, collection data, eDNA data) will be presented by early adopters as concrete showcases on how to use DwC-DP, while GBIF will present how it supports DwC-DP through their Integrated Publishing Toolkit (IPT) and infrastructure. Finally, we will explain the next steps for DwC-DP and how you can contribute or provide feedback.

Session: 6798937-1**7020785**

21/10/25 | 14:10

Room: Ballroom A

ORAL • EN

From Observations to Interactions: iNaturalist and the Expanding Landscape of Biodiversity Data Sharing with DwC-DP

Presenter

Carrie Seltzer

Authors

Carrie Seltzer (iNaturalist • United States)

John Wieczorek (Rauthiflor LLC • Argentina)

Abstract

iNaturalist now hosts over 250 million biodiversity occurrence records representing more than 500,000 unique taxa—making it one of the largest platforms for community-contributed biodiversity data. Since 2012, iNaturalist has used the Darwin Core Archive (DwC-A) format to share its research-grade observations with GBIF and other partners. While effective for basic occurrence sharing, DwC-A has not supported richer connections—especially organism interactions—found in the platform’s underlying data.

The Darwin Core Data Package (DwC-DP) offers a new opportunity. This flexible and extensible format allows iNaturalist to represent not just Occurrences and their associated Media (images, sounds), but also relationships between those Occurrences—OrganismInteractions

—such as predation, pollination, parasitism, and other vital ecological connections. This illustration uses community-generated Observation Fields that capture interactions even though these are not currently controlled fields in the core iNaturalist data model.

This presentation will highlight how iNaturalist’s data maps to DwC-DP, illustrating both continuity and advancement over DwC-A. While Occurrence remains a foundational element, DwC-DP brings structure to a richer ecosystem of data, enabling iNaturalist to capture and communicate ecological knowledge that was previously invisible in shared datasets.

Attendees will see a concrete comparison between the two Darwin Core formats through the lens of iNaturalist’s experience, showing how the transition enhances what can be shared without disrupting what already works. This case sets the stage for subsequent talks by establishing core concepts—Occurrences and Media—while introducing Interactions as an example of what DwC-DP newly enables. It demonstrates how the new standard supports both incremental improvements and novel capabilities for data providers and consumers alike.

Session: 6798937-1**7009288**

21/10/25 | 14:30

Room: Ballroom A

ORAL • EN

From Flat to Structured: Enhancing Natural History Collection Datasets in GBIF Using Darwin Core Data Packages

Presenter

Jörg Holetschek

Authors

Jörg Holetschek (Botanic Garden & Botanical Museum Berlin • Germany)**Röpert Dominik** (Botanic Garden & Botanical Museum Berlin • Germany)**Droege Gabi** (Botanic Garden & Botanical Museum Berlin • Germany)**Berendsohn Walter G.** (Botanic Garden & Botanical Museum Berlin • Germany)**Fichtmueller David** (Botanic Garden & Botanical Museum Berlin • Germany)**Paule Juraj** (Botanic Garden & Botanical Museum Berlin • Germany)**Escobari Vargas Andrea Belen** (Botanic Garden & Botanical Museum Berlin • Germany)**Güntsch Anton** (Botanic Garden & Botanical Museum Berlin • Germany)

Abstract

With a collection of currently about 4 million specimens, the Botanic Garden & Botanical Museum Berlin (BGBM) houses the largest herbarium in Germany. Complementary to this main collection, the seed bank, the DNA bank and the living collection in the botanical garden with more than 32,000 documented accessions are important components of the institution (BGBM Press 2022). The herbarium is partly digitized with high-resolution voucher images, sporadically accompanied by photographs of the respective living organism. Herbarium specimens and their images are published to the Global Biodiversity Information Facility (GBIF), digital records of tissues and DNA samples to the Global Genome Biodiversity Network (GGBN, Dröge et al. 2016), and extracted sequences to the International Nucleotide Sequence Database Collaboration (INSDC, Karsch-Mizrachi et al. 2025).

Until recently, GBIF was centered around the concept of occurrences using Darwin Core (Wieczorek et al. 2012) or ABCD (Access to Biological Collections Data, Holetschek et al. 2012). Although it was possible to publish material samples, their relation to the original specimen was lost. In order to overcome this limitation and to be able to model complex relationships between entities, GBIF has introduced Darwin Core Data Packages. They are based on Frictionless Data, a toolkit for transparent FAIR (findable, accessible, interoperable, reusable; Wilkinson et al. 2016) data sharing. Darwin Core Data Packages will enable publishing structured biodiversity data about organisms, observations, specimens, material samples, media objects, sequences, biotic interactions – and, above all, all their complex relationships.

We will discuss the results of a pilot study in which the diverse collection data of the BGBM were published to GBIF with this new approach. Darwin Core Data Packages allowed to include tissue and DNA samples and their lineage from specimens, the images of organisms before being collected, and DNA sequences – information previously not shared with GBIF.

Session: 6798937-1**7009182**

21/10/25 | 14:42

Room: Ballroom A

ORAL • EN

Modeling Complex Marine Survey Data Using the Darwin Core Data Package

Presenter

Yi-Ming Gan

Authors**Yi-Ming Gan** (Royal Belgian Institute of Natural Sciences • Belgium)**John Wieczorek** (Rauthiflor LLC under contract to GBIF • Argentina)**Cecilie Svenningsen** (Global Biodiversity Information Facility (GBIF) • Denmark)**Pablo Deschepper** (Royal Belgian Institute of Natural Sciences • Belgium)**Charlie Plasman** (Royal Belgian Institute of Natural Sciences • Belgium)**Anton P. Van de Putte** (Royal Belgian Institute of Natural Sciences • Belgium)**Tim Robertson** (Global Biodiversity Information Facility (GBIF) • Denmark)**Abstract**

The BROKE-West fish dataset originates from a pelagic survey conducted in the Southern Ocean during the 2006 BROKE-West voyage. Since its initial publication in 2008 as a flat Darwin Core Archive (DwCA) occurrence table, the dataset has undergone significant evolution. Although rich in associated data, the original version included only species occurrence records. In 2016, it was used to test the extended MeasurementOrFact (eMoF) extension developed by OBIS, which enabled the inclusion of environmental and biological measurements. In 2023, survey design and sampling context were incorporated through the Humboldt Extension.

Today, the dataset has been fully restructured using the proposed Darwin Core Data Package (DwC-DP), a model that overcomes the structural limitations of the DwCA star schema. DwC-DP enables the expression of previously unpublished ancillary information and allows for the clear linkage of survey design, sampling events, occurrences, materials, community-level measurements, individual measurements, environmental measurements, and material relationships (e.g., prey items derived from stomach samples). This transformation offers a test case for evaluating how DwC-DP addresses long-standing challenges in representing complex biodiversity survey data.

From the perspective of a GBIF and OBIS node, adopting this new model presents significant opportunities. DwC-DP offers a richer structure that represents the complexity of biodiversity data. However, these benefits come with challenges. DwC-DP is more complex to implement and contains more identifiers, requiring more effort in transforming and maintaining the data. This may require shifts in data modeling, tooling, and workflows. Addressing these issues through capacity building, guidance, and tooling will be important to realise DwC-DP's full potential.

Session: 6798937-1**7020632**

21/10/25 | 14:55

Room: Ballroom A

ORAL VIRTUAL • EN

From A To DP - DwC-DP Captures The Full Story Of A Citizen Science And DNA Metabarcoding Survey

Presenter

Cecilie Svenningsen

Authors

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Tim Robertson (Global Biodiversity Information Facility (GBIF) • Denmark)

Abstract

‘Insektmobilen’ was a nationwide Danish research initiative (2017–2020) that combined citizen science insect surveys with DNA metabarcoding, while also contributing to the entomological collections of the Natural History Museum of Denmark (Svenningsen & Tøttrup, 2024). The resulting dataset is currently published as a Darwin Core Archive (DwC-A) Occurrence core with extensions for extended Measurements or Facts, Multimedia, Event, and DNA-derived data.

However, the limitations inherent in the DwC-A’s star schema arrangement restrict the integration of multiple identification types (morphological and DNA-based) and prevent proper linkage between multimedia, DNA data, and their respective sampling events.

Re-publishing the dataset using the proposed Darwin Core Data Package (DwC-DP) framework overcomes these limitations. DwC-DP allows for multiple identification records per sample, connects multimedia and DNA data directly to events, supports detailed referencing of collection materials, and recognises the contributions of all agents, including citizen scientists. The dataset also leverages Humboldt Extension terms (TDWG Humboldt Extension Task Group, 2024) to describe surveys and sampling targets, capturing the methodological richness of the project.

While mapping to DwC-DP enables a more comprehensive and flexible representation of the data, it also introduces challenges, especially for nested sampling designs. Publishers must carefully choose the level of detail to include to ensure usability and clarity for data consumers. We will present our data mapping and share the lessons we learnt along the way.

References

Svenningsen C, P. Tøttrup A (2024). Insektmobilen - National citizen science and DNA metabarcoding survey of flying insects in June 2018 and 2019. Version 1.11. Natural History Museum of Denmark. Occurrence dataset <https://doi.org/10.15468/m48e3e> accessed via GBIF.org on 2025-05-15.

TDWG Humboldt Extension Task Group. 2024. Humboldt Extension Vocabulary List of Terms. Biodiversity Information Standards (TDWG).

Session: 6798937-1**7018835**

21/10/25 | 14:06

Room: Ballroom A

ORAL VIRTUAL • EN

Characterizing paleontological specimens for maximal alignment with global data practices

Presenter

Holly Little

Authors

Holly Little (Smithsonian Institution National Museum of Natural History • United States)**Alex Lawrence** (Smithsonian Institution National Museum of Natural History • United States)**Talia Karim** (University of Colorado Boulder • United States)**Erica Krimmel** (United States)**Lindsay Walker** (University of Kansas Biodiversity Institute (Symbiota Support Hub) • United States)

Abstract

Paleontological specimens can vary widely from the smallest single cell protist or pollen grain, to trays of molluscs or fossil samples from cores, slabs like preserved tree canopies or trackways, and, of course, to the largest dinosaurs. Each of these examples has inherent characteristics requiring careful consideration of how to best represent that specimen in a digital record affecting discoverability and fitness-for-use of the data. Previous work (Little 2018, Little et al. 2021) has shown that there are known challenges in mapping paleontological specimen data to existing data standards. While most biological and paleontological specimens share similar fundamental data (evidence of a taxon at a place and time collected by a person), the addition of geological context adds multidimensional complexity, and variations in the preservation of paleontological materials can impact data requirements for documenting what is present. Assessing the nuances of the data across heterogeneous paleontological specimens will help to make comprehensive recommendations for communicating their inherent complexity.

Through coordination with the paleontology collections community, we are conducting an assessment to characterize the various types of paleontological specimens in our collections to document the data requirements for clearly describing them and their associated information. Our aim is to ensure consistency and discoverability in what is represented in the data and to enable better alignment with existing or developing global data practices. This effort will result in a resource consisting of example records, use cases for testing new data formats, highlights of key data classes, and implementation guidelines for standards like Darwin Core. Importantly, these results can be used to evaluate new developments like the Darwin Core Data Package to ensure paleontological specimen data can be mobilized, discovered, and used interoperably. Here we share an overview of this process and initial results.

Little 2018, <https://doi.org/10.3897/biss.2.25437>Little et al. 2021, <https://doi.org/10.3897/biss.5.75646>

Session

6802864-1

Symposium

21/10/25 | 14:00

Room: Ballroom B1

Integrative tools, data platforms and applications to address freshwater biodiversity research (Part 1)

Organizers

Jaime Ricardo Garcia Marquez

Eren Turak

Thilina Surasinghe

Yusdiel Torres Cambas

Thomas Tomiczek

Vanessa Bremerich

Merret Buurman

Kristi Bego

Paula Torre Zaffaroni

Description

The degradation of freshwater ecosystems and the decline of their biodiversity has triggered efforts to compile, standardize and publicly share fragmented freshwater biological data, and freshwater-specific geospatial datasets. This involves the integration of cutting-edge earth observation products to map hydrographical networks at high spatial resolution and at large geographical scales, the development of new processing tools, models and workflows that account for the longitudinal connectivity in freshwater ecosystems while integrating geospatial and biological data and call for the adoption of FAIR (Findable-Accessible-Interoperable and Reusable) and CARE (Collective Benefit, Authority to Control, Responsibility, Ethics) standards, as well as STAC (Spatio Temporal Asset Catalogs) specification for geospatial information. This session invites contributions that explore integrative approaches for advancing the standardization of freshwater biodiversity databases, and developing hydrological and environmental datasets relevant to the protection and restoration of freshwater species and ecosystems. The thematic scope of the session also includes change detection and causal attribution, biodiversity forecasting, spatial prioritization and other modelling applications using both biological and geospatial information on pressures, drivers, ecosystem structure and function. We encourage studies focusing on data interoperability and/or integration of large-scale biological and environmental datasets in models and scenarios to support freshwater conservation and management.

Session: 6802864-1**7020269**

21/10/25 | 14:05

Room: Ballroom B1

ORAL • EN

Environment90m - globally standardized environmental variables for spatial freshwater biodiversity science at high resolution

Presenter

Jaime Ricardo Garcia Marquez

Authors

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Giuseppe Amatulli (Italy)

Sami Domisch (Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) • Germany)

Abstract

The current loss of freshwater habitats and biodiversity calls for an immediate mobilization and application of existing data and tools to develop sound strategies for their long-term conservation. However, one particular challenge for obtaining a baseline regarding the spatial distribution of freshwater habitats and biodiversity, species distribution modelling and conservation planning frameworks is the need for standardized high-resolution environmental information, which ideally can provide a characterization of freshwater habitats anywhere in the world. To address this challenge, we present the Environment90m dataset which provides a total of 106 variables for each of the 726 million sub-catchments of the Hydrography90m dataset, corresponding to single stream segments. Specifically, Environment90m includes 47 variables related to topography and hydrography, 19 climate variables for the observation period of 1981-2010, as well as projections for 2041-2070 and 2071-2100 under the Shared Socioeconomic Pathways (SSPs) 1.26, 3.70 and 5.85, and three global circulation models (UKESM, MPI and IPSL). Moreover, Environment90m includes 22 land cover categories, 16 soil variables and two variables related to nitrogen deposition. For land cover, we also provide the annual time-series data from 1992-2020. In addition, Environment90m includes information on aridity and modelled streamflow. Summary statistics (mean, min, max, range, sd) are provided for all continuous variables while for categorical data, the proportion of each category is calculated within each of the sub-catchments. The data is available at <https://hydrography.org/environment90m>. To facilitate data download and processing, we provide dedicated functions within the hydrographr R-package. For all underlying calculations, we used the open-source tools GDAL/OGR, GRASS-GIS and AWK, so that custom data can be easily generated using the hydrographr R-package. Environment90m, along with the tools, provides an array of opportunities for research and application in spatial freshwater biodiversity science, specifically biogeographical analyses and conservation in freshwater ecosystems.

Session: 6802864-1**7020606**

21/10/25 | 14:15

Room: Ballroom B1

ORAL • EN

The GeoFRESH platform for integrative freshwater geospatial data processing

Presenter

Vanessa Bremerich

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Sami Domisch (Leibniz Institute of Freshwater Ecology and Inland Fisheries, Department of Community and Ecosystem Ecology • Germany)

Abstract

Large-scale predictive modeling, including species distribution models (SDMs), is increasingly vital for understanding and forecasting freshwater biodiversity patterns under changing environmental conditions. However, the effective use of such models in freshwater ecology is often hindered by the challenges of managing and processing hydrologically relevant high-resolution geospatial data and accounting for the inherent longitudinal and lateral connectivity of freshwater ecosystems.

To address these challenges, we developed GeoFRESH (<https://geofresh.org>), an open-access, web-based platform that facilitates the preparation of freshwater-specific, analysis-ready geospatial data for any location worldwide. Based on the Hydrography90m high-resolution global stream network, GeoFRESH enables users to (i) upload and visualize point coordinates, (ii) assign each point to the closest stream segment, (iii) annotate points with a suite of 104 local and upstream-aggregated topographic, climatic, land-cover, and soil variables, (iv) get information for over 1.4 million lakes integrated in the stream network and their individual drainage basins, (v) generate summary plots, and (vi) export processed data for further use in modeling workflows.

Planned next steps are adding an online point-and-click catchment delineation tool, an interactive online map editor for easy ‘point- snapping’, and an application programming interface (API), along with a set of functions that allow accessing GeoFRESH from within the hydrographr R package for easy integration into efficient workflows. Further, we intend to include spatial information on barriers across Europe and offer interactive connectivity functionalities. The GeoFRESH platform enables researchers to integrate ecologically meaningful information into large-scale predictive modeling tools and analysis workflows for freshwater ecosystems.

Session: 6802864-1**7030338**

21/10/25 | 14:25

Room: Ballroom B1

ORAL • EN

Virtual Research Environments as a tool to enable reproducible research workflows

Presenter

Merret Buurman

Authors

Jaime García Márquez

Merret Buurman

Vanessa Bremerich

Markus Konkol Konkol

Afroditi Grigoropoulou

Sami Domisch

Abstract

Freshwater science is data-driven science. The data required for investigating questions related to freshwater biodiversity is heterogeneous and so are the tools that are used to analyse the data. The workflow to find, download, assemble and analyse required datasets can be quite a patchwork: Tedious to carry out, to document, to reproduce.

Various R packages have been developed to make biodiversity data access and analysis easier, e.g. *rgbif*, *hydrographr*, *specleanr*. However, a researcher still needs to install them (which can be cumbersome, especially on computers running Windows). Additional analysis tools may be written in other languages such as Python or Bash, or may require conflicting package versions, leading to errors when installing. This poses a barrier to people wanting to reproduce an analysis. In addition, considerable computing resources are needed for analyses spanning large river basins.

Virtual Research Environments (VREs) enable researchers to do their data-driven science online, overcoming these obstacles and thus contributing to more reproducible science. The AquaINFRA project (<https://www.aquainfra.eu>) is developing such a VRE featuring a growing number of freshwater-related functionality, such as upstream catchment delineation or connectivity analysis. All tools can be used without having to install them. Besides offering an API, which allows users to access the tools from R or any other scripting language (via HTTP), the tools are integrated into Galaxy, a research computing platform widely used in the bioinformatics community [1]. One feature of Galaxy is a workflow canvas that allows to chain tools together in a graphical way. Complex data processing chains can be displayed visually, and re-run with one click. These workflows can be easily shared with colleagues, and easily modified to use different parameters or a different

Session: 6802864-1**7020043**

21/10/25 | 14:40

Room: Ballroom B1

ORAL • EN

OneWater Data Platform: Towards FAIR water data ecosystem in France

Presenter

Yvan Le Bras

Authors

Eric Lecaude (BRGM • France)

Isabelle Braud (INRAE • France)

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Véronique Chaffard (IRD • France)

Sylvain Grellet (BRGM • France)

Abstract

In France, the national research and innovation program ‘OneWater – Eau Bien Commun’ (2022-2032) addresses a wide range of key scientific issues to help protect and manage water as a common good. Made up of several projects that will generate a large amount of highly heterogeneous data, ranging from sensor data to social science data, samples and model-based data.

To process, share and re-use heterogeneous datasets and ultimately generate new knowledge, the national ‘OneWater FAIR Water Data Platform’ ambition is to go beyond a simple data catalog by fostering a FAIR Water Data ecosystem based on international standards and implementing semantic web interoperability producing FAIR compliant data by DNA.

This communication will present the approach that is being implemented in the OneWater Data Platform project and its first results.

1/ The first overview of the water community needs, obstacles and practice. The resulting first action plan. And the first common use cases that will serve as examples to build the OneWater platform.

2/ The definition of how to reach high FAIRness level within the OneWater Data community by specifying how the FAIR principles of Wilkinson *et al.* 2016 are interpreted for Water data in the light of the existing international standards and best practices (OGC, W3C, INSPIRE, RDA). The produced FAIRness analysis templates for various numerical resources (data sets, protocols, software, catalogs, vocabularies, software codes) and their first application on datasets from the national French Water Information System.

3/ OneWater’s FAIR Data platform architecture definition around well-known and most recent interoperability standards, best practices and their open-source implementations. It also takes into account the latest FAIR Open Science prototyping exercises such as the use of platforms like Galaxy, the associated recommendations and the results of pilot projects such as the OGC Open Science Persistent Demonstrator.

Session: 6802864-1

7019915

21/10/25 | 14:55

Room: Ballroom B1

ORAL VIRTUAL • EN

Communicating interdisciplinary research to aid timely responses amid emerging environmental risk

Presenter

Paula Torre Zaffaroni

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Abstract

Environmental crises can open opportunities for interdisciplinary research, but urgency requires tools that translate scientific findings into actionable information. In August 2022, a massive fish kill took place in the Oder River, Germany, following an extensive bloom of *Prymnesium parvum*, a brackish-water alga. This event coincided with one of the region's driest and hottest summers on record. In response, an interdisciplinary, multi-institutional project was launched to investigate the bloom's causes, the river's ecological status, and its recovery dynamics. With heatwaves expected to increase in frequency and salt inputs to the river still unregulated, similar events may occur again. This makes it essential not only to understand the causes, but also to support risk assessment and early response.

A key challenge is to integrate and communicate results across spatial, temporal, and disciplinary scales, in a way that supports both scientific analyses and decision-making. Within the ODER-SO project, we leveraged Earth Observation to reconstruct chlorophyll dynamics and harmonize them with sparse in-situ monitoring. To do so, we processed the Sentinel-2 archive covering the Oder catchment using CR2CC (Cloudless Reference-Ready Sentinel-2 Composite) and structured the output into a datacube. Building from this, we developed a web-based, data visualization dashboard to bring together near real-time chlorophyll concentration dynamics and its long-term trends, environmental monitoring data from various sources (including temperature, discharge, and nutrients), and the applied results from project experiments (e.g., lab experiments on *Prymnesium* growth conditions).

The ODER-SO dashboard was designed with multiple user groups in mind including researchers in academia and in environmental offices, and decision-makers, to facilitate the translation of complex and heterogeneous data into an interpretable and timely format. This presentation illustrates an approach to strengthening the interface between science and decision-making in the context of fast-developing environmental crises.

Session: 6802864-1**7013882**

21/10/25 | 15:05

Room: Ballroom B1

ORAL • EN

The Danube Fish Database: documenting species distributions across a major European river basin

Presenter

Yusdiel Torres Cambas

Authors

Yusdiel Torres Cambas (Leibniz Institute of Freshwater Ecology and Inland Fisheries • Germany)

Abstract

The Danube River Basin (DRB) harbors the highest fish species richness among European rivers, yet native populations face growing threats from industrialization, hydrological alterations, invasive species, pollution, hydropower developments, and climate change. Spanning across 19 countries, the DRB presents conservation challenges that demand coordinated, transboundary data sharing. The present database compiles and standardizes fish occurrence datasets, which have previously been unavailable, fragmented, and often restricted by federal agencies, research institutes, and conservation organizations. Following the data collation, formatting, and quality control, we wrapped all the R-code we employed into a new `danubeoccurR` R-package, to facilitate and streamline the entire process for reproducibility and possible re-use in other regions and datasets. The collated dataset also integrates data from public sources and national monitoring programs. It contains 100,308 occurrence records across 113 fish species, representing 29 families and 17 orders, with a temporal range from 1856 to 2024. Each record in the database provides taxonomic details, geographic coordinates, the date of the observation, and a reference to the original data source. This database provides a vital resource for developing evidence-based management strategies in the DRB by supporting fish community conservation, invasive species monitoring, and climate impact assessments.

Session: 6802864-1**7020478**

21/10/25 | 15:15

Room: Ballroom B1

ORAL • EN

Open science approaches on assessing global aquatic insect biodiversity

Presenter

Afroditi Grigoropoulou

Authors

Afroditi Grigoropoulou (Leibniz Institute for freshwater ecology and inland fisheries • Germany)

Jaime Garcia Marquez (Germany)

Yusdiel Torres-Cambas (Germany)

Thomas Tomizcek (Germany)

Marlene Schuerz (Austria)

Vanessa Bremerich (Germany)

Sami Domisch (Leibniz Institute for freshwater ecology and inland fisheries • Germany)

Abstract

Freshwater ecosystems are highly biodiverse, and aquatic insects represent a major component of biodiversity while being widely used as water quality indicators. Despite their ecological relevance, global-scale assessments of aquatic insect distributions remain constrained by fragmented occurrence data and a lack of scalable hydrographic data processing tools. This work represents an integrative workflow that addresses these limitations by combining three components: (i) a standardised global database of aquatic insect occurrences, (ii) open-source geospatial tools for freshwater-specific environmental data processing, and (iii) a global-scale analysis of aquatic insect ecological niche breadth across biomes worldwide.

First, we developed the Global EPTO Database including over 50 datasets of genus-level georeferenced records for Ephemeroptera, Plecoptera, Trichoptera, and Odonata (EPTO), attributed with topographic predictors relevant to freshwater biodiversity modelling. The database enables global-scale mapping of taxonomic richness, highlighting biodiversity hotspots and knowledge gaps worldwide. Second, to support scalable geospatial processing, we developed the hydrographr R package that enables delineating upstream basins, calculating network-based distances, and aggregating high-resolution datasets (e.g. Hydrography90m, SoilGrids250m, ESA CCI Land Cover) within drainage basins. We have integrated the functionalities of the package into reproducible workflows under two case studies of: i) species distribution modelling and ii) connectivity assessment in a river fragmented by dams. Finally, using these data and tools, we analysed global patterns of ecological niche breadth for aquatic insects, showing that assemblage-level niche width does not consistently narrow towards the tropics, as often assumed, but instead might reflect macroevolutionary and dispersal processes.

This talk aims to showcase a valuable contribution to spatial freshwater biodiversity science, which includes the first comprehensive and standardised global dataset of aquatic insect occurrences, intuitive tools for complex hydrographic data processing, and novel insights into the spatial patterns of ecological niche breadth of aquatic insects at the global scale.

Session **6796330-1**

Symposium

21/10/25 | 14:00

Room: Ballroom B2

Improving data management strategies, sharing and FAIRness of DNA-derived Biodiversity Data (Part 1)

Organizers

Tobias Frøslev

Joana Pauperio

Saara Suominen

Miwa Takahashi

Vanessa Yepes Navarez

Erika Montoya Cadavid

Ricardo Ortiz Gallego

Description

Every lifeform in the world, from viruses to whales, contains a bio-molecular footprint that informs about their occurrence and biology. DNA based methods are transformative tools for biodiversity detection and monitoring. Environmental DNA (eDNA) metabarcoding in particular is expected to massively accelerate the field by enabling detection of entire biological communities from soil, water, and air samples. However, the detection of biodiversity from environmental samples (using eDNA) generates larger data sets unlike traditional methodologies in which each DNA sequence comes from an isolated individual.

Despite its potential, standardized sharing and integration of metabarcoding data and other DNA-associated biodiversity data has remained limited until now. Best practices for FAIR data sharing include submitting raw sequence data to INSDC (International Nucleotide Sequence Database Collaboration) short read archives (e.g. ENA, SRA) and sharing the processed and interpreted biodiversity records (e.g., Amplicon Sequence Variants, ASVs and Operational Taxonomic Units, OTUs) through biodiversity databases like those of the Global Biodiversity Information Facility (GBIF.org) and Ocean Biodiversity Information System (OBIS.org).

We invite contributions that address:

- New tools and pipelines for improved sharing of DNA-derived biodiversity data.
- Approaches for better integration of DNA-derived data with other biodiversity data.
- Remaining challenges and solutions for achieving FAIR DNA-derived biodiversity data.
- Non-technical aspects that infrastructures should consider, such as legal frameworks, domain specific data culture etc.

This session will include discussions on best practices and solutions to enhance the FAIRness of DNA-derived biodiversity data for biodiversity research, with a main focus on eDNA and metabarcoding data. We will seek to share the initiatives, strategies and experiences that have been proposed regarding the management and final disposal of this information as a useful tool for decision-making on environmental matters.

Session: 6796330-1**7020338**

21/10/25 | 14:00

Room: Ballroom B2**ORAL • EN**

One Year of Progress with the GBIF Metabarcoding Data Toolkit

Presenter

Tobias Frøslev

Authors

Tobias Frøslev (Global Biodiversity Information Facility • Denmark)

Thomas Stjernegaard (Global Biodiversity Information Facility • Denmark)

Dmitry Schigel (Global Biodiversity Information Facility • Denmark)

Tim Robertson (Global Biodiversity Information Facility • Denmark)

Abstract

DNA metabarcoding has transformed biodiversity monitoring by enabling the detection of comprehensive biological communities from environmental samples like soil, water, and air. However, the volume, complexity, and structure of these datasets present challenges for standardized sharing and integration into global biodiversity data infrastructures.

In response, GBIF launched a new programme in 2024 focused on improving the management, publication, and FAIRness of DNA-derived biodiversity data. At its core is the Metabarcoding Data Toolkit (MDT), a lightweight, open-source application that helps data holders format and publish metabarcoding datasets through GBIF using intuitive templates and visualizations. The MDT supports key data management tasks, including mapping to standardized vocabularies, incorporating non-Darwin Core fields, and preparing submission-ready archives.

Now one year into the pilot phase, this session will provide an update on the programme's development and implementation, share lessons learned from participating GBIF nodes, and outline the next steps toward broader adoption. A short demonstration of the MDT will showcase its current capabilities and planned improvements based on user feedback.

Session: 6796330-1**7020936**

21/10/25 | 14:15

Room: Ballroom B2

ORAL • EN

Towards FAIR eDNA: OBIS Australia's Efforts in Standardising and Publishing Marine eDNA Data

Presenter

Sachit Rajbhandari

Authors

Sachit Rajbhandari (NCMI, CSIRO • Australia)**Eric Raes** (The Minderoo Foundation • Australia)**Philipp Bayer** (The Minderoo Foundation • Australia)**Matthew C. Smith** (CSIRO • Australia)**Andrew Bissett** (Environment CSIRO, Australian Microbiom • Australia)**Bruce Deagle** (ANFC, CSIRO • Australia)**Jodie Van De Kamp** (Environment, CSIRO • Australia)**Pascal Craw** (Environment, CSIRO • Australia)**Miwa Takahashi** (Environomics Future Science Platform, CSIRO • Australia)**Katherine Tattersall** (NCMI, CSIRO • Australia)

Abstract

Environmental DNA (eDNA) is increasingly used for biodiversity monitoring, providing insights into species presence across ecosystems. As eDNA datasets grow, interoperability and accessibility are crucial. OBIS Australia (OBIS-AU), Australia's node of the UNESCO IODE Ocean Biodiversity Information System, hosted by CSIRO National Collections and Marine Infrastructure Research Unit, promotes use of the DNA Derived Data Extension in Darwin Core (DwC) to standardise publication of eDNA and metabarcoding data. OBIS-AU has published over 26 million eDNA records to the OBIS.

OBIS-AU is collaborating with the Minderoo Foundation, Australian Microbiome Initiative, CSIRO Marine National Facility Research Vessel Investigator (RVI), and the Australian National Fish Collection to advance marine eDNA data sharing through global biodiversity platforms. OBIS-AU is supporting data publication for CSIRO's new shipboard eDNA sampling capability through improved eDNA workflows and metadata integration. OBIS-AU is a member of the "Making eDNA FAIR" project, aiming to develop a FAIR eDNA metadata checklist integrating existing standards with new eDNA-specific terms.

Recording eDNA-derived species occurrences present several challenges. One example is taxonomic ambiguity, often caused by incompleteness in reference databases like GenBank, WoRMS, BOLD, or SILVA. Linking eDNA sequence reads to biodiversity occurrence records is complex and requires infrastructure integrating sequence data, metadata, and taxonomy. Technical barriers, limited engagement, and lack of incentives hinder open access to eDNA data. OBIS-AU is addressing these challenges by exploring tools like GBIF's MDT, OBIS's PacMAN pipeline, and AI-based tools to assist data publishers. OBIS-AU has published eDNA data using DwC Occurrence Core and DNA Derived Data Extension and is now testing a publication model with the DwC Event Core to better capture sampling context and improve integration, interoperability, and reuse of complex eDNA datasets. OBIS-AU intends to align with the new DwC Data Package to support modular publishing of marine biodiversity data.

Session: 6796330-1**7020421**

21/10/25 | 14:30

Room: Ballroom B2

ORAL • EN

The Swedish ASV portal for Molecular Biodiversity data: making eDNA data open and FAIR

Presenter

Rasa Bukontaite

Authors

Rasa Bukontaite (SWEDISH MUSEUM OF NATURAL HISTORY • Sweden)

Tobias Andermann (Biodiversity Data Lab Department of Organismal Biology Uppsala University Sweden • Sweden)

Maria Prager (Department of Biological and Environmental Sciences, Gothenburg University • Sweden)

Anders Andersson (KTH Royal Institute of Technology • Sweden)

Daniel Lundin (Department of Biology and Environmental Science, Linnaeus University • Sweden)

Abstract

Metabarcoding data derived from environmental DNA (eDNA) or specimen bulk-samples hold great promise for large-scale biodiversity monitoring programs. Many such metabarcoding datasets have already been generated in recent years, across terrestrial and aquatic systems. However, the accessibility and interoperability of these data are limited, if they are only available as raw sequencing files on long-term storage databases such as ENA. To make these data more FAIR—findable, accessible, interoperable, and reusable—we developed the Swedish ASV-portal, integrated into the Swedish Biodiversity Data Infrastructure (SBDI).

ASVs are the most granular unit of metabarcoding derived sequences, as they represent clusters of reads with 100% sequence identity. The ASV-portal allows searches based on sequence (BLAST) or taxonomy, marker gene and/or primer sequences. The occurrences of the matches can be displayed in the Living Atlas platform to which the ASV-portal is connected. We also provide the R-package ASVoccur that allows streamlined import of data from the ASV-portal directly into R and provides functionality for merging datasets and performing aggregation at different taxonomic levels. To ensure comparability between datasets, the portal applies standardized taxonomic annotation schemes using the nf-core/ampliseq pipeline, and the annotations are regularly updated as reference databases improve.

Integration with global biodiversity data platforms such as the Global Biodiversity Information Facility (GBIF) further extends the reach and impact of the ASV portal. This interoperability enables the linking of genetic data with other biodiversity observations, facilitating comprehensive ecosystem assessments and supporting evidence-based conservation efforts. The portal's user-friendly interface and support for standard data formats and protocols make it accessible to a broad range of users, from bioinformaticians and ecologists to policy-makers and conservationists. By enabling efficient data sharing and reuse, the Swedish ASV Portal plays a pivotal role in fostering transparency, reproducibility, and collaborative research to support global biodiversity science and conservation.

Session: 6796330-1**7018435**

21/10/25 | 14:45

Room: Ballroom B2

ORAL VIRTUAL • EN

A TDWG and GSC collaborative initiative to develop an environmental DNA (eDNA) metadata checklist

Presenter

Miwa Takahashi

Authors

Miwa Takahashi (Commonwealth Scientific and Industrial Organisation • Australia)**Joana Paupério** (European Molecular Biology Laboratory – European Bioinformatics Institute (EMBL-EBI) • United Kingdom)**Peter Woollard** (European Molecular Biology Laboratory – European Bioinformatics Institute (EMBL-EBI) • United Kingdom)**Tobias Frøslev** (Global Biodiversity Information Facility • Denmark)**Luke R. Thompson** (Mississippi State University • United States)**Katherine Silliman** (Mississippi State University • United States)**Stephen Formel** (Formel Data Services • United States)**Christopher Hunter** (GigaScience Press • Hong Kong)**Camila Babo** (CIBIO – Research Centre in Biodiversity and Genetic Resources • Portugal)**Kristy Deiner** (Switzerland)

Abstract

Environmental DNA (eDNA) derived data, particularly DNA sequences and species occurrence records, are powerful resources for a range of applications, including biodiversity monitoring, biosecurity, and agricultural bio-surveillance. An important part of eDNA data's value lies in its reusability, which can be enhanced through use of metadata that adheres to FAIR (Findable, Accessible, Interoperable, Reusable) data principles. While FAIR practices are gaining recognition within the eDNA community, adoption remains limited. A key barrier is that existing data standards, including Darwin Core (DwC) and the Minimum Information about any (x) Sequence (MlxS), lack sufficient terms to fully describe eDNA workflows, from sampling and processing to bioinformatic outputs. To address this challenge, we have initiated a collaborative eDNA Task Group supported by the Biodiversity Information Standards (TDWG) and Genomic Standards Consortium (GSC) organisations. We aim to build upon current standardisation efforts to develop a comprehensive and interoperable eDNA metadata checklist for formal integration into the MlxS and DwC frameworks. Our goal is to ensure compatibility with and seamless adoption by major biodiversity and sequence data infrastructures, such as Global Biodiversity Information Facility (GBIF), Ocean Biodiversity Information System (OBIS), and International Nucleotide Sequence Database Collaboration (INSDC). This talk will present progress of the TDWG/GSC joint eDNA initiative, including our collaborative efforts with related working groups and initiatives, such as eDNAqua-plan, the Darwin Core Data Package (DwC-DP), DNA-derived data extension to DwC, Minimum Information about any Ancient Sequence (MInAS), and the FAIR eDNA (FAIRe) initiatives. We invite contributions and collaboration to help shape a shared metadata framework that supports the growth, reuse, and long-term utility of eDNA data worldwide.

Session: 6796330-1**7020235****21/10/25 | 15:00****Room:** Ballroom B2**ORAL • EN**

A standards-based platform for eDNA metabarcoding data standardization and publishing

Presenter

Katherine Silliman

Authors

Katherine Silliman (Northern Gulf Institute, Mississippi State University • United States)**Luke Thompson** (Northern Gulf Institute, Mississippi State University • United States)**Bayden Willms** (Northern Gulf Institute, Mississippi State University • United States)**Carter Rollins** (Northern Gulf Institute, Mississippi State University • United States)**Miwa Takahashi** (Commonwealth Scientific and Industrial Research Organisation • Australia)**Stephen Formel** (Formel Data Services • United States)

Abstract

Metabarcoding of environmental DNA (“eDNA”) has emerged as a powerful technique for marine biodiversity and environmental monitoring, enabling detection of taxa ranging from microbes to plankton to large vertebrates. As the volume of eDNA data grows exponentially, robust systems for data publication, organization, and access are essential for facilitating reproducible research, enabling evidence-based natural resource planning, and ensuring the long-term preservation and utility of these valuable biodiversity records. The Ocean DNA Explorer represents a significant advancement in marine eDNA data management, providing an integrated solution for standardization, exploration, and dissemination of biodiversity data. This platform accepts eDNA data and metadata through standardized templates that implement the recently developed FAIR eDNA (FAIRe) metadata checklist, which consists of terms sourced from established data standards such as MIxS, Darwin Core (DwC), and the DNA-derived data extension to DwC. Researchers can generate project-specific templates for either Google Sheets or Excel. The platform’s PostgreSQL database is open-source, open-access, and accessible through APIs. It further facilitates data publishing to the international biodiversity repositories, OBIS and GBIF, through the edna2obis pipeline. Initially developed to support NOAA ‘Omics and NOAA Ocean Exploration users, the Ocean DNA Explorer continues to evolve through user feedback, driving ongoing improvements to its database structure, curation protocols, visualization capabilities, and training resources.

Session: 6796330-1**7022667**

21/10/25 | 15:15

Room: Ballroom B2**ORAL VIRTUAL • EN**

Improving interoperability towards FAIR eDNA by aligning data standards

Presenter

Camila Babo

Authors

Camila Babo (BIOPOLIS-CIBIO • Portugal)

Emilie Boulanger (Ocean Biodiversity Information Systems (OBIS) • France)

Peter Woollard (EMBL's European Bioinformatics Institute • United Kingdom)

Joana Veríssimo (BIOPOLIS-CIBIO • Portugal)

Saara Suominen (UNESCO - Intergovernmental Oceanographic Commission • France)

Veera Norros (Finnish Environment Institute • Finland)

Abstract

Environmental DNA (eDNA) is rapidly transforming biodiversity monitoring and research, with data being produced, shared and reused at increasing rates. However, metadata commonly used to describe eDNA workflows, from sampling to bioinformatic analysis, remains limited and inconsistently reported. Commonly used metadata frameworks, such as the Darwin Core (DwC) from the Biodiversity Information Standards (TDWG) and the Genomic Standards Consortium's Minimum Information about any (X) Sequence (MlxS) checklist, were not specifically designed for eDNA applications, resulting in fragmented metadata representation across platforms. This practice hinders interoperability and defies FAIR principles (Findability, Accessibility, Interoperability, and Reusability). To address this, we are developing alignment models within the EU Horizon-funded eDNAqua-Plan project to map and harmonise metadata standards across the aquatic biodiversity monitoring workflow. Although other standards exist, we focused our efforts on DwC and MlxS as these are the most widely adopted within the eDNA community. We aim to identify gaps, resolve overlaps, and improve the compatibility between standards by building upon previous efforts between DwC and MlxS core under the TDWG framework, focusing specifically on eDNA applications. These alignment models support better data integration by ensuring that field names across different metadata standards are clearly defined, matched, and, where needed, extended. This will facilitate a more seamless data exchange between projects and improve discoverability in biodiversity repositories, supporting data reusability and large-scale analysis across datasets. This talk will cover the current status of this work, including the alignment progress from the DNA-derived extension from DwC and the MlxS Core checklist. This effort is a collaboration with related initiatives such as the FAIR-eDNA (FAIRe) and highlights how these alignment efforts can serve as a foundation for improved community-driven standards. We invite feedback from the wider biodiversity and eDNA community to refine these models and collectively improve metadata consistency and FAIRness within eDNA research.

Session **6802919**

Symposium

21/10/25 | 14:00

Room: Tolima

Harmonizing In Situ and Earth Observation (EO) for Biodiversity Assessment

Organizers
Antonio Ferraz
Michael Harfoot
Maria Santos

Description

Understanding biodiversity dynamics requires the integration of in situ and Earth Observation (EO) data, yet this process presents significant challenges in data processing, harmonization, and matching across different sources. While in situ data provides critical insights into biodiversity characteristics, its spatial and temporal coverage remains limited. EO data, on the other hand, offers systematic, repeatable, and scalable measurements with high spatial and temporal continuity.

Integrating these complementary data sources is essential for comprehensive biodiversity assessments, but it requires advanced techniques to bridge existing gaps. Machine Learning and Artificial Intelligence approaches provide promising solutions by leveraging the unique properties of each data type, facilitating seamless integration, and enhancing predictive capabilities.

This session invites contributions that explore innovative strategies for data fusion, highlight methodological advances in AI-driven biodiversity assessments, and demonstrate the potential benefits of integrating multi-source environmental data. We welcome studies that address key challenges, propose novel frameworks, and showcase real-world applications of AI-enhanced biodiversity monitoring using EO time-series.

Session: 6802919**7020502**

21/10/25 | 14:05

Room: Tolima

ORAL • EN

OpenNature: integrating fragmented biodiversity data and products to improve biodiversity knowledge and make it accessible to all.

Presenter

Michael Harfoot

Authors

Michael Harfoot (Vizzuality & Dalhousie University • United Kingdom)**Francis Gassert** (Vizzuality • Spain)**Alison Johnston** (University of St Andrews • United Kingdom)**Scott Loarie** (iNaturalist • United States)**Oisín Mac Aodha** (University of Edinburgh • United Kingdom)**Brian Maitner** (University of Southern Florida • United States)**Carsten Meyer** (iDiv • Germany)**Craig Mills** (World Resources Institute • United Kingdom)**Laura Pollock** (McGill University • Canada)**Drew Purves** (Google Deepmind • United Kingdom)

Abstract

The state of nature continues to decline despite proliferating biodiversity metrics and increasingly stringent policies. At the same time, new technologies including citizen science, bioacoustics, camera traps, eDNA and earth observation are substantially expanding the amount of ecological data collected, whilst increasingly sophisticated processing algorithms are converting that data into knowledge. However, that data and knowledge is fragmented and in many cases not as accessible as it should be. For example, derived products such as indicators or basic information such as species range maps often have licenses with constraints (e.g. not for commercial use), or are not open at all. Derived data products are compiled and distributed by different organisations often in different formats and with different licenses. The difficulty in accessing, integrating and using this data and knowledge impedes decisions affecting biodiversity, made by businesses, local governments, park managers, conservationists, and communities. And the problem is exacerbated in regions with fewer resources and diverse languages, creating a significant barrier to effective biodiversity management.

OpenNature is a partnership of researchers, private organisations and NGOs, working to address these issues. Its ultimate aim is to produce better biodiversity knowledge and make it available to all and, in so doing, to empower society to make more informed, nature- positive decisions.

Here, we will introduce OpenNature and its initiatives. One such is OpenNatureAI, an attempt to develop an open, AI-powered system that integrates diverse biodiversity data—maps, reports, APIs, Earth Observation data etc—to train models that can make estimates of the distributions and status of otherwise data poor species and regions. We will discuss the challenges of integrating these data. Of equal importance to the modelling component, OpenNatureAI aims to synthesise multiple information streams into knowledge that is useful and accessible to diverse users, especially those under-served by the current landscape of tools.

Session: 6802919**7020655**

21/10/25 | 14:15

Room: Tolima

LIGHTNING TALK • EN

Spatiotemporal prediction of flowering using satellite indices: a multiscale approach to functional connectivity analysis in agricultural landscapes.

Presenter

Laura Perez

Authors

Laura Perez (Data Observatory • Chile)

Javier Lopatin (Universidad Adolfo Ibañez • Chile)

Dylan Craven (Universidad mayor • Chile)

Abstract

The global expansion of human activities has led to widespread landscape fragmentation, which compromises functional connectivity and threatens the provision of key ecosystem services, such as pollination. This study aims to predict spatial variations in floral density and native bee abundance across multiple spatial scales in agricultural landscapes. To achieve this goal, we are taking an integrated approach that combines field monitoring, remote sensing, phenological metrics, and connectivity modeling. This approach allows us to assess the impact of habitat loss on bee populations and their ability to provide pollination services. Using multispectral drones and Sentinel-2 satellite imagery, we map the spatiotemporal distribution of flowering, which serves as an indicator of high-quality pollinator habitats. We incorporate these data into circuit theory based connectivity models (Omniscape) to visualize ecological flows and identify critical conservation areas. Following FAIR principles, we will make our results publicly available through platforms such as the Data Observatory Chile and collaborative repositories. This will facilitate their integration into public policy and early warning systems. Additionally, we promote collaboration among scientists, beekeepers, and farmers by providing open-access digital tools that visualize floral resources and pollination potential. Ultimately, this research supports designing resilient, biodiverse agricultural landscapes through open science and cross-sector engagement. By identifying spatial mismatches between biodiversity and land use, we prioritize conservation actions in vulnerable areas. Furthermore, the project promotes inclusive territorial governance based on data transparency and participatory planning, which are critical components for climate adaptation, long-term food security, and biodiversity conservation.

Session: 6802919

7020417

21/10/25 | 14:20

Room: Tolima

LIGHTNING TALK VIRTUAL • EN

Predicción de estados funcionales de humedales altoandinos mediante datos locales, teledetección y aprendizaje automático

Presenter

Mailén Lallement

Authors

Mailén Lallement (ITAMA -CONICET • Argentina)

Paula Torre Zaffaroni (Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) • Germany)

Matías Braun (Research Group GREEN, University of Nebrija -Universidad Nebrija (UAN) • Spain)

Abstract

Los humedales altoandinos (*mallines*) son ecosistemas críticos del norte de la Patagonia argentina. Estos ambientes sostienen procesos hidrológicos clave y una alta biodiversidad, pero se encuentran cada vez más afectados por la expansión de forestaciones exóticas, la presión ganadera y la intensificación de la variabilidad climática. No obstante, la subrepresentación de estos ambientes en las bases de datos de biodiversidad regionales a globales ocasiona extrapolaciones erróneas sobre su estado ecológico. Presentamos un enfoque integrador que combina observación satelital, datos ecológicos de campo, información meteorológica y aprendizaje automático para predecir los estados funcionales de los *mallines*. El estudio se centra en la cuenca del río Chacabuco, donde procesamos imágenes Sentinel-2 para analizar la variación espectral intra e interanual, generando indicadores relacionados con la actividad de la vegetación, la presencia de agua superficial y la humedad del suelo. Asimilamos estos datos con bases de datos abiertas que incluyen niveles freáticos, composición vegetal, contenido de carbono y métricas de productividad. A partir de esta integración, entrenamos modelos supervisados de aprendizaje automático para identificar clases funcionales de humedales en función de sus dinámicas hidrológicas y de vegetación. Los análisis preliminares realizados en años con condiciones climáticas contrastantes revelaron respuestas divergentes entre *mallines*. La variabilidad en la humedad superficial y en la actividad vegetal sugiere efectos de amortiguación subterránea en sitios más resilientes, y señales de alerta temprana, como descensos abruptos en el verdor o anomalías de humedad, en los más sensibles. Este enfoque ofrece una herramienta concreta para anticipar transformaciones funcionales en humedales altoandinos, articulando datos satelitales, observaciones locales y ciencia de datos. Al visibilizar estos ecosistemas poco representados, se avanza hacia la construcción de bases de datos más representativas y de sistemas de conservación mejor fundamentados.

Session: 6802919**7020506**

21/10/25 | 14:25

Room: Tolima

LIGHTNING TALK • EN

A machine learning approach to species distribution modelling using remote sensing and citizen science data

Presenter

Mélisande Teng

Authors

Mélisande Teng (Mila, Université de Montréal • Canada)

Amna Elmustafa (Arizona State University • United States)

Benjamin Akera (Canada)

Hager Radi Abdelwahed (Mila • Canada)

Yoshua Bengio (Mila, Université de Montréal • Canada)

Hugo Larochelle (Mila • Canada)

David Rolnick (Canada)

Abstract

Biodiversity is declining at an unprecedented rate, impacting ecosystem services necessary to ensure food, water, and human health and well-being. Understanding the distribution of species and their habitats is crucial for conservation policy planning. However, traditional methods in ecology for species distribution models (SDMs) generally focus either on narrow sets of species or narrow geographical areas and there remain significant knowledge gaps about the distribution of species. A major reason for this is the limited availability of data traditionally used, due to the prohibitive amount of effort and expertise required for traditional field monitoring. The wide availability of remote sensing data and the growing adoption of citizen science tools to collect species observations data at low cost offer an opportunity for improving biodiversity monitoring and enabling the modelling of complex ecosystems. In this talk, we present our work developing machine learning methods for species distribution modelling using satellite images from Sentinel-2 and observation data from citizen science databases such as eBird and eButterfly. We discuss the possibilities and limitations of this work for scalably modelling properties of ecosystems worldwide.

Session: 6802919**7020038**

21/10/25 | 14:30

Room: Tolima

LIGHTNING TALK VIRTUAL • EN

Integrating eDNA and Remote Sensing for Scalable Soil Microbiome Biodiversity Assessment

Presenter

Andjin Siegenthaler

Authors**Andjin Siegenthaler** (Faculty of Geo-Information Science and Earth Observation, University of Twente • Netherlands)**Andrew K. Skidmore** (Faculty of Geo-Information Science and Earth Observation, University of Twente • Netherlands)**Haidi Abdullah** (Faculty of Geo-Information Science and Earth Observation, University of Twente • Netherlands)**Elnaz Neinavaz** (Faculty of Geo-Information Science and Earth Observation, University of Twente • Netherlands)**Abstract**

Understanding biodiversity dynamics at large spatial scales necessitates the integration of in situ and Earth Observation (EO) data. This study explores innovative methodologies that combine environmental DNA (eDNA) metabarcoding with remote sensing to assess forest microbiome biodiversity across diverse ecosystems and spatial scales.

By aligning eDNA data with hyperspectral imagery from AVIRIS-NG and DESIS platforms, we developed machine learning models to predict the spatial distribution of forest microbial communities. Gaussian Processes techniques were employed to model and map the diversity and distribution of forest microbial communities at fine spatial resolutions. These models explained significant variance in microbial diversity metrics, highlighting the potential of remote sensing to capture ecological patterns traditionally assessed through labor-intensive fieldwork.

Our approach addresses the challenges of harmonizing point-based in situ and EO data by demonstrating that remote sensing can serve as a proxy for habitat characteristics influencing microbial diversity. This integration facilitates scalable biodiversity assessments, enabling the monitoring of microbial diversity and ecosystem function across large and complex landscapes.

The findings underscore the promise of combining eDNA and remote sensing for comprehensive biodiversity monitoring. By leveraging the strengths of both data types, we can enhance predictive capabilities and gain deeper insights into the spatial dynamics of forest microbiomes, contributing to more informed conservation and land management strategies.

Session: 6802919**7020807**

21/10/25 | 14:35

Room: Tolima

LIGHTNING TALK • EN

Opportunities for monitoring aquatic fungi with earth observation data

Presenter

Eirik Aasmo Finne

Authors**Eirik Aasmo Finne** (The Norwegian College of Fishery Science, UiT The Arctic University of Norway • Norway)**Teppo Rämä** (Faculty of Biosciences, Fisheries and Economics, UiT The Arctic University of Norway • Norway)**Jennifer Anderson** (Swedish University of Agricultural Sciences, Department of Aquatic Sciences and Assessment • Sweden)**Abstract**

Aquatic fungi (AF) are key parts of lentic biodiversity, where their ecosystem functions include biodegradation of organic matter and pollutants, nutrient cycling, and acting as parasites on animals and plants. However, the biodiversity and ecological roles of AF have for a long time been underappreciated. AF are missing from all large-scale ecosystem monitoring initiatives, there are large knowledge gaps of AF ecology and taxonomy, and the public awareness of AF is limited at best.

Integration of eDNA metabarcoding data, in situ measurements of environmental variables, and earth observation (EO) products is essential to explain patterns of AF biodiversity dynamics and establishing monitoring of these organisms. We perform a feasibility study for the potential of EO-data to inform AF monitoring based on data from the Swedish monitoring network SITES. This network encompasses 6 lakes between latitudes 56° N and 68° N, and provides a time series from the last decade with 18S metabarcoding data and in situ measurements of physical and chemical water properties. This data is combined with key remote sensing variables from freely available satellite programs, including water surface temperature (thermal infrared sensor, Landsat 8), and turbidity and chlorophyll-a concentrations (Multispectral Imager, Sentinel-2). The combination of these three data sources enables validation of the EO-data, and opportunities for associating AF diversity and environmental change.

The results from this feasibility study will be included in downstream development of novel Essential Biodiversity Variables (EBVs) for AF and to form recommendations for the use of EO-derived variables to inform AF monitoring.

Session: 6802919**7008796**

21/10/25 | 14:40

Room: Tolima

LIGHTNING TALK • EN

FAIRification and AI-Readiness for Biodiversity Digital Twins

Presenter**Claus Weiland****Authors****Claus Weiland** (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**Daniel Bauer** (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**Desalegn Chala** (Natural History Museum • Norway)**Dag Endresen** (Natural History Museum • Norway)**Marcella Orwick-Rydmark** (Natural History Museum • Norway)**Gabriela Zuquim** (CSC – IT Center for Science • Finland)**Danaële Puechmaille** (EUMETSAT – European Organisation for the Exploitation of Meteorological Satellites • Germany)**Zakaria Kehel** (ICARDA – International Center for Agricultural Research in the Dry Areas • Morocco)**Jonas Grieb** (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**Abstract**

The European Green Deal addresses a wide array of critical topics regarding the interaction and exchange between society and ecosystems involving human-induced climate change, biodiversity loss, and deforestation. To support the development of appropriate and sustainable mitigation strategies, both political frameworks as well as large-scale scenario forecast and simulation infrastructures such as Destination Earth (DestinE) and the Green Deal Data Space (GDDS) are currently implemented. Setting-up the data spaces for DestinE and GDDS requires the consolidation and harmonization of vast amounts of data, among them data from long-term biodiversity monitoring (e.g. using eDNA), near real-time data captured by IoT devices (e.g. camera traps) and large-scale Earth observation data.

Key tools for integration and assessment of such data have been developed in the DestinE-linked Biodiversity Digital Twin project (BioDT). Biodiversity digital twins (DTs) provided digital replicas of particular phenomena of the biosphere. For FAIR-compliant reuse, repurposing and cross-platform portability, they are packaged using the RO-Crate specification: Resulting datasets as well as computational workflows are bundled as digital objects and annotated with rich machine-interpretable metadata using schema.org and its extensions Bioschemas and Croissant (high-level metadata supporting AI-Readiness).

We have developed a pilot study to migrate and functionally integrate BioDT's digital twin for crop wild relatives (DT CWR, doi:10.3897/rio.10.e125192) in DestinE's Data Lake (DEDL). Major objectives of the workflow.earth prototype is to enhance visibility and long-term availability of DT CWR, and to improve its prediction capabilities using DEDL's near data processing services and – in perspective

– the orchestrated interplay with other digital twins (e.g. Climate Change Adaptation DT).

In this presentation, we will demonstrate the deployment of agrobiodiversity workflows in DEDL with workflow.earth and the publication of model and results as web-based FAIR Digital Objects building on RO-Crate and FAIR Signposting.

Session

6799145-1

Symposium

21/10/25 | 14:00

Room: Caldas

Spatial biodiversity data products for reporting and decision-making - are we there yet? (Part 1)

Organizers

Tobias Andermann

Jakob Nyström

Description

Addressing the global biodiversity crisis requires spatial data products showing biodiversity metrics – current state, changes, and scenarios – that are interpretable and actionable for policy and decision-making. Examples of use cases include biodiversity monitoring, reporting in adherence with the GBF, prioritization of conservation projects, spatial planning for infrastructure projects, and corporate impact and risk reporting. Producing such maps requires predictive biodiversity models that can learn the complex relationships between biodiversity, environmental factors and anthropogenic pressures. In this session, we deep dive into the state-of-the-art of predictive biodiversity modeling on local, national, and global scales. We highlight and discuss which types of models are most appropriate for different objectives and contexts. Further, we examine best practices for evaluating predictive performance and quantifying uncertainty in such models. We critically discuss to what extent current data products are appropriate for making decisions with potentially substantial financial and ecological consequences. This session will be a hybrid of scientific talks, panel discussions, and audience engagement. The aim is to identify current limitations in spatial biodiversity modeling and to map a way forward to improving the state-of-the-art in this field.

Session: 6799145-1**7018626**

21/10/25 | 14:10

Room: Caldas

ORAL • EN

eBird Status and Trends: leveraging model ensembles to evaluate quality and uncertainty of predictions made from participatory science data

Presenter

Tom Auer

Authors

Tom Auer (Cornell Lab of Ornithology • United States)

Abstract

A global network of participatory scientists has contributed almost 2 billion observations to eBird over the past 23 years. While this is one of the largest biodiversity datasets in the world, extracting usable biological information from these data poses challenges, particularly related to spatial bias and changing observation processes. The eBird Status and Trends project uses state-of-the-art machine learning modeling to address these challenges and generate standardized, full-annual cycle, high spatiotemporal resolution predictions of relative abundance for almost 3000 bird species globally. While predictions from this type of modeling can provide the best available information on biodiversity and are valuable for policy and decision-making, many global maps of ecological variables are released without accompanying indicators of quality or spatial information on the limits of applicability, which are necessary for assessing reliability and utility. We will discuss how the eBird Status and Trends project uses ensemble-based methods and accompanying models of sampling coverage to: 1) identify limits of reliable predictions, 2) generate scale appropriate measures of predictive performance, and 3) quantify uncertainty. We will present examples of relative abundance predictions alongside performance, uncertainty, and limitation metrics. Additionally, we will explore practical application examples, highlighting the potential utility of this information to guide complementary sampling efforts, and briefly demonstrate how these data products can directly inform conservation prioritization, policy guidance, and other decision-making processes. Including these indicators of reliability helps advance the utility and trustworthiness of spatial biodiversity predictions, moving us closer to products that are actionable and ready for the demands of ecological decision-making.

Session: 6799145-1**7020884**

21/10/25 | 14:25

Room: Caldas

ORAL • EN

A Novel Framework for Defining Minimally Modified Reference Areas for Biodiversity Monitoring as an Alternative to Using Protected Areas

Presenter

Robert McElderry

Authors

Charbel El Khoury (ETH Zurich • Switzerland)

Robert McElderry (ETH Zurich • Switzerland)

Abstract

Evaluating ecosystem change and monitoring progress toward conservation priorities requires the setting of appropriate baselines. High-quality baseline values for reference conditions are critical for proper evaluation, but can be difficult to define for many measures of biodiversity. Although protected areas often include pristine areas where natural conditions may be measured, there is a large variety of restrictions governing the regulated use of protected areas. As an alternative, we developed an algorithm that identifies minimally human-modified terrestrial pixels that can be used as reference areas, and we compared our reference areas with the World Database on Protected Areas (WDPA). We selected reference areas across all potential land covers and ecoregions to ensure spatial and ecological representativeness of “natural” conditions.

In this poster, we show how well protected areas around the globe capture “natural” landscapes and whether they constitute adequate baselines for what a pristine area should look like.

Key research questions include:

1. Protection coverage: What proportion of reference areas fall within WDPA boundaries, and how does this vary by IUCN strictness of protection ranking?
2. Ecological representativeness: Do protected areas encompass the full diversity of ecoregions and land cover types needed for comprehensive reference conditions?
3. Ecosystem Intactness: How well does protection status predict remote sensing-derived ecosystem level metrics in comparison with reference areas?

Preliminary results indicate relatively poor protection of much of the reference areas that we identified. Protected areas also poorly represent the vast variety of ecoregions. Overall ecosystem intactness declines from strict reserves to multiple-use areas, but there is broad variability that is only partially described by size of protected area. Together, these results suggest that baseline values of “nature” may be better found in areas not modified by humans, which for some ecoregions are often not located within protected areas.

Session: 6799145-1**7015553**

21/10/25 | 14:40

Room: Caldas

ORAL • EN

PhyloFun - Spatial Phylogenetics of Fungi in Norway for Biodiversity Management

Presenter

Veerle van Winden

Authors

Veerle van Winden (Natural History Museum of Oslo • Norway)

Mika Bendiksby (Natural History Museum of Oslo • Norway)

Brent Mishler (University of Berkeley • United States)

Miguel Naranjo-Ortiz (Natural History Museum of Oslo • Norway)

Abstract

Fungi are among the most understudied branches of life, despite their great diversity and crucial ecological roles. The PhyloFun project explores patterns of fungal diversity from an evolutionary perspective using Norway as a model. PhyloFun integrates occurrence records with phylogenetic information to carry out a spatial phylogenetic assessment. Occurrence data are harvested from various online data repositories, including both observational as well as specimens-based records. In addition, PhyloFun uses DNA sequence data systematically produced within the NorBol barcoding project combined with sequences harvested from GenBank. To reduce imbalance in taxon and marker sampling, PhyloFun also produces new DNA sequence data from both fungarium specimens and freshly collected materials. An existing, systematically organised framework, Nature in Norway (NiN), provides an important and innovative data source, with which to compare the distribution patterns of clades at all levels. With its extensive fungal occurrence data, its diverse habitat, and the NiN system Norway represents an ideal location to undertake this research. Focusing on Norway as a model system, the PhyloFun project hopes to assess how evolutionary relationships shape fungal community composition across spatial scales.

Session: 6799145-1**7020808**

21/10/25 | 14:55

Room: Caldas

ORAL • EN

BIOSCANN - A national scale predictive model for detecting high-conservation value forests

Presenter

Tobias Andermann

Authors

Tobias Andermann (Uppsala University • Sweden)

Johan Häggmark (Sweden)

Patrik Olsson (Sweden)

Alice Högström (Sweden)

Abstract

As we approach the short- to medium-term implementation deadlines of major international biodiversity agreements, such as the United Nation's Kunming-Montreal Global Biodiversity Framework and the European biodiversity strategy, there is a pressing need for high-quality data products to guide large-scale conservation prioritization decisions. In this study, we implement a deep learning segmentation approach for detecting high biodiversity-conservation-value forests using a set of remote sensing data products. This approach has enabled us to produce a national data product of continuous coverage for Sweden, with an unprecedented accuracy of 91% and a high-detail spatial resolution of 10-meter pixel size, significantly advancing on existing approaches. Sweden serves as a good test case for the here developed approach, as it is home to a large portion of Europe's remaining old-growth forests and is also characterized by robust biodiversity and environmental data availability. Our approach allowed us to identify over 50,000 km² of potential high conservation value forest (HCVF) at high confidence, which has the potential to considerably improve efficiency in manual inventory efforts. With its high accuracy and spatial resolution, our data product offers substantial utility for decision-makers at different administrative scales, and directly addresses the goals set by large international biodiversity conservation plans. While this study focuses on detecting high conservation value forests in Sweden, the presented model serves as a proof-of-concept implementation that can be adapted and applied for modeling other regions and biodiversity metrics.

Session

6799127

Symposium

21/10/25 | 14:00

Room: Valle

Overcoming Barriers to Biodiversity Data Sharing and Use in Asia: Success Stories and Lesson Learned

Organizers

Melissa Jean-Yi Liu

Jerome Chie-Jen Ko

Mao-Ning Tuanmu

Vijay Barve

Description

Asia's remarkable diversity—spanning biodiversity, topography, languages, and cultures—presents unique challenges for biodiversity data mobilization and use. Key obstacles include language barriers, limited capacity for data mobilization, and a traditionally conservative research environment that hinders open data sharing. However, in recent years, growth in citizen science contributions, cross-sector collaborations, as well as support from GBIF Asia regional support team and Asia nodes have contributed to a growing awareness of the value of open biodiversity data.

This symposium will showcase successful initiatives in standardized biodiversity data management, sharing, and application across Asia, with emphasis on how these align with GBIF, TDWG, and other global data standards. Selected case studies will demonstrate effective implementation of open data principles, successful policy integration, and innovative approaches to capacity building. Presentations will highlight collaboration between government agencies, research institutions, NGOs, and citizen scientists, including specific examples of data integration into regional and global biodiversity observation networks.

The session will produce a synthesis of best practices, practical solutions for overcoming regional challenges, and recommendations for strengthening Asia's contribution to global biodiversity data networks. Participants will gain actionable insights for implementing similar initiatives in their contexts.

Session: 6799127

7020532

21/10/25 | 14:05

Room: Valle

ORAL • EN

Unlocking Biodiversity Data Use in Asia: Lessons from Taiwan's TBN--GBIF Two-Layer Model

Presenter

Jerome Chie-Jen Ko

Authors

Jerome Chie-Jen Ko (Taiwan Biodiversity Information Facility • Taiwan)

Li-Chung Lu (Taiwan Biodiversity Research Institute • Taiwan)

Huiling Chang (Taiwan)

You-cheng Yu (Taiwan Biodiversity Research Institute • Taiwan)

Ping Huang (Taiwan Biodiversity Research Institute • Taiwan)

Chih-Yi Tsai (Taiwan Biodiversity Research Institute • Taiwan)

Jheng-Sin Song (Taiwan Biodiversity Research Institute • Taiwan)

Yihong Chang (Word Gleaner Ltd • Taiwan)

Mao-Ning Tuanmu (Biodiversity Research Center, Academia Sinica • Taiwan)

Abstract

Globally standardised biodiversity data are abundant on the Global Biodiversity Information Facility (GBIF), yet Asia's hotspots face linguistic, licensing and technical barriers that limit reuse. Taiwan addresses this gap with a two-layer model in which GBIF supplies datasets while the Taiwan Biodiversity Network (TBN) localises them for policy use.

We analysed a 2024 GBIF snapshot of downloads initiated in Taiwan (3,353 events) together with international downloads of Taiwan-origin records, and compared these with complete TBN download logs for 2018–2024 (39,091 events classified by intended use). Since TBN adopted CC-BY licensing in 2018, domestic uptake has grown by a mean 106 % per year, reaching 13,127 downloads in 2024. Half of these requests supported environmental-impact assessments, 29% scientific research and 4% education, demonstrating that open licensing, coupled with a portal tailored to local audiences, supports regulatory decision-making. Within Taiwan, GBIF usage in 2024 amounted to only one-quarter of TBN's total, underscoring the need for a local interface even as GBIF provides international reach.

TBN's success rests on three operational features: it supplies metadata and vernacular taxon names in the local language, easing linguistic barriers; it partners closely with citizen-science projects, offering publishing assistance and options for masking sensitive localities; and it imports GBIF data bimonthly – along with feeds from eBird and iNaturalist – augmenting each harvest with Taiwan-specific administrative units and elevation values so users can query and report records in ways that match national conservation practice. Remaining challenges include establishing a citation-tracking loop that returns use cases to data providers and securing resources to reconcile taxonomic updates across sources.

Taiwan's experience shows that pairing a national localisation layer with GBIF can transform raw occurrence records into policy insight and cross-border collaboration. We invite Asian partners to adopt similar two-layer strategies to unlock the transformative power of unified biodiversity information.

Session: 6799127**7011575**

21/10/25 | 14:20

Room: Valle

ORAL • EN

Building a Bridge for Data Sharing: Practical Experiences in Integrating Biodiversity Data via Taiwan Biodiversity Database Portal System

Presenter

Jin-Ying Lee

Authors

Jin-Ying Lee (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Chun-I Chang** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Mao-Ning Tuanmu** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)

Abstract

The Taiwan Biodiversity Information Alliance (TBIA) is a cross-institutional collaborative initiative established in 2021, comprising government agencies, academic institutions, and collection-based institutions. Its core mission is to facilitate the integration of biodiversity data across Taiwan. In 2023, TBIA launched the “Biodiversity Database Portal System” (<https://tbiadata.tw/en-us/>), a unified platform that aggregates species occurrence data maintained by alliance partners. The portal enables users to filter, query, and download biodiversity data from multiple sources through a single access point. To support smoother data integration during the alliance’s early operations, TBIA members drafted and published Taiwan’s National Biodiversity Data Standard, based on Darwin Core. Using this standard as a foundation, the development team collaborated with alliance partners to gather practical requirements and designed a recommended API specification for data integration. Most alliance partners have since developed APIs accordingly, successfully connecting their occurrence data to the system. For those unable to develop their own APIs, TBIA encourages data publication through the Integrated Publishing Toolkit (IPT) hosted and managed by Taiwan Biodiversity Information Facility (TaiBIF), allowing data to be integrated into our system via TaiBIF’s API services. However, inconsistencies in data formats—such as variations in scientific names, dates, geographic coordinates, and quantity—remain common and require additional conversion and processing by the development team. Additionally, to address concerns related to sensitive species occurrence data, the portal includes a coordinate generalization mechanism to reduce ecological risk from precise location disclosure. This session will share TBIA’s hands-on experiences in API design, data mapping, and processing, with the goal of providing practical guidance for other teams pursuing cross-institutional data integration in the field of biodiversity informatics.

Session: 6799127**7021041**

21/10/25 | 14:35

Room: Valle

ORAL VIRTUAL • EN

Recent Trends of Biodiversity Information in Japan

Presenter

Showtaro Kakizoe

Authors

Showtaro Kakizoe (National Museum of Nature and Science • Japan)**Aino Ota** (National Museum of Nature and Science • Japan)**Utsugi Jinbo** (National Museum of Nature and Science • Japan)

Abstract

Japan is recognized as a biodiversity hotspot with a highly endemic fauna and flora, and has contributed data to GBIF since its founding in 2001. In Asia, Japan leads in “Preserved specimen” records and ranks third in “Human observation records”. This presentation highlights three uniquely Japanese approaches to biodiversity information—“museum,” “digital archives,” and “taxonomic checklists”—tracing their historical context and recent developments.

First, specimens linked to occurrence data enable rigorous, evidence-based biodiversity research through morphology, DNA, and stable isotope analyses. Museums and universities curate these collections, and Japan’s Science Museum Net (S-Net) coordinates specimen data aggregation. However, Japan’s hundreds of mainly public museums face chronic understaffing, budget shortfalls, administrative consolidation, and challenges in preserving both professional and amateur collections. The presentation examines how these institutions innovate to supply high-quality specimen data despite limited resources.

Second, Japan is promoting a national “digital archives” infrastructure—a framework for collecting, preserving, and disseminating contents, metadata and/or thumbnails of diverse digital and analog resources. The National Diet Library operates “Japan Search”, a cross-sectoral portal that harvests metadata from various content providers, including S-Net, enabling unified search and access. Several domestic digital- archive projects will be introduced.

Finally, publishing comprehensive taxonomic checklists is vital for ensuring accurate global understanding of Japan’s taxa and taxonomic research. Although Japan is strong in taxonomic study, it has lagged in broadcasting national checklists internationally. Last year the team released FernGreenList ver. 2.0 via GBIF. The presentation will share preliminary analyses of FernGreenList, review other available Japanese checklists, and preview forthcoming datasets.

By examining these three strands of activity, this talk aims to spark discussion on challenges and solutions in biodiversity information that will be increasingly relevant across Asia and beyond.

Session: 6799127**7020578**

21/10/25 | 14:50

Room: Valle

LIGHTNING TALK • EN

Constraints and Avenues of Bugs Distribution Modelling in India

Presenter

Mamta Sharma

Authors**Mamta Sharma** (Institute of Environment and Sustainable Development, Banaras Hindu University • India)**Purushothaman Chirakkuzhyil Abhilash** (Institute of Environment and Sustainable Development, Banaras Hindu University • India)**Abstract**

The most diverse group of organisms, insects are a worldwide concern due to climate change. The changes in their spatial pattern can impact the interactions and ecosystem structure of an area, posing threats to human health and food security. Through the use of widely applied Species Distribution Modelling (SDM) techniques, insect distributions are mapped globally based on occurrence data, and species past, current and future spatial projections are developed. However, the regional perspective of modelling studies, can reveal research focus, gap areas and alignment with global developments to support management decisions. In this study we collected the SDM researches on insects for India, exploring habitat requirement of the taxa. The study identifies the magnitude and direction insect SDMs, and define central species groups, modelling methods, environmental variables, occurrence sources and applied science areas in Indian context. The study highlights critical need to prioritize national biodiversity data management as climate change adaptation measure and promoting advanced biogeographic research for evidence-based actions.

Session: 6799127

7020577

21/10/25 | 14:55

Room: Valle

LIGHTNING TALK VIRTUAL • EN

Harnessing Citizen Science for Urban Biodiversity: Insights from the Hyderabad Annual Tree Biodiversity Survey

Presenter

Ashwin A

Authors

Ashwin A (WWF-INDIA, Intern • India)

Farida Tampal (WWF-INDIA • India)

Lavanya Bhat (India)

Ram Dayal Vaishnav (The Naturalist School • India)

Vijay Barve (India)

Abstract

Rapid urbanization, particularly in fast-growing cities like Hyderabad, India, poses a significant threat to biodiversity. This necessitates innovative approaches to studying and conserving urban ecosystems. The Hyderabad Annual Tree Biodiversity Survey, a citizen science initiative spearheaded by WWF-India, Hyderabad office, has been instrumental in this effort. Conducted in both 2024 and 2025, the survey engaged approximately 200 volunteers to map and analyze the city's tree diversity and associated fauna.

Using a custom web application and iNaturalist, participants surveyed over 900 trees, an increase from 750 in the previous year. These surveys covered more than 110 species across 26 locations, up from 23 in 2024, meticulously documenting the faunal biodiversity hosted by these trees. The results revealed that native tree species support significantly higher animal biodiversity than introduced species, reaffirming last year's findings.

Notably, over 80% of the surveyed trees were avenue trees (trees planted on roadside), showcasing a vibrant biodiversity and indicating several ecological traits within the city environment. An analysis of the Air Quality Index (AQI) at the surveyed locations was also conducted. Approximately 60% of the trees belonged to regions reporting "Poor" AQI, and emerged as a critical factor which is impacted the biodiversity in urban regions.

This dataset has been published on the Global Biodiversity Information Facility (GBIF), making it accessible for the scientific community to download and utilize for a more detailed analysis. These findings underscore the crucial importance of native flora and environmental quality for urban biodiversity. The survey's success demonstrates the power of citizen science in generating robust ecological data while fostering community involvement in conservation efforts. This study advocates for prioritizing native species in urban planning and improving air quality to enhance biodiversity, offering a scalable model for citizen-driven research in urban ecology.

Session: 6799127**7005087**

21/10/25 | 15:00

Room: Valle

LIGHTNING TALK VIRTUAL • EN

Disseminating citizen science data in India - a case study of SeasonWatch and GBIF

Presenter

Geetha Ramaswami

Authors

Geetha Ramaswami (Nature Conservation Foundation • India)

SeasonWatch Citizen Scientist Network (Nature Conservation Foundation • India)

Abstract

Citizen science has been a powerful tool in generating information on biodiversity in a collaborative way. However, data sharing mechanisms are often not adequate, and as such information may not reach a wide majority of end-users. The Global Biodiversity Information Facility provides an ideal opportunity to curate and disseminate citizen science data in the universal DarwinCore format for diverse end users. SeasonWatch is a citizen science project of India, documenting climate change through changing tree phenology. Contributors register one or more trees with the programme, and measure the quantity of leaves, flowers, and fruits on these trees once a week. An additional monitoring format allows for one-time phenology observations as well. This case study will look at the process of data collection, verification, and curation in SeasonWatch, and how this dataset is now the second-largest from India on GBIF. We also discuss how uploading data on the GBIF platform has improved access to citizen contributed tree phenology data to researchers across the world.

Session

6803214

Symposium

21/10/25 | 14:00

Room: Cauca

Matching decision-making needs with actionable data product to drive biodiversity monitoring impact

Organizers

Laurent Chmiel

Silas C. Principe

Description

Biodiversity observation organizations generate an unfathomable quantity of high-quality, reliable, and up-to-date data covering most of Earth. This data offers scientific insights into pressing biodiversity issues, but effectively integrating it into decision-making processes remains challenging and complex, requiring time, skills, and resources. This complexity creates a gap that prevents decision-makers from making use of the data they need to support their decisions. Bridging this gap is crucial to achieving the Kunming-Montreal Global Biodiversity Framework's goals, particularly Target 21. How can the scientific community better understand the needs of decision-makers? Could highly transformed and aggregated data-driven products, such as accessible dashboards, be a solution to increase data uptake from non-specialists?

This session will explore potential dialogue between decision-makers and biodiversity observation organizations, along with best practices, challenges, and solutions for ensuring biodiversity data is fit-for-purpose and readily actionable at local, regional, and global levels. We will aim to identify strategies to turn biodiversity data into readily available insights supporting conservation policies and management actions worldwide.

Session: 6803214**7020063**

21/10/25 | 14:10

Room: Cauca

ORAL • EN

A grammar towards operationalization of Essential biodiversity variables

Presenter

Guillaume Body

Authors

Guillaume Body (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Mathieu Basille (Patrinat (OFB-MNHN-CNRS-IRD) • France)

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Wiebke Pressé (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Florian Barnier (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Abstract

Essential biodiversity variables (EBVs) are a key step between raw data and broad indicators. EBVs are basic pieces of knowledge about the state of biodiversity, from genes to ecosystems, resulting from analysis of raw data. EBVs can then be combined in various ways to produce indicators or assessments of the status of biodiversity elements. Biodiversa+, the European Biodiversity Partnership, has developed a complete EBV grammar to enhance the operationalization of EBVs for governance and policy-making, through a formalization of a specific vocabulary addressing the “when”, “what”, “which”, and “where”, “how” questions of biodiversity data. In this talk, we will present the first steps of EBV standardisation, management and visualization allowed by the EBV grammar.

Session: 6803214**7020394**

21/10/25 | 14:20

Room: Cauca

ORAL • EN

Tracing the impact of a national observatory in biodiversity research and initiatives: successes and areas for improvement

Presenter

Christine M. Laney

Authors

Christine M. Laney (National Ecological Observatory Network (NEON), Battelle • United States)**Katherine M. Thibault** (National Ecological Observatory Network (NEON), Battelle • United States)**Eric Sokol** (National Ecological Observatory Network (NEON), Battelle • United States)**Sara Paull** (National Ecological Observatory Network (NEON), Battelle • United States)**Hugh Cross** (National Ecological Observatory Network (NEON), Battelle • United States)

Abstract

The investment required to support long-term, standardized monitoring of natural ecosystems and their biodiversity can be immense, but the return on such investment will be far greater. Recent improvements to shared data and modeling frameworks have the capacity to greatly enhance the usability and usefulness of existing and future biodiversity data. The U.S. National Ecological Observatory Network (NEON) monitors plants, algae, arthropods, small mammals, birds, fish, and microbes using standardized protocols across 81 field sites in ecosystems across the United States, alongside a suite of environmental data. NEON also archives over 100,000 new biological and environmental samples each year and provides both samples and observational data freely to research communities worldwide. Here, we trace the impacts of the use of NEON's samples and data to date, how NEON's partnerships with other networks has expanded and improved over time, and reflect on the successful strategies for increasing use and the remaining challenges. We also present areas in which new technologies and frameworks have the potential to greatly improve use of this major resource over coming decades to ultimately realize the goal of understanding and forecasting changes in biodiversity across scales of space and time.

Session: 6803214**7020247**

21/10/25 | 14:30

Room: Cauca

ORAL • EN

Scaling science to action: a framework to deliver defensible and actionable science to practitioners and decision-makers worldwide

Presenter

Viviana Ruiz-Gutierrez

Authors

Viviana Ruiz-Gutierrez (Cornell Lab of Ornithology • United States)

Abstract

Although participatory science initiatives are generating unprecedented volumes of ecological data globally, decision-makers have only recently begun to leverage this valuable resource. One of the primary obstacles to broader use is the limited availability of defensible and accessible data-products-or, data that has already been analyzed and translated into actionable science. This challenge is most pronounced in developing nations, where analytical capacity in both public and private sectors is often limited.

For this panel, we would like to share our experience of working alongside partners across sectors and disciplines to leverage the strengths of participatory science data to inform policy, conservation, management, and nature-based solutions. Our work leverages the strengths of eBird- the world's largest biodiversity monitoring program, with over 1.9 billion records worldwide. Over the past decade, we have refined a framework to link science with decision-makers. This includes working closely with state and federal partners to validate and build trust in available information, publishing real-world use cases, and leveraging advances in computational biology to scale and disseminate our information.

As a result, our data products have been used to directly inform conservation actions, management, strategies, and regulatory frameworks. For example, the general permitting process for wind energy developments for the US Fish and Wildlife Service. The value and credibility of our work is evidenced by the more than 2.5 million downloads of our data products over the past five years, including decision-makers and partners such as US Geological Survey, Birdlife International, Environment and Climate Change Canada, Earthjustice, among others. Our work exemplifies how academic institutions can work alongside practitioners and decision-makers to generate information that is defensible and actionable, at high spatial and temporal resolutions worldwide.

Session: 6803214**7015017**

21/10/25 | 14:40

Room: Cauca

ORAL • EN

Realising the potential of interoperable data products to improve the outlook for marine biodiversity: lessons from EMODnet

Presenter

Tom Webb

Authors

Tom Webb (University of Sheffield • United Kingdom)

Joana Beja (VLIZ • Belgium)

Salvador Jesús Fernández Bejarano (Lifewatch ERIC • Spain)

Elvira Ramos (IHCantabria • Spain)

Samuel Sainz-Villegas (IHCantabria • Spain)

Karline Soetaert (Royal Netherlands Institute for Sea Research • Netherlands)

Stolte Willem (Deltares • Netherlands)

Charles Troupin (University of Liège • Belgium)

Benjamin Weigel (INRAE • France)

Abstract

Policies responding to increasing pressures on marine biodiversity require adequate data and information to support their implementation and to monitor their effectiveness. Marine biodiversity science has made significant progress generating and aggregating biodiversity data, however turning this into evidence-based knowledge useful to decision makers remains a significant challenge. ‘Data products’ provide processed data to address specific user needs, and are widely used in climate science, geosciences, and remote sensing, but the development of biodiversity data products is challenging due to the complexity of biological systems and of the data derived from surveys designed without explicit biodiversity policy or management guidance. A wide range of potential products of interest may include distributional data for thousands of individual taxa, requiring advanced statistical methods to model patterns in biodiversity using heterogeneous and sparse source data with biases in spatial, temporal, and taxonomic coverage. We illustrate these challenges using data products created within the Biology thematic lot of the European Marine Observation and Data Network (EMODnet), and we propose that the EMODnet Biology approach, which involves providing clear, open and reproducible documentation of the product creation process with a strong emphasis on the computational tools needed to link source data to higher-level data products, can productively support decision making at the European scale. Furthermore, this approach provides part of the essential infrastructure required to maximise the financial benefits of FAIR data, and data products play a key role in empowering users to make maximum use of existing biodiversity data to help to understand and manage our seas.

Session

6798937-2

Symposium

21/10/25 | 16:00

Room: Ballroom A

Darwin Core Data Package: an updated model and format for exchanging biodiversity data (Part 2)

Organizers

Kate Ingenloff

John Wieczorek

Peter Desmet

Yi Ming Gan

Jörg Holetschek

Description

In this session we will present the Darwin Core Data Package (DwC-DP), a new model and format for sharing biodiversity data. DwC-DP is designed to overcome the limitations of Darwin Core Archives (such as the star schema) and introduces a semantic model for biodiversity data. This model consists of a number of related tables (e.g. Events, Occurrences, Agents, Assertions) that aim to capture the diversity of biodiversity data in a common model, while still feeling familiar to data publishers. As a format, DwC-DP builds upon the Data Package standard and expresses data as CSV files and technical information as a machine-readable metadata file (similar to Darwin Core Archives). DwC-DP is the result of an extended iterative approach supported by the Global Biodiversity Information Facility (GBIF) and based on a wide range of use cases. Some of these use cases (e.g. survey data, collection data, eDNA data) will be presented by early adopters as concrete showcases on how to use DwC-DP, while GBIF will present how it supports DwC-DP through their Integrated Publishing Toolkit (IPT) and infrastructure. Finally, we will explain the next steps for DwC-DP and how you can contribute or provide feedback.

Session: 6798937-2**7020859**

21/10/25 | 16:00

Room: Ballroom A

ORAL • EN

Darwin Core Data Package: A Practical Evolution to Support Richer, Deeper, and New Biodiversity Data Sharing

Presenter

John Wieczorek

Authors

John Wieczorek (Rauthiflor LLC • Argentina)

Tim Robertson (Global Biodiversity Information Facility (GBIF) • Denmark)

Abstract

After nearly two decades of success with Darwin Core and the Darwin Core Archive (DwC-A), the biodiversity informatics community faces the need to share data that are both richer in detail and deeper in structure than existing formats support. The Darwin Core Data Package (DwC-DP) emerges as a direct response to this need—not as a replacement, but as a natural, practical evolution of a trusted standard. This presentation introduces DwC-DP as the result of six years of iterative, use case-driven development and testing, designed to extend the capabilities of Darwin Core without discarding its simplicity or adoption base.

The journey began with the Unified Model—a comprehensive conceptual design proven to meet complex use cases, but too burdensome for everyday use. DwC-DP captures the “sweet spot” of that design: flexible enough to support emerging data types (e.g., Nucleotide Analyses, Organism Interactions, Survey Targets, Phylogenetic Trees), while retaining usability for current data publishers.

Key features include modular schemas, a clearly event-based structure, and reusable extension patterns for concepts like Agent Roles, Media, Assertions, Protocols, and References. DwC-DP supports both flattened and nested forms, empowering users to adopt the level of complexity appropriate to their data.

This talk will demystify DwC-DP for audiences ranging from cautious data providers to advanced integrators, highlighting its role as a community-informed technical foundation—supported by GBIF, governed by TDWG, and shaped by global feedback. Attendees will leave with a clearer sense of how DwC-DP enables more science and better decision-making without requiring a disruptive shift for those already using Darwin Core.

Session: 6798937-2**7015382**

21/10/25 | 16:20

Room: Ballroom A

ORAL • EN

Two Decades of ABCD: Advancing Structured Biodiversity Data Sharing

Presenter

Anton Güntsch

Authors**Anton Güntsch** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**David Fichtmueller** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Jörg Holetschek** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Gabi Droege** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Walter G. Berendsohn** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Abstract**

ABCD (Access to Biological Collection Data, <https://abcd.tdwg.org/>) is a TDWG (Biodiversity Information Standards) standard that was developed by a broad international collaboration to create a structured framework for capturing and exchanging biodiversity data.

ABCD was implemented as a hierarchical XML schema, allowing it to interoperate seamlessly with standardized software components. This design enables diverse applications such as data publication, harvesting and aggregation, quality control, and access through data portals. By facilitating harmonized exchange and integration of primary biodiversity data, ABCD supports robust scientific workflows and analyses (Holetschek et al. 2012, <https://doi.org/10.1080/11263504.2012.740085>).

Over the past two decades, ABCD has undergone continuous refinement to align with the evolving needs of the biodiversity informatics community. In parallel with the widely used Darwin Core standard (Wieczorek et al. 2012, <https://doi.org/10.1371/journal.pone.0029715>), ABCD plays a vital role in promoting the harmonization, mobilization, and dissemination of biodiversity data across both national and international infrastructures. Domain-specific extensions for ABCD play a central role for special-interest networks, like the Global Genome Biodiversity Network (GGBN, Droege et al. 2016, <https://doi.org/10.1093/database/baw125>). An important example of the use of ABCD at the national level is the establishment of standardized data flows between domain data centers and central aggregation and data analysis platforms in NFDI4Biodiversity in Germany (Glöckner et al. 2020, <https://doi.org/10.5281/zenodo.3943645>).

The latest iteration of the standard, ABCD version 3.0, introduces a significant architectural enhancement: the semantic definitions of data elements are now decoupled from their structural representation in XML. This modularization promotes greater flexibility in how the standard can be applied and reused, facilitating integration into emerging data ecosystems and enhancing interoperability (Fichtmueller et al. 2019, <https://doi.org/10.3897/biss.3.37214>). In particular, ABCD contributes to the emerging “Darwin Core Data Package” a new initiative aimed at enabling the global exchange and reuse of structured collection and observational data based on Frictionless Data technology (<https://frictionlessdata.io/>).

Session: 6798937-2**7019768**

21/10/25 | 16:31

Room: Ballroom A

ORAL VIRTUAL • EN

Seamless Integration: How DiSSCo's openDS Facilitates Data Interoperability with the Darwin Core Data Package

Presenter

Sam Leeflang

Authors

Sam Leeflang (Naturalis Biodiversity Center • Netherlands)

Tim Robertson (Global Biodiversity Information Facility • Denmark)

Abstract

The Distributed System for Scientific Collection (DiSSCo) has been following the developments of the Darwin Core Conceptual Model and the Darwin Core Data Package (DwC-DP) with great interest. DiSSCo is an emerging European Research Infrastructure Consortium (ERIC) aimed at accelerating the digitisation of Europe's Natural History Collections. Vital to this acceleration is the exchange of knowledge, ideas, and tools, which can be done through the DiSSCo infrastructure. Essential for the infrastructure is a collective language in the form of data standards, which we call open Digital Specimen (openDS).

The development of openDS has been done in parallel to the development of the Darwin Core Conceptual Model. OpenDS has reached production maturity after it has gone through a public review in 2024. OpenDS is a document focussed specification optimized for data curation, where each document represents a Fair Digital Object (FDO). This means that openDS is broader than the specimen information but also contains models to capture annotations and provenance. As the openDS Digital Specimen and Digital Media models are developed on top of existing TDWG standards and the work on the Darwin Core Conceptual Model, they can be seen as an implementation of the conceptual model. Translations between openDS and DwC-DP, both implementations of the conceptual model, can therefore be made without any loss in data.

During the session, DiSSCo will share their experience with implementing both the conceptual model in the form of openDS and the translation from openDS to the DwC-DP.

DiSSCo will be able to create DwC-DP for any of their data, showing how specimen from Natural History Collections can be mapped to DwC-DP.

Session: 6798937-2**7019798**

21/10/25 | 16:44

Room: Ballroom A

ORAL • EN

Implementation Status of the Darwin Core Data Package (DwC DP) at GBIF

Presenter

Federico Méndez

Authors

Federico Méndez (GBIF Secretariat • Denmark)

Abstract

The implementation of the Darwin Core Data Package (DwC-DP) goes beyond enabling publishing mechanisms, it also benefits from data services that support search, discovery, and exploration. GBIF.org currently offers a robust data indexing platform, including an API and data portal. A large proportion of the available data has been published using the existing Darwin Core Archive (DwC-A) standard. While DwC-A's simplicity has enabled effective aggregation within a centralized infrastructure, the richer modeling capabilities of the new DwC-DP introduce both opportunities and challenges for future data services.

To address this, the GBIF Secretariat is developing a phased roadmap for data ingestion and discovery services based on the new DwC-DP. The roadmap includes: enabling the publishing and registration of DwC-DP datasets; extending dataset catalogs to support discovery; facilitating exploration of dataset structures and schemas; and, in the near future, implementing global data services for cross-dataset querying and downloads, comparable to those currently available on GBIF.org.

This presentation provides a status update on the development of this roadmap. It demonstrates how a DwC-DP dataset can be published, ingested, and explored through its internal structure via a test data portal. Finally, it outlines upcoming service enhancements for both the current DwC-A platform and the evolving DwC-DP based infrastructure.

Session: 6798937-2**7016769**

21/10/25 | 16:56

Room: Ballroom A

ORAL • EN

Implementing the proposed DwC-DP format in GBIF: data publishing tools

Presenter

Mikhail Podolskiy

Authors

Mikhail Podolskiy (GBIF • Denmark)

Abstract

The GBIF Integrated Publishing Toolkit (IPT) has enabled the publication of thousands of datasets in a robust and user-friendly way for more than a decade. This success is due in part to the simplicity and clarity of the Darwin Core standard, as well as the straightforward workflows the IPT provides for data publishers.

As the data model supporting the mobilization of more complex biodiversity data evolves, so too must the infrastructure. Traditional schemas like Darwin Core have served the community well, but they limit the expression of richer biodiversity information. To address this, GBIF is working towards introducing the new Darwin Core Data Package (DwC-DP), designed to better represent complex relationships among biodiversity entities.

While DwC-DP opens exciting possibilities for linking entities and supporting diverse data types, it also presents significant challenges for developers and data publishers. We must balance this increased richness with usability, ensuring that tools like the IPT remain accessible to a broad community. Key challenges include managing data model versions, providing user guidance for complex schemas, and ensuring that schema governance and validation workflows are transparent and sustainable.

This presentation will offer a vision for implementing DwC-DP support in the IPT, including design decisions, current state and limitations, and planned improvements.

We aim to inspire contributions and ideas from the TDWG community to improve tooling and practices, ultimately helping to lower the barriers to publishing high-quality, richly structured biodiversity datasets.

Session: 6798937-2

7009601

21/10/25 | 17:06

Room: Ballroom A

ORAL VIRTUAL • EN

Darwin Core Data Package public review process

Presenter

Steve Baskauf

Authors

Steve Baskauf (Darwin Core Maintenance Group • United States)

Abstract

The TDWG Vocabulary Maintenance Specification (VMS, provides a mechanism for making a set of coordinated changes to a vocabulary. The Darwin Core Data Package (DwC-DP) falls into this category of coordinated additions to the Darwin Core standard In this presentation, I will describe how the public review process described by the VMS applies to the DwC-DP proposal. Specifically, I will detail: what is under review, how the proposed changes will be added to the standard and its documentation, and how the public can provide comments to participate in the public review.

Session

6802864-2

Symposium

21/10/25 | 16:00

Room: Ballroom B1

Integrative tools, data platforms and applications to address freshwater biodiversity research (Part 2)

Organizers

Jaime Ricardo Garcia Marquez

Eren Turak

Thilina Surasinghe

Yusdiel Torres Cambas

Thomas Tomiczek

Vanessa Bremerich

Merret Buurman

Kristi Bego

Paula Torre Zaffaroni

Description

The degradation of freshwater ecosystems and the decline of their biodiversity has triggered efforts to compile, standardize and publicly share fragmented freshwater biological data, and freshwater-specific geospatial datasets. This involves the integration of cutting-edge earth observation products to map hydrographical networks at high spatial resolution and at large geographical scales, the development of new processing tools, models and workflows that account for the longitudinal connectivity in freshwater ecosystems while integrating geospatial and biological data and call for the adoption of FAIR (Findable-Accessible-Interoperable and Reusable) and CARE (Collective Benefit, Authority to Control, Responsibility, Ethics) standards, as well as STAC (Spatio Temporal Asset Catalogs) specification for geospatial information. This session invites contributions that explore integrative approaches for advancing the standardization of freshwater biodiversity databases, and developing hydrological and environmental datasets relevant to the protection and restoration of freshwater species and ecosystems. The thematic scope of the session also includes change detection and causal attribution, biodiversity forecasting, spatial prioritization and other modelling applications using both biological and geospatial information on pressures, drivers, ecosystem structure and function. We encourage studies focusing on data interoperability and/or integration of large-scale biological and environmental datasets in models and scenarios to support freshwater conservation and management.

Session: 6802864-2**7021007**

21/10/25 | 16:00

Room: Ballroom B1

ORAL • EN

Maximizing the value of large-scale data in land to water restoration projects

Presenter

Andres Felipe Suarez Castro

Authors

Andres Felipe Suarez Castro (Griffith University • Australia)**Dale Robertson** (U. S. Geological Survey, Upper Midwest Water Science Center • United States)**Liliana Pagliero** (Australian Rivers Institute, Griffith University • Australia)**Mohammad Hassan Ranjbar** (Australian Rivers Institute, Griffith University • Australia)**Bernhard Lehner** (Department of Geography, McGill University • Canada)**Simon Linke** (CSIRO • Australia)**David Hamilton** (Australian Rivers Institute, Griffith University • Australia)

Abstract

Changes in land use have disrupted natural nutrient cycles, leading to declines in freshwater biodiversity and water quality worldwide. Restoration approaches that consider the interface between terrestrial and aquatic systems are thus key to build resilience in water ecosystems. However, despite billions of dollars spent in water quality monitoring programs, decision makers are confronted with inadequate information to prioritize landscape restoration that benefits freshwater systems. Here, we present an adaptable framework to integrate remote sensing, hydrological, land use and socio ecological data to prioritize the restoration of catchments. This framework was applied to different case studies across North America, Oceania and South America. For each region, we used novel large-scale datasets to identify areas with the highest sources of nutrient runoff and predict loads of TP and TN entering lakes. These models were combined with zero-dimensional models, which are easy to implement, to mechanistically predict lake-wide nutrient concentrations based on inflow nutrients, lake residence time and other physical characteristics. We used this information to prioritize the selection of sites where restoration could benefit biodiversity and ecosystem services by reducing the impact of nutrient sources associated with multiple sources including land cover change, farm fertilizers and manure. Our results show that models based on large scale datasets had a high model estimation performance of total loads and yields sources. We also show how the framework can be applied at multiple spatial scales, from single lakes to entire catchments and regions, and how uncertainty in potential restoration outcomes increases in areas with poor water quality monitoring data. By applying our framework to prioritise for lake restoration, we show the importance of accounting for links between terrestrial and freshwater ecosystems to maximize benefits of restoration across the land to water interface, particularly in data poor regions.

Session: 6802864-2**7014724**

21/10/25 | 16:15

Room: Ballroom B1

ORAL VIRTUAL • EN

The freshwater biodiversity forecasting tool to support conservation planning and scenario evaluation at broad spatial scales

Presenter

Eren Turak

Authors

Eren Turak (NSW Department of Climate Change, Energy, the Environment and Water • Australia)**Rajesh Thapa** (University of New England • Australia)**Glenn Manion** (Cryzan Pty Ltd • Australia)**Michael Drielsma** (NSW Department of Climate Change, Energy, the Environment and Water • Australia)**Savrina Carrizo** (NSW Department of Climate Change, Energy, the Environment and Water • Australia)**Jamie Love** (NSW Department of Climate Change, Energy, the Environment and Water • Australia)

Abstract

We developed a freshwater biodiversity forecasting tool to inform spatial prioritisation of conservation and restoration actions in the Australian State of NSW (801,428 km²). The three output types are: 1) spatial layers of biodiversity condition; 2) benefit surfaces for conservation and restoration actions; and 3) forecasts of biodiversity condition under spatially-explicit management scenarios including climate adaptation scenarios.

The first stage of development of the tool was confined to rivers. The condition layer was based on biological intactness index scores calculated for over 3,240 river monitoring sites from macroinvertebrate data collected using a standardised sampling protocol. Modelled condition index scores were calculated for each of 164,580 river sub-catchments (median surface area= 2.2 km²) in Australia's National Catchment Boundaries database using multiple linear regression. The variables used in the model were calculated from pressure and driver data extracted for all sub-catchments. We then used the condition layer together with river types based on macroinvertebrate assemblages collected from reference sites to estimate a biodiversity persistence index for each sub-catchment. The tool enables the aggregation and reporting of persistence at any spatial scale and for any type of classification e.g. land use, tenure, ecosystem type. We generated forecasts of future condition and persistence by altering the driver and pressure layers to reflect expected changes under future management and climate change scenarios.

This tool can be modified for use at local to global spatial scales. We developed a version of the tool using the global HydroATLAS datasets which is available for the 6377 HydroBASINS of NSW (median surface area= 134.1 km²). Forecasts at that spatial scale are likely to be less useful for some of the intended applications of this tool in NSW but these global datasets are likely to be maintained more regularly and consistently into the future compared with most national and sub-national datasets.

Session: 6802864-2**7019847**

21/10/25 | 16:30

Room: Ballroom B1

ORAL • EN

Modelling freshwater fish species' distributions considering the impact of river fragmentation in mainland Spain

Presenter

Lide Izeta-Zalduendo

Authors

Lide Izeta-Zalduendo (Instituto de Biodiversidad y Medioambiente BIOMA, Universidad de Navarra • Spain)**Rafael Miranda** (Instituto de Biodiversidad y Medioambiente BIOMA, Universidad de Navarra • Spain)**Amaia A. Rodeles** (Centro de Investigación Mariña (CIM), Universidade de Vigo • Spain)**María Morán-Luis** (IHCantabria - Instituto de Hidráulica Ambiental de la Universidad de Cantabria • Spain)**Alexia M. González-Ferreras** (IHCantabria - Instituto de Hidráulica Ambiental de la Universidad de Cantabria • Spain)**Francisco J. Peñas** (IHCantabria - Instituto de Hidráulica Ambiental de la Universidad de Cantabria • Spain)**José Barquín** (IHCantabria - Instituto de Hidráulica Ambiental de la Universidad de Cantabria • Spain)**David Galicia** (Instituto de Biodiversidad y Medioambiente BIOMA, Universidad de Navarra • Spain)

Abstract

Freshwater ecosystems are globally at risk, with one quarter of its fauna threatened with extinction according to the assessments from the International Union for Conservation of Nature. Riverine fish are an especially vulnerable group, since their movement is constrained to the river network. Barriers like dams and weirs interrupt the longitudinal connectivity of the river network, altering the natural flow, temperature and sedimentation, degrading the habitat, and hindering the movement of the individuals up and downstream. In Europe, barriers affect 51% of fish species. Spain is a particularly interesting area to study the effect of barriers on freshwater fish due to the large number of barriers to longitudinal connectivity and the high degree of endemism of its fish species. Species distribution models were built for native freshwater fish to determine the role of barriers in species' distributions. Presence-absence data were obtained from the Spanish Fish Chart, the most complete database to date of the Spanish freshwater fishes, containing more than 100,000 records of fish presence in Spain. Barrier data were compiled from regional, national and European databases and snapped to the river network. The impact of the river network's degree of fragmentation on the species distribution models was determined through the performance of the model.

Session: 6802864-2**7020789**

21/10/25 | 16:45

Room: Ballroom B1

ORAL • EN

Freshwater biodiversity data publishing enables the integration of species occurrences with other conservation products to generate vital conservation support tools

Presenter

Laban Musinguzi

Authors

Laban Musinguzi (National Fisheries Resources Research Institute • Uganda)

Vianny Natugonza (Maritime Institute, Busitema University • Uganda)

Abstract

The conservation of freshwater biodiversity lags behind terrestrial and marine biodiversity because data and information limitations to support conservation are greatest in freshwater ecosystems. Because freshwater ecosystems support disproportionately more species than the other ecosystems, the limitations in data are a disadvantage to many species. Data and information on freshwater biodiversity are not only limited because few freshwater ecosystems are considered for regular monitoring, but existing data is also scattered in non-user-friendly formats, limiting accessibility and use. Therefore, aggregating available data is desirable to make it accessible everywhere to guide freshwater biodiversity conservation and research. This presentation will demonstrate how the mobilization, aggregation, and publication of previously scattered data on the occurrence of freshwater fishes of Uganda enabled the integration of the species occurrences with other conservation products including HydroBasins, the global red list for threatened species, and IUCN's frameworks for regional assessments and mapping freshwater taxa to generate critical decision support tools to guide freshwater conservation research decision making. The conservation tools developed include a dedicated information dissemination platform, standard species distribution maps, a national red list for the species, and an index to prioritize habitats for protection. The national red list was the first for the fishes of the country, enabling the species to catch up with terrestrial taxa with national red lists. With increasing evidence on the use of the generated conservation tools in research, capacity building, and advocacy, data mobilization and subsequent integration in other data and information products to generate decision support tools has potential to facilitate freshwater conservation and research actions.

Session: 6802864-2**7020482**

21/10/25 | 17:00

Room: Ballroom B1

ORAL • EN

Integrating freshwater fish biodiversity for area prioritization in Colombia

Presenter

Thomas Tomiczek

Authors

Thomas Tomiczek (Leibniz Institute for freshwater ecology and inland fisheries • Germany)**Jaime Ricardo Garcia Marquez** (Leibniz Institute for freshwater ecology and inland fisheries • Germany)**Sami Domisch** (Leibniz Institute for freshwater ecology and inland fisheries • Germany)

Abstract

The increasing anthropogenic pressures on freshwater biodiversity raise the important question, how well is it represented within protected areas? We address this question using the freshwater fish fauna of a neotropical biodiversity hotspot, specifically Colombia, as a case study, home to 1616 freshwater fish species and one of the global freshwater biodiversity hotspots. We employ species distribution modelling and spatial prioritization analyses to estimate (i) how the Colombian fish fauna is covered by the existing protected areas, and (ii) to which degree alternative protected area configurations may have the potential to increase the number of fish species under protection. We compiled 238,278 geographic occurrences for 1313 freshwater fish species across Colombia and neighboring countries and cleaned the species data by harmonizing the nomenclature and revising the geo-referenced coordinates. Using the GMTED-digital elevation model, we delineated a stream network and extracted the corresponding 38150 sub-catchments that served as spatial units for the analysis. We then used an ensemble of modelling algorithms to project potentially suitable habitats of single fish across the study area. We finally used integer linear programming to account for 30 % of each fish' suitable habitat within newly-delineated priority areas, i.e. hypothetical protected areas. We found that the newly-delineated priority areas overlap only by 25.2 % with the existing protected area network.

Strikingly, the required amount of area for protection is similar to that of the existing protected areas, reflecting however a major mismatch between the two. Moreover, we found that endemic and threatened species, especially in the Magdalena-Cauca and Pacific-Choco basins contributed towards the newly-delineated priority areas that would be integral for an efficient freshwater fish protection. Our results highlight the high discrepancy between freshwater biodiversity conservation and protected areas in Colombia, and guide the integration of those areas with high ecological value yet reduced anthropogenic impact.

Session: 6802864-2

7020485

21/10/25 | 17:15

Room: Ballroom B1

ORAL • ES

Priorización espacial para la conservación de ecosistemas acuáticos en la Orinoquía colombiana hacia la meta 30x30

Presenter

Elkin A. Noguera-Urbano

Authors

Elkin A. Noguera-Urbano (Instituto Humboldt • Colombia)

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Leidy Marcela Cepeda (Instituto Humboldt • Colombia)

Lina María Sánchez-Clavijo (Instituto Humboldt • Colombia)

Maria Cecilia Londoño (Instituto Humboldt • Colombia)

Juliana Delgado (The Nature Conservancy TNC • Colombia)

Abstract

La región de la Orinoquía colombiana alberga una alta diversidad biológica y constituye uno de los principales reservorios de agua dulce del país, pero enfrenta crecientes presiones antrópicas que amenazan sus ecosistemas. En este contexto, se implementó un enfoque de planificación sistemática de la conservación (PSC), integrando variables biológicas, ecológicas y socioeconómicas, para priorizar espacialmente áreas de conservación de ecosistemas acuáticos. El estudio delimitó 4.243 microcuencas como unidades de planificación, incorporando distribuciones de 458 especies clave, ecosistemas estratégicos (ríos, humedales, bosques riparios), índices de integridad ecológica, conectividad hidrológica y restricciones espaciales como áreas protegidas. Mediante el uso del paquete prioritizr y sus algoritmos de programación lineal entera, se generaron escenarios de priorización con una meta de conservación del 30%. Los resultados evidencian áreas prioritarias con alta conectividad estructural, identificando corredores y núcleos de conservación relevantes en la Orinoquía. La inclusión de restricciones del RUNAP orienta las prioridades hacia zonas de piedemonte y alta montaña, mientras que su exclusión resalta áreas en la altillanura y la transición amazónica. Las soluciones muestran una fuerte asociación con ecosistemas acuáticos, validando la robustez del enfoque. Este trabajo proporciona una base técnica sólida para orientar decisiones de conservación en la región y contribuir al cumplimiento de metas globales como la protección del 30% de los ecosistemas de aguas interiores para 2030.

Session

6796330-2

Symposium

21/10/25 | 16:00

Room: Ballroom B2

Improving data management strategies, sharing and FAIRness of DNA-derived Biodiversity Data (Part 2)

Organizers

Tobias Frøslev

Joana Pauperio

Saara Suominen

Miwa Takahashi

Vanessa Yepes Navaez

Erika Montoya Cadavid

Ricardo Ortiz Gallego

Description

Every lifeform in the world, from viruses to whales, contains a bio-molecular footprint that informs about their occurrence and biology. DNA based methods are transformative tools for biodiversity detection and monitoring. Environmental DNA (eDNA) metabarcoding in particular is expected to massively accelerate the field by enabling detection of entire biological communities from soil, water, and air samples. However, the detection of biodiversity from environmental samples (using eDNA) generates larger data sets unlike traditional methodologies in which each DNA sequence comes from an isolated individual.

Despite its potential, standardized sharing and integration of metabarcoding data and other DNA-associated biodiversity data has remained limited until now. Best practices for FAIR data sharing include submitting raw sequence data to INSDC (International Nucleotide Sequence Database Collaboration) short read archives (e.g. ENA, SRA) and sharing the processed and interpreted biodiversity records (e.g., Amplicon Sequence Variants, ASVs and Operational Taxonomic Units, OTUs) through biodiversity databases like those of the Global Biodiversity Information Facility (GBIF.org) and Ocean Biodiversity Information System (OBIS.org).

We invite contributions that address:

- New tools and pipelines for improved sharing of DNA-derived biodiversity data.
- Approaches for better integration of DNA-derived data with other biodiversity data.
- Remaining challenges and solutions for achieving FAIR DNA-derived biodiversity data.
- Non-technical aspects that infrastructures should consider, such as legal frameworks, domain specific data culture etc.

This session will include discussions on best practices and solutions to enhance the FAIRness of DNA-derived biodiversity data for biodiversity research, with a main focus on eDNA and metabarcoding data. We will seek to share the initiatives, strategies and experiences that have been proposed regarding the management and final disposal of this information as a useful tool for decision-making on environmental matters.

Session: 6796330-2**7020861**

21/10/25 | 16:00

Room: Ballroom B2

ORAL • EN

European Nucleotide Archive data model and developments for improving eDNA derived data sharing

Presenter

Joana Paupério

Authors

Joana Paupério (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Rajkumar Devaraj (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Eugene Ivanov (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Vishnukumar Balavenkataraman Kadhivelu (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Ankur Lathi (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Peter Wollard (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Colman O'Cathail (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Guy Cochrane (EMBL-EBI - European Bioinformatics Institute • United Kingdom)

Abstract

DNA based methods are powerful tools that are increasingly used for biodiversity research. The analysis of environmental DNA (eDNA) using metabarcoding techniques enables comprehensive species detections and descriptions of communities and their function. This approach is becoming widely used for downstream applications in biodiversity monitoring and conservation. For meaningful interpretation, the eDNA derived data needs to be shared in a standardised, findable, accessible and interoperable way, therefore following FAIR (Findable, Accessible, Interoperable and Reusable) principles.

eDNA derived data consists of the raw sequence reads and the interpreted data, that includes the sets of sequences derived after bioinformatics processing (Amplicon Sequence Variants (ASVs) or Operational Taxonomic Units (OTUs)), their presence in the analysed sample and associated taxonomic identification (ASV/OTU tables). The raw reads and associated sample metadata are often shared through the International Nucleotide Sequence Database Collaboration (INSDC), that joins the European Nucleotide Archive (ENA), the National Centre for Biotechnology Information (NCBI), and the DNA Data Bank of Japan (DDBJ). The interpreted species occurrences are usually made available through biodiversity databases (e.g. GBIF, OBIS). However, data sharing is often performed with minimal metadata and lacks the appropriate linkage between sequence and biodiversity data repositories.

Here we will present the current developments in the ENA data model to promote the submission of eDNA derived data, including sample metadata following international standards, raw sequence data and new implementations for ASV/OTU sequences and associated taxonomic annotations. In the scope of previous and ongoing projects, ENA has interacted with the community and collaborated in the discussions around eDNA metadata standards and the definition of the requirements for deposition and access to eDNA derived data.

Current implementations align with the identified requirements and move towards improved data sharing and interoperability of eDNA derived data.

Session: 6796330-2**7014912**

21/10/25 | 16:15

Room: Ballroom B2**ORAL • EN**

The role of the ERGA community in building capacity to adhere to best practices for FAIR reference genome production

Presenter

Robert Waterhouse

Authors

Robert Waterhouse (SIB Swiss Institute of Bioinformatics • Switzerland)

Abstract

The European Reference Genome Atlas (ERGA) initiative significantly advances data management, sharing, and the FAIRness (Findable, Accessible, Interoperable, Reusable) of biodiversity genomics data across Europe. ERGA's mission to generate high-quality reference genomes for diverse European species is underpinned by a strong commitment to robust data stewardship and open science principles. By adopting and promoting FAIR standards throughout its workflows, from sample collection and metadata documentation to genome assembly and annotation, ERGA ensures that genomic data are systematically curated and easily discoverable by the broader scientific community. ERGA's operations emphasise standardised protocols and interoperable formats that facilitate seamless integration with global databases and initiatives, such as the European Nucleotide Archive (ENA) and the Earth BioGenome Project. This approach not only improves the long-term usability and visibility of data but also supports cross-disciplinary research in conservation biology, evolutionary studies, and ecosystem monitoring. In addition, ERGA plays a critical role in developing best practices for data sharing and access, addressing ethical and legal considerations, such as data sovereignty and benefit-sharing. ERGA aims to foster a responsible data ecosystem that balances openness with equity, with an emphasis on supporting researchers with information, guidelines, and access to community discussion forums so they can more easily achieve high standards of data production as well as data FAIRness. Through training programmes and capacity-building initiatives, ERGA also enhances digital literacy and data management skills among European researchers, further embedding FAIR principles into the fabric of biodiversity genomics. Ultimately, ERGA strengthens Europe's leadership in genomic data stewardship, ensuring that biodiversity data remains impactful, accessible, and ethically managed for current and future scientific endeavours.

Session: 6796330-2**7008265**

21/10/25 | 16:30

Room: Ballroom B2**ORAL • EN**

MiCoDa: the Microbial Community Database

Presenter

Stephanie Jurburg

Authors

Stephanie Jurburg (Helmholtz Center for Environmental Research • Germany)**Clara Arboleda Baena** (German Centre for Integrative Research (iDiv) Halle-Jena-Leipzig • Germany)**Anahita Kazem** (Friedrich Schiller University Jena • Germany)**Birgitta Koenig-Ries** (Friedrich Schiller University Jena • Germany)**Antonis Chatzinotas** (Helmholtz Center for Environmental Research (UFZ) • Germany)**Maria Jose Alvarez Blanco** (Germany)**Andre Soibelman Glock Lorenzoni** (German Center for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig • Germany)**Santiago Castillo Rivadeneira** (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig • Germany)

Abstract

Data collection, management, and reuse are increasingly important in the life sciences. In microbial ecology, sequencing has altered our relationship to the invisible microbial world and created massive amounts of reusable microbiome data, but these data are hard to integrate and underused. To foster sequence data reuse, we created the Microbial Community Database (MiCoDa), an open database of 16S rRNA amplicon sequencing data. Through manual curation and dedicated bioinformatics processing, MiCoDa unifies over 35,000 microbiome samples under consistent species definitions, allowing users to examine microbiomes across studies easily and without the need for advanced computational resources or bioinformatics know-how. The MiCoDa web interface allows users to explore, filter, and download ready-to-use species tables and fosters interoperability between INSDC databases, publication DOIs, and soon, the Global Biodiversity Information Facility (GBIF). MiCoDa data was collected from sequence archives as well as through community-oriented data collection and reuse events organized yearly across Latin America, Africa, and soon, Asia. Currently, we are validating AI-driven methods for dataset identification and metadata extraction and working towards an automated update protocol that can keep pace with the accelerating rate of nucleotide data production. Fostering microbiome data reuse globally may not only advance science, but may serve to invert knowledge flows in microbial ecology.

Session: 6796330-2**7015342**

21/10/25 | 16:45

Room: Ballroom B2**ORAL • EN**

Supporting multi-proxy ancient environmental DNA research through community curation within the Neotoma Paleoecology Database

Presenter

Trisha Spanbauer

Authors

Trisha Spanbauer (University of Kentucky • United States)

John Williams (University of Wisconsin-Madison • United States)

Socorro Dominguez (University of Wisconsin-Madison • United States)

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Rachel Meyer (UC Santa Cruz • United States)

Jonathan Nelson (University of Wisconsin-Madison • United States)

Vilma Perez (University of Adelaide • Australia)

Dilli Prasad Rijal (The Arctic University of Norway • Norway)

Kathleen Stoof-Leichsenring (Alfred Wegener Institute for Polar and Marine Research • Germany)

Abstract

Ancient environmental DNA (aeDNA) is genetic material accumulated over time in sediments and other depositional environments and, like eDNA, aeDNA can be used to analyze changes in biodiversity. However, unlike eDNA, aeDNA has the ability to decipher past biodiversity changes over timescales of hundreds to millions of years. The field of aeDNA research is growing rapidly with dozens of new sites being added to the literature yearly, yet data reuse and synthesis is uncommon in this emerging field. For the aeDNA community, the Neotoma Paleoecology Database is an important resource for data integration, because of Neotoma's large data volume (Neotoma holds over 10,000,000 paleo-observations over the past 2.6Myr across a range of terrestrial, lacustrine, and marine proxy types) and because of well-developed models for storing information about stratigraphic depth, age estimates, and age uncertainties, which are essential when integrating many records from many locations.

Here, we share recent efforts focused on the technical dimensions of integrating aeDNA data into the Neotoma Paleoecology Database while simultaneously building a community-focused structure of data governance using FAIR and CARE principles. These efforts include an initial focus on building templates for aeDNA metabarcoding data and their accompanying ASV/OTU tables for upload to Neotoma, updating the Neotoma data schema to support data and metadata specific to aeDNA research, and looking to integrate, where possible, other standards developed by the paleogenomics/genomics community. This integration will allow for aeDNA data to be compared to traditional paleoecological biodiversity data that is housed in Neotoma, including pollen, diatoms, vertebrates, plant macrofossils, ostracods, etc.

Combining the rapidly growing numbers of aeDNA datasets with paleoecological data, geochronological controls and age depth models, and other paleoenvironmental proxies contained within Neotoma has the potential to generate transformative inferences about macroecological processes over broad temporal and spatial scales.

Session: 6796330-2**7020495****21/10/25** | 17:00**Room:** Ballroom B2**ORAL • EN**

A multi-evidence approach for flagging taxonomic misidentifications in marine eDNA metabarcoding datasets

Presenter

Pieter Provoost

Authors

Pieter Provoost (UNESCO • Belgium)

Saara Suominen (Belgium)

Silas Principe (Belgium)

Ward Appeltans (Belgium)

Abstract

Environmental DNA (eDNA) metabarcoding is increasingly recognized as a cost-effective and non-invasive tool for biodiversity monitoring and early detection of invasive species in marine ecosystems. As a result, the number of eDNA metabarcoding datasets submitted to the Ocean Biodiversity Information System (OBIS) has grown substantially in recent years. However, this influx of data introduces new challenges related to data quality and reliability. A key step in eDNA bioinformatics pipelines is taxonomic annotation, where operational taxonomic units (OTUs) or amplicon sequence variants (ASVs) are assigned to taxa based on comparison to reference sequence databases, using approaches such as sequence similarity search or machine learning classification. The accuracy of these assignments is highly sensitive to factors such as the completeness and curation of the reference database, the taxonomic resolution of the marker used in the assay, and the choice of algorithm parameters such as identity thresholds or confidence cutoffs. Also, the relative ease and low cost of generating eDNA data has led to large volumes of records being produced, making it increasingly difficult to manually verify taxonomic identifications and detect potential errors. To address these issues, we present a method for flagging potential misidentifications in eDNA metabarcoding datasets, by integrating molecular evidence, reference database completeness, known species distributions, environmental parameters, and ecological traits.

Session

6960773-8

Symposium

21/10/25 | 16:00

Room: Tolima

Applied Research & Policy Integration - Global Knowledge & Policy (Contributed Oral Presentations)

Organizers

Francisco Pando

Henrique M. Pereira

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-8**7013952**

21/10/25 | 16:00

Room: Tolima

ORAL • EN

From Data to Diets: Building the World Food Map to Integrate Biodiversity and Strengthen Global Food Systems

Presenter

Chris Vogliano

Authors

Chris Vogliano (Wageningen University & Research • Netherlands)

Jenny Gallo (Bioversity International | CIAT • Colombia)

Abstract

The World Food Map is a novel, open-access geospatial platform developed to integrate edible biodiversity metadata and support the diversification of global food systems. Its purpose is to document and visualize commonly consumed foods, neglected and underutilized species (NUS), and centers of crop origins to empower decision makers for more diverse, sustainable and health-supportive diets and food systems.

Methods include the integration of over 1,500 foods identified through 1200+ key informant interviews across 100+ countries via the Global Diet Quality Project (2021–2025), categorized by food group and mapped by country. To address gaps in species representation, a global partner network is being developed—including Kew Gardens, Crops for the Future, and the Periodic Table of Food Initiative (PTFI)—to consolidate and harmonize existing data on taxonomy, nutrient composition, geolocation, climate resilience, and cultural significance. A landscape analysis and consultations with leading experts are guiding the identification and prioritization of edible species and associated metadata.

Results to date include the initial mapping of commonly consumed foods by country, identification of key bioregions and crop centers of origin for select crops, and integration of emerging food composition data from PTFI. Crops that emerge from this research will inform the next round of inspirational foods to be analyzed by PTFI using their standardized and high-resolution protocols for comprehensive biomolecule profiling. This collaboration will enable the identification of a globally representative list of culturally, nutritionally, and ecologically important foods, many of which currently lack composition data.

The project demonstrates the power of interdisciplinary collaboration and data interoperability to bridge nutrition, biodiversity, and policy. Conclusions highlight the importance of continued investment in open-access, metadata-linked systems like the World Food Map to drive evidence-based strategies for improving dietary diversity, climate resilience, cultural heritage, and food system sustainability.

Session: 6960773-8**7010216**

21/10/25 | 16:10

Room: Tolima

ORAL • EN

Mapping threats to the world's freshwater biodiversity

Presenter

Christophe Brabant

Authors

Christophe Brabant (McGill University • Canada)

Lars Iversen (McGill University • Canada)

Laura Pollock (McGill University • Canada)

Abstract

Earth has entered an era of unparalleled human activities, resulting in dramatic biodiversity loss worldwide. Nowhere is this more true than in freshwater ecosystems, which are both the richest habitats on Earth as well as the most threatened globally. Although the major anthropogenic pressures in freshwater ecosystems have been studied, effective conservation action remains limited due to the lack of spatial data on threats to freshwater species. Here, we use comprehensive data from the *International Union for the Conservation of Nature* to map the impact of 45 threats to all assessed freshwater amphibians, reptiles, fish, mammals, dragonflies, and molluscs. Using a novel threat mapping method, we create maps that illustrate the impact of threats to species, globally. Our results highlight the most acute overlap of threats occurring in Europe and northwestern Africa, with pollution and agriculture as the major threats to freshwater biodiversity. We find three threats that impact, on average, close to one-fourth of freshwater species anywhere on Earth. Additionally, we find an association between threat intensity and extinction risk, particularly for the impact of pollutants. Finally, we provide evidence that freshwater species are nearly universally more impacted than terrestrial ones, for any threat anywhere on Earth. Our assessment reports global evidence of the

far-reaching and dramatic impacts of anthropogenic activities. We hope the resulting threat maps can provide the baseline knowledge needed for future mitigation actions and conservation initiative in freshwater systems. A baseline urgently needed in order to support sustainable planning for various domains of human activities and assist in setting conservation priorities for watersheds at risk.

Session: 6960773-8**7020970**

21/10/25 | 16:20

Room: Tolima

ORAL • EN

How Socio-Ecological Research Supports Decision Making? A systematic review

Presenter

Cristian Cruz-Rodríguez

Authors

Cristian Cruz-Rodríguez (Université de Montréal • Canada)**Nicolas Urbina-Cardona** (Pontificia Universidad Javeriana • Colombia)**Maria Cecilia Londoño-Murcia** (Instituto Humboldt • Colombia)**Timothée Poisot** (Université de Montréal • Canada)

Abstract

Over the past 50 years, many tools have been developed to monitor biodiversity; yet, its loss continues around the world. In response, scientists, policymakers, and practitioners have created a variety of approaches aimed at generating useful information to support both biodiversity conservation and human well-being. Still, important gaps exist in how these different frameworks actually connect with real-world decision-making. To explore this issue, we conducted a systematic review to answer the question: What is the current state of research on socio-ecological systems and biodiversity, and how are these studies being used to inform decisions? We found that progress has been made over the past few decades. However, despite the range of methods now available, decision-making is still slow to adopt new perspectives and often remains anchored in the Millennium Ecosystem Assessment approach. Biodiversity studies also tend to rely on land cover as an indirect indicator instead of using direct measures. In many cases, research focuses on local-scale analyses that are valuable for understanding specific contexts but make it harder to apply insights more broadly. We also saw clear differences in how participatory processes are approached. In the Global North, research often emphasizes involving a wide range of stakeholders. In contrast, studies in the Global South typically focus on engaging local communities, reflecting different sociopolitical contexts and priorities. Another strong trend is the focus on developing new methods and tools. While these are undoubtedly important, there's been less attention paid to generating long-term, systematic knowledge about how socio-ecological systems work over time. Overall, our findings point to an urgent need to better connect socio-ecological research with decision-making. This means encouraging more inclusive, integrative, and context-aware approaches that reflect the complexity of both local realities and global challenges.

Session: 6960773-8**7019938**

21/10/25 | 16:30

Room: Tolima

ORAL • EN

Knowledge from non-English-language studies broadens contributions to conservation policy and helps to tackle bias in biodiversity data

Presenter

Louise McRae

Authors

Filipe Serrano (Universidade de São Paulo • Brazil)

Valentina Marconi (Institute of Zoology, ZSL • United Kingdom)

Louise McRae (Institute of Zoology, ZSL • United Kingdom)

Abstract

Local ecological evidence is key to informing conservation. However, many global biodiversity indicators often neglect local ecological evidence published in languages other than English, potentially biasing our understanding of biodiversity trends in areas where English is not the dominant language. Focussing on Brazil, a megadiverse country with a thriving national scientific publishing landscape, we assess how well bilingual literature searches can both improve coverage of biodiversity data for a country where English is not the primary language.

We conducted a comprehensive screening of articles containing abundance data for vertebrates published in 59 Brazilian journals (articles in Portuguese or English) and 79 international English-only journals. These were grouped into three datasets according to journal origin and article language (Brazilian-Portuguese, Brazilian-English and International).

Our results showed that including data published in Brazilian journals, especially those published in Portuguese, strongly increased representation of Brazilian vertebrate species (by 10 times) and populations (by 7.6 times) in the dataset. Meanwhile, international journals featured a higher proportion of threatened species. There were no marked differences in spatial or temporal coverage between datasets, in spite of different bias towards infrastructures. We found that population trends in international journals showed stronger and more frequent decreases in average abundance than those in national journals, regardless of whether the latter were published in Portuguese or English.

Collecting data from local sources markedly further strengthens global biodiversity databases by adding species not previously included in international datasets. Furthermore, the addition of these data helps to understand spatial and temporal biases that potentially influence abundance trends at both national and global level. We show how incorporating non-English-language studies in global databases and indicators could provide a more complete understanding of biodiversity trends and therefore better inform global conservation policy.

Session: 6960773-8

7020810

21/10/25 | 16:40

Room: Tolima

ORAL • EN

Monitoring Mammal Diversity in Suburban Forests: Snapshot USA at Purgatory Creek Natural Area, San Marcos, Texas

Presenter

Tatiana Velasquez-Roa

Authors

Tatiana Velasquez-Roa (Texas State University • United States)

Iván Castro-Arellano (Texas State University • United States)

Abstract

The Snapshot USA initiative represents a nationwide collaboration aimed at systematically monitoring mammal populations through standardized camera trap protocols across a wide range of ecological and urban gradients. As part of this initiative, the Integrative Ecology Lab from Texas State University has conducted a three-year study (2022–2024) in the Purgatory Creek Natural Area, a suburban forest ecosystem in San Marcos, Central Texas. Fifteen camera traps were deployed annually, resulting in 5,870 wildlife detections (99% were mammals). A total of 15 mammal species were identified, spanning 11 families and six taxonomic orders. The most frequently recorded species were white-tailed deer (*Odocoileus virginianus*, 60% of detections), wild boar (*Sus scrofa*, 14%), gray fox (*Urocyon cinereoargenteus*, 9%), northern raccoon (*Procyon lotor*, 7%), and Bryant’s fox squirrel (*Sciurus niger*, 3%). Less frequently detected species such as the coyote (*Canis latrans*), nine-banded armadillo (*Dasypus novemcinctus*), and virginia opossum (*Didelphis virginiana*) contributed to the site’s biodiversity profile. This study demonstrates the value of standardized, long-term monitoring in capturing spatial and temporal patterns of mammal diversity in suburban landscapes. The findings contribute to a growing national dataset that supports cross-site comparisons and informs conservation strategies in rapidly developing regions. By integrating local-scale data into a national framework, this work highlights the importance of open, interoperable biodiversity data for evidence-based urban planning and ecological resilience.

Session: 6960773-8

7016116

21/10/25 | 16:50

Room: Tolima

ORAL • EN

Mapping the use of biodiversity in Brazil

Presenter

Sonia Carvalho Ribeiro

Authors

Sonia Carvalho Ribeiro (Federal University of Minas Gerais UFMG • Brazil)

Abstract

We explore the challenges involved in combining, harmonizing, and analyzing diverse datasets related to the production, trade, conservation, and socio-economic value of biodiversity-based products and services across in Brazil. This is critical for advancing sustainable development, conservation strategies, and the valuation of sociobiodiversity. Data integration in biodiversity markets involves: Linking **ecological data** (e.g., species distribution), with **economic data** (e.g., prices, trade volumes, value chains) and **socio-cultural data** (e.g., traditional knowledge, community use) to inform policy, regulation, and sustainable development strategies. By mapping the utilization of native species (NS) from Brazil's biodiversity across eleven industrial sectors: foodstuffs, beverages, textiles, clothing, leather, wood, pulp and paper, biofuels, pharmaceuticals, rubber and furniture we show that there exists a diverse range of NS use in industrial products (48%) and activities (73%). These economic activities represent potential annual exports of approximately USD \$50 billion. However, we found that only 1% of the potential business, USD \$500 million of annual exports, is consolidated and can be traced to such products. We show that biodiversity markets and larger annual revenues locate in municipalities away from places in which biodiversity products originate. Therefore, the biodiversity business in Brazil remains largely untapped. This prompts a critical examination of the role of biodiversity within the Brazilian industry and its alignment with the Brazilian Biodiversity Law and the Nagoya Protocol. Our study is a pioneering effort that provides strategic recommendations.

Session: 6960773-8**7021003**

21/10/25 | 17:00

Room: Tolima

ORAL • ES

Tecnologías y archivos de la biodiversidad. Una aproximación histórica a la conformación y conservación del conocimiento botánico y ambiental.

Presenter

Verónica Matallana-Chaves

Authors

Verónica Matallana-Chaves (Universidad Nacional de Colombia • Colombia)

Abstract

Esta presentación explora el impacto de las tecnologías digitales en la reinterpretación y democratización de los archivos botánicos en Colombia al enfocarse en la integración y el uso de datos científicos históricos del Instituto de Ciencias Naturales de la Universidad Nacional de Colombia, que abarcan desde el siglo XIX hasta el siglo XXI. Las colecciones albergadas en este instituto, y en alto riesgo de pérdida por problemas infraestructurales, no solo documentan la biodiversidad de la región sino que reflejan las dinámicas coloniales, epistemológicas y sensoriales subyacentes a la producción de conocimiento botánico.

La investigación parte de mi tesis, “Desecación de la observación. Un análisis sensorial de la conformación del Herbario de José Jerónimo Triana”, la cual integró metodologías disciplinares de la historia, la botánica y los estudios sociales de la ciencia. El diálogo establecido entre las prácticas de colecta botánica en distintos momentos de la historia de la ciencia en Colombia me permitió examinar cómo las herramientas digitales —desde bases de datos de libre acceso hasta plataformas interactivas— han transformado la accesibilidad y la reinterpretación de estos datos.

Conectar la ciencia de datos y la historia ambiental con los debates sobre nuevas ontologías, la descolonización de las prácticas biológicas y los discursos sobre conservación ambiental se torna importante para plantear el debate sobre cómo las herramientas digitales moldean los registros botánicos y los usos —contemporáneos e históricos— de los repositorios de biodiversidad. Al destacar tanto el potencial como los retos de estas tecnologías, la investigación contribuye a una reflexión crítica sobre la conformación y acceso de datos botánicos en la construcción de futuros más inclusivos y participativos en la biología.

Session: 6960773-8**6999910**

21/10/25 | 17:10

Room: Tolima

ORAL • EN

Cutting Out the Middlemen: How Blockchain Tools Can Decolonize Conservation Finance

Presenter

Gabriel Nunes

Authors

Gabriel Nunes (GainForest • Brazil)

David Dao (GainForest | ETH Zurich • Switzerland)

Abstract

Despite billions invested in conservation annually, less than 1% reaches Indigenous peoples and local communities performing critical ecosystem stewardship (Gjefsen, 2021). This exclusion persists because funding structures prioritize large international corporate intermediaries over direct investment in frontline conservationists. Additionally, funding databases only report the first recipient in the chain of granting and regranting, making it impossible to track if funds reach local communities (Rainforest Foundation Norway, 2024).

We present an alternative: Ecocerts, blockchain-based impact certificates developed by GainForest (a non-profit organization focused on data-driven conservation) and the Hypercerts Foundation. Ecocerts create immutable records of conservation impact achieved by local communities, offering a direct and transparent mechanism to fund conservation work.

These digital impact certificates connect grassroots organizations with individuals and institutions seeking to support conservation. Communities quantify and validate their ecological impact through diverse data sources, including satellite imagery, biodiversity monitoring, and community-reported metrics, providing communities with both international visibility and verified access to funding.

In a recent case study, GainForest's Gitcoin round 23, "Hypercerts for Nature Stewards," employed quadratic funding—a mechanism that weights contributions based on the number of donors rather than contribution size—to distribute funds to 29 grassroots projects in 15 days. The initiative attracted 921 donors who contributed \$4,119.53 in direct funding in two weeks, which activated a matching pool of 20,000 USD. Additionally, the Celo Foundation distributed its climate-focused funds to eight local initiatives through the Ecocerts platform, totaling 2,175 CEL0 tokens (approximately \$3,500) per initiative. Blockchain-based smart contracts, reduced fund's distribution time from months to less than three days. Through Ecocerts, we showcase a model that: a) Democratizes conservation finance making it truly participatory; b) Centers local data as evidence of impact, ensuring ground up accountability; c) Channels resources directly to communities for verifiable conservation efforts; d) Replaces top-down reporting with community-led verification

Session: 6960773-8**7014170**

21/10/25 | 17:20

Room: Tolima

ORAL VIRTUAL • EN

Global spring ecosystem ecology and conservation

Presenter

Lawrence Stevens

Authors

Lawrence Stevens (Springs Stewardship Institute • United States)

Abstract

Springs ecosystems develop where groundwater reaches the earth's surface, both on land and underwater. Small but abundant, bio- culturally and economically diverse and interactive, springs support intrinsic and extrinsic attributes of the landscapes in which they emerge; however, springs are widely appropriated and threatened by humans. We present a global review of springs' ecological characteristics and values, describing management and conservation solutions to improve scientific understanding and stewardship. 1) Springs are natural windows into groundwater, humanity's last reserve of freshwater. 2) They provide critical baseflow for most rivers on Earth, but have been widely ignored in river hydrogeology. 3) Springs are hotspots of endemic species, in arid, temperate, tropical, and submarine settings, sustaining many endangered species and many thousands of rare, endemic, poorly- known, and unprotected springs-dependent species.

4) North American springs commonly support 10-25% of regional vascular plant gamma-diversity. 5) By functioning as ambush habitat for predators and stop-over habitat for migrating species, springs exert broad keystone ecological interactivity across landscapes. 7) Their cultural significance includes sites inhabited by divine beings, where miracles occur, and where human cultures have emerged. 8) Springs globally sustain subsistence agriculture, domestic, and emergency water supplies for more than a billion people, and their economic values is multiple billions of dollars/yr through those uses, hot springs balynology, recreation, and water bottling. Mitigating anthropogenic impacts to groundwater the supported spring requires an insular conservation strategy differing from those for protection of large landscapes or wide-ranging species, one focused on care for small, vital habitat patches within landscapes. Such a strategy requires sound scientific data, agreement on lexicon and classification, and strong educational outreach to youth, the public, and managers, and simple, effective and incentivized methodologies. The Springs Stewardship Institute's Springs Online database is designed for these purposes. What's good for springs is good for all things.

Session

6799145-2

Symposium

21/10/25 | 16:00

Room: Caldas

Spatial biodiversity data products for reporting and decision-making - are we there yet? (Part 2)

Organizers

Tobias Andermann

Jakob Nyström

Description

Addressing the global biodiversity crisis requires spatial data products showing biodiversity metrics – current state, changes, and scenarios – that are interpretable and actionable for policy and decision-making. Examples of use cases include biodiversity monitoring, reporting in adherence with the GBF, prioritization of conservation projects, spatial planning for infrastructure projects, and corporate impact and risk reporting. Producing such maps requires predictive biodiversity models that can learn the complex relationships between biodiversity, environmental factors and anthropogenic pressures. In this session, we deep dive into the state-of-the-art of predictive biodiversity modeling on local, national, and global scales. We highlight and discuss which types of models are most appropriate for different objectives and contexts. Further, we examine best practices for evaluating predictive performance and quantifying uncertainty in such models. We critically discuss to what extent current data products are appropriate for making decisions with potentially substantial financial and ecological consequences. This session will be a hybrid of scientific talks, panel discussions, and audience engagement. The aim is to identify current limitations in spatial biodiversity modeling and to map a way forward to improving the state-of-the-art in this field.

Session: 6799145-2**7020479**

21/10/25 | 16:05

Room: Caldas

ORAL • EN

The Agrobiodiversity Crisis: The urgent need for tools to monitor the global decline of crop biodiversity

Presenter

James Borrell

Authors

James Borrell (Royal Botanic Gardens Kew • United Kingdom)

Sophie Jago (United Kingdom)

Felix Lim (United Kingdom)

Carolina Tovar (United Kingdom)

Sam Pironon (Queen Mary University of London • United Kingdom)

Marybel Soto Gomez (United Kingdom)

Abstract

Globally we face two concurrent and interlinked biodiversity crises. While the rapid decline in wild biodiversity is well documented, the magnitude and rate of decline in agrobiodiversity is comparatively overlooked. Agrobiodiversity, the species and genetic diversity of plants and animals we use for agriculture, underpins global food systems and is the facet of biodiversity upon which we most directly depend.

Without food security there can be little progress towards the Global Biodiversity Framework goals. Whilst indicators for monitoring wild biodiversity are proliferating, a major gap exists in our capability to monitor agrobiodiversity. This talk will illustrate how existing datasets and tools from conservation can be co-opted to urgently monitor agrobiodiversity – from farms to nations – and highlight persistent gaps where novel tools and metrics are needed. We identify challenges, including predictive models that can integrate the ecological, socioeconomic and agronomic drivers that shape patterns of crop diversity. We report examples from Ethiopia and Peru seeking to identify spatial hotspots of threatened agrobiodiversity through a framework combining remote sensing, bioclimatic modelling, landscape genomics, socioeconomic surveys, crop production statistics, ex situ collection databases and competing land use pressures. We discuss how decision makers can be empowered to act on these data through *in situ* and *ex situ* conservation, to safeguard the sustainability, resilience and productivity of food systems and help meet humanity's needs at least cost to nature.

Session: 6799145-2**7020441**

21/10/25 | 16:20

Room: Caldas

ORAL • EN

Harnessing biodiversity, trait, and satellite data to forecast global agricultural pest risk with AI: A scalable framework for biodiversity monitoring

Presenter

Colleen Miller

Authors

Colleen Miller (University of Minnesota • United States)

Megan Barkdull (LA County Natural History Museum • United States)

Richard Sharp (WWF • United States)

Rebecca Chaplin-Kramer (WWF • United States)

Justin Johnson (University of Minnesota • United States)

Sara Emery (Cornell University • United States)

Mia Lippey (University of California, Davis • United States)

David Mulla (University of Minnesota • United States)

Abstract

Understanding where and when agricultural pests will cause damage is a longstanding ecological and food security challenge, and one now made urgent by rapid climate and land-use change. This presentation shares the goals and early outputs of a new interdisciplinary project that combines biodiversity data, evolutionary and ecological principles, and remote sensing in a knowledge-guided AI framework to forecast pest outbreaks globally.

We focus on Lepidopteran pests, economically important, well-documented insects with strong ecological and phylogenetic data coverage, and explore how functional traits (e.g., dispersal mode, body size, host specificity), evolutionary history, and environmental change interact to shape global patterns of pest risk. Inspired by previous work creating a pest control living database which combined field measures, trait data and earth observations, we pilot an AI-driven approach to global biodiversity modeling that includes phylogenetics. Our models integrate satellite-derived vegetation dynamics, climate anomalies, and historical land use with Lepidopteran data to generate spatiotemporal forecasts of outbreak likelihood under varying environmental contexts.

Rather than relying solely on data-driven machine learning, we use knowledge-guided AI techniques that incorporate biological constraints, such as thermal tolerances and known host associations, directly into predictive architectures. This approach improves generalizability across space and time and aligns outputs with known biological mechanisms. We expect this novel integration of AI techniques with ecological and evolutionary information to demonstrate improved accuracy and interpretability compared to traditional statistical models and uninformed ML methods.

Our goal is to produce scalable, policy-relevant insect biodiversity data products that anticipate biological responses to global change. We highlight how this framework supports pest monitoring and decision-making for conservation and agricultural resilience. This talk will preview our modeling approach, share early framework approaches, and invite feedback on aligning biodiversity AI products with user needs for global pest models integrated across biology and earth observation science.

Session: 6799145-2**7013337**

21/10/25 | 16:35

Room: Caldas

ORAL • EN

Data uncertainties in spatial conservation plans: which ones are important?

Presenter

Heini Kujala

Authors

Heini Kujala (Natural History Museum of Finland, University of Helsinki • Finland)

Abstract

The urgency of reversing biodiversity decline is reflected in the increasing ambition of national and international conservation policies, such as the Kunming–Montreal Global Biodiversity Framework and the EU Biodiversity Strategy and Restoration Law, to protect and restore nature. Spatial conservation prioritisation is a powerful conservation planning tool that optimises the placement of conservation measures in space, so that benefits can be simultaneously maximised for many species within budgetary constraints. These tools are increasingly used to guide both conservation and land use decision-making. Uncertainties in input data and how these affect conservation solutions, have long been of central interest to both conservation scientists and practitioners. Because conservation priority maps are underpinned by biodiversity data, the greatest effort has traditionally focused on perfecting their accuracy. What is perhaps less well understood is that in spatial resource-allocation problems, some data influence the final solution far more strongly than others. Resolving uncertainties in these highly influential data layers is thus more important for the stability and accuracy of the priority solution. Using examples from different conservation case studies, I show that uncertainties in conservation costs, threats or habitat condition often outweigh the impact of individual biodiversity data on conservation plans. In addition, I show that the decisions we make on which data to include and how we modify them before their use may have larger impacts on the prioritisation result than uncertainties in any individual species data.

Understanding how different data types and their use affects spatial priorities is useful as it helps to focus our data improvement efforts to those uncertainties that matter.

Session: 6799145-2

7015931

21/10/25 | 16:50

Room: Caldas

ORAL • EN

Integrating eDNA and Ecological Modeling for Early Biodiversity Assessment: A Tool for ESG, MRV, and Compliance with International Standards

Presenter

Daniel Silva Sierra

Authors

Daniel Silva Sierra (Corporación Científica Ingeobosque • Colombia)

Ana Milena Jiménez Guerra (Corporación Científica Ingeobosque • Colombia)

Laura Floréz Botero (Corporación Científica Ingeobosque • Colombia)

Abstract

Rapid and effective characterization of soil and aquatic biodiversity is key to meeting international conservation and sustainability standards. This study presents a methodological workflow that integrates environmental DNA (eDNA) with ecological niche modeling to anticipate the presence of threatened and endemic species. Soil and water samples were collected from 95 sites in the Orinoquia region, and processed by NatureMetrics® using metabarcoding techniques, resulting in FASTQ files and abundance tables. Sequences were clustered into operational taxonomic units (OTUs), and for each, ecological niches were modeled using MaxEnt, based solely on eDNA detection points and environmental variables from WorldClim (bioclimatic) and SoilGrids (edaphic). In parallel, niche models were developed for known endemic species in the region. Spatial overlap between niches was quantified using the Schoener’s D index, with significant similarity defined as $D = 0.70$. This comparison enabled the identification of morphospecies whose potential distributions strongly overlap with known endemics, despite lacking reference genomes. Results suggest that spatial patterns derived exclusively from eDNA enable rapid and efficient screening for critical habitats, facilitating compliance with Performance Standard 6 (IFC, IDB). Furthermore, the approach aligns with the Taskforce on Nature-related Financial Disclosures (TNFD) by providing robust spatial metrics for biodiversity-related risk management. The methodology also strengthens Monitoring, Reporting, and Verification (MRV) activities for projects involving carbon credits, biodiversity credits, and habitat banking. Finally, this tool directly contributes to Sustainable Development Goals (SDGs) 6, 13 and 15, by enhancing technical capacities for terrestrial conservation and proactive assessment of environmental impacts linked to climate change, supporting evidence-based decision-making aligned with international standards.

Session

6803288

Symposium

21/10/25 | 16:00

Room: Valle

From Data to Decisions: Advancing Biodiversity Monitoring through Species Population EBVs

Organizers

Elkin Tenorio

Walter Jetz

Helena Olaya

Melodie McGeoch

Nerieth Leuro

Laura Garcia

Juan Carlos Rey

Description

This symposium explores methodological advances and applications of Species Population Essential Biodiversity Variables (EBVs). As the UN Global Biodiversity Framework drives demand for standardized biodiversity metrics, this session provides a platform to share experiences in developing Species Population EBVs that effectively integrate disparate raw data into standardized information products. Participants will explore the complete workflow of creating robust biodiversity information - from initial data curation of field observations, remote sensing data, and biological collections, to model development and evaluation, particularly addressing challenges that arise in the absence of expert knowledge.

The session welcomes contributions showcasing how Species Population EBVs capture critical biodiversity dynamics including: (i) contraction, shifts, and expansion of geographic distributions (including potential extinctions and alien invasions), and (ii) losses and gains in species population sizes across large spatial, temporal, and taxonomic scales. Through this symposium, we aim to foster dialogue about best practices, tools, and methodologies while demonstrating how these models can effectively contribute to environmental decision-making - from conservation planning to ecosystem management and climate change adaptation. By featuring data integration methodologies, large-scale empirical findings, specific use case demonstrations, and aggregate indicator products, the session provides a comprehensive horizon scan of current Species Population EBV production and identifies key opportunities for advancing research and application in support of biodiversity monitoring worldwide.

Session: 6803288**7018620**

21/10/25 | 16:05

Room: Valle

ORAL • EN

Developing Species Population EBVs by Standardizing Participatory Science Data through Machine Learning Workflows to Track Avian Population Dynamics

Presenter

Tom Auer

Authors

Tom Auer (Cornell Lab of Ornithology • United States)

Abstract

The Kunming-Montreal Global Biodiversity Framework (GBF) underscores the urgent need for cost-effective and standardized metrics for monitoring species' populations at scale. Participatory science platforms like eBird provide unprecedented volumes of observational data on biodiversity, but translating this wealth of information into robust Essential Biodiversity Variables (EBVs) presents significant analytical challenges. These include integrating information about interobserver variation, spatial and temporal biases in data collection, and changes in observation processes over time. The eBird Status and Trends project addresses these challenges using state-of-the-art analytical approaches, including Double Machine Learning trend models, to generate relative abundance estimates for almost 3000 species and trends estimates for almost 1000 species, with data volumes growing at a rate that would at least double or triple this taxonomic coverage in the next five years. These approaches integrate species observational data with large-scale remote sensing data to generate standardized, high-resolution data products on biodiversity that are crucial for conservation decision-making, policy, and planning under the GBF. Here we describe the workflow for generating two Species Population EBVs from eBird participatory science data. The first is a "proportion of population" metric at 3km and weekly resolution that can serve as a standardized proxy for species density, useful for identifying areas of high concentration and importance, particularly for migratory species. The second is estimated trends in relative abundance at 27km spatial resolution, providing critical information on population loss and gain across species' ranges. We will demonstrate how these methods can be adapted to other regions and taxa, present use cases highlighting their value in biodiversity monitoring, management, and decision-making, and discuss extensions to estimate Community Composition EBVs.

Session: 6803288**7020826**

21/10/25 | 16:20

Room: Valle

ORAL • EN

Production, delivery, and use of Global Species Population EBVs

Presenter

Walter Jetz

Authors

Walter Jetz (Yale University • United States)

Abstract

This talk will give a general introduction to Species Population (SP) EBVs and pinpoint examples, challenges and opportunities for their successful implementation and use. I will first discuss the motivation and characteristics of the SP EBV concept, and the range of monitoring and planning use cases it addresses. I will then give an overview of the suite of data harmonization, integration, and modelling steps and solutions required for an empirical delivery of SP EBVs at scale. I will highlight example implementations and specifically go over the end-to-end solution provided by Map of Life. I will close by giving examples of the growing range and depth of use cases these global empirical products are enabling and discuss the tremendous need and potential of globally standardized, fine-scale information for monitoring and managing biodiversity change.

Session: 6803288**7020137**

21/10/25 | 16:35

Room: Valle

ORAL VIRTUAL • EN

Expanding Wallace EcoMod to calculate biodiversity change indicators from species distribution models for conservation management and planning

Presenter

Mary Blair

Authors

Mary Blair (American Museum of Natural History • United States)

Andrea Paz (Canada)

Gonzalo Pinilla-Buitrago (Mexico)

Daniel López-Lozano (United States)

Bethany A. Johnson (United States)

Beth Gerstner (United States)

Jamie Kass (Japan)

Elkin A. Noguera-Urbano (Colombia)

Jorge I. Velásquez-Tibatá (Colombia)

Robert P. Anderson (United States)

Abstract

Wallace EcoMod is an open-source, instructive, and interactive R-based software application with a graphical user interface that supports accessible, open, expandable, flexible, interactive, instructive, and reproducible species distribution modeling (SDM) workflows. Wallace allows users to build SDMs by harnessing existing R packages in a Graphical User Interface (GUI). Our development team continually maintains and advances Wallace in response to user-community feedback, such as recent enhancements for metadata reporting and the ability to manage multiple species' models in a single session. Here, as a result of a co-development process with the Colombia Biodiversity Observation Network (BON), we describe an expansion of Wallace's functionalities aimed at conservation management and planning. We have added functions from two new R packages (maskRangeR and changeRangeR) that enable quantifications of species' geographic ranges by post-processing SDM outputs with remote sensing and other data. Further, Wallace users can now calculate biodiversity change metrics such as range size, the upper bounds of IUCN's extent of occurrence and area of occupancy, percent suitable land cover, protected area representativeness, and projected trends under future scenarios. Users can also calculate and compare measures of species richness and endemism by overlapping SDM outputs across multiple species. We also have now achieved integration between Wallace and the existing Colombia BON tool BioModelos, which enables expert validation of occurrence records and species range estimates. Wallace can now directly access vetted occurrence data from BioModelos and return a payload containing the masked model and biodiversity metrics, as well as relevant metadata, facilitating expert review and iterative model refinement. These enhancements not only advance regional conservation workflows, but can now be expanded for interoperability with other regional or global biodiversity platforms.

Session: 6803288**7020012**

21/10/25 | 16:30

Room: Valle

ORAL • EN

Biodiversity Monitoring Strategy for Chile: Leveraging Standardized Environmental Reporting and Public Baseline Initiatives

Presenter

Juan Saez-Hidalgo

Authors

Juan Saez-Hidalgo (Institute of Ecology and Biodiversity • Chile)**Paola Poch** (Institute of Ecology and Biodiversity • Chile)**Julián Caro** (Institute of Ecology and Biodiversity • Chile)**Daniel Ortiz** (Institute of Ecology and Biodiversity • Chile)**Rosvita Gonzáles** (Institute of Ecology and Biodiversity • Chile)**Karina Martínez-Tillería** (Institute of Ecology and Biodiversity • Chile)**Ricardo Segovia** (Institute of Ecology and Biodiversity • Chile)

Abstract

Chile is currently advancing two key public initiatives essential to modernizing biodiversity data management: standardized biodiversity data reporting required by environmental assessments and the creation of a comprehensive public baseline designed to track temporal dynamics across 11 environmental components, including terrestrial, aquatic, and marine biodiversity. These initiatives present an opportunity to implement a high-resolution, nationwide biodiversity monitoring strategy. Nonetheless, significant challenges remain, particularly in integrating and standardizing sampling event data. To overcome this, the BIODATA team at the Institute of Ecology and Biodiversity (IEB) has developed field mappings to align Chilean biodiversity reporting with the Humboldt Core extension of the Darwin Core standard and proposed a structured data model to capture biodiversity sampling events. This facilitates the integration of data reporting by environmental assessments into key platforms such as the Plataforma Tecnológica Línea de Base Pública (PTLBP), developed by Chile's Ministry of Environment. While further enhancements in data quality are needed, these foundational steps significantly advance Chile's capability for coordinated and effective long-term biodiversity monitoring.

Session: 6803288**7020619**

21/10/25 | 17:05

Room: Valle

ORAL VIRTUAL • EN

Delivering 1km resolution global species distribution EBV: progress and challenges

Presenter

Beth Gerstner

Authors

Beth Gerstner (United States)

Kevin Winner (Yale University • United States)

John Wilshire (Yale University • United States)

Walter Jetz (Yale University • United States)

Abstract

As international conservation efforts aim to address biodiversity loss driven by climate change and anthropogenic disturbance, accurate, high-resolution data on species distributions—captured as species distribution essential biodiversity variables (SD EBVs)—has become a critical resource for policymakers and stakeholders. Currently, much of this data is publicly accessible through species range maps (e.g., IUCN Red List) and occurrence records (e.g., GBIF). However, these sources are fundamentally incomplete and subject to various biases. Thus, building a comprehensive SD EBV framework at spatial resolutions relevant to conservation action requires scalable species distribution models (SDMs). Our team has been developing and refining global 1 km² SDMs that accommodate a wide range of taxa—from vertebrates to invertebrates, common to rare species, and generalists to specialists—each with distinct modeling challenges. A key advancement has been the implementation of target group background (TGB) sampling, which mitigates sampling bias by drawing background points from the same distribution as occurrences from a group of taxonomically or ecologically relevant species. Early applications of this approach have improved model performance, especially in under-sampled regions and across geopolitical and biogeographic gradients. In this talk, we will share insights from our work producing, curating, and validating global SD EBVs, and highlight the integration of novel approaches, such as TGB sampling, to improve model predictions. We will also discuss ongoing challenges— including data gaps, computational constraints, and the complexity of modeling across taxa—and outline the next steps toward building a comprehensive, robust global SD EBV framework to support biodiversity conservation.

Session **6960773-3**

Symposium

21/10/25 | 16:00

Room: Cauca

Digital Technologies & AI (Contributed Oral Presentations)

Organizers
Andre Zerger

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-3**7014935**

21/10/25 | 16:00

Room: Cauca

ORAL • EN

What matters for cross-taxonomic bioacoustic models ?

Presenter

Gagan Narula

Authors

Gagan Narula (EarthSpeciesProject • Switzerland)

David Robinson (EarthSpeciesProject • Australia)

Marius Miron (EarthSpeciesProject • Spain)

Masato Hagiwara (EarthSpeciesProject • United States)

Keen Sara (EarthSpeciesProject • United States)

Milad Alizadeh (EarthSpeciesProject • United Kingdom)

Emmanuel Chemla (EarthSpeciesProject • Mexico)

Matthieu Geist (EarthSpeciesProject • France)

Olivier Pietquin (EarthSpeciesProject • France)

Abstract

Recent work has shown that cross-taxonomic transfer learning does occur in bioacoustics AI, such as from birds to whales (Ghani et al 2023) and human speech to gibbon vocal identity (Cauzinille et al 2024). Although these are promising results, they are limited in scope by the number of taxonomic groups used for training and evaluation, the size of the training data, and the number of ethological tasks.

Predictive model outputs trained for classification and detection tasks are constrained to a fixed number of sound categories, and fine-tuning on a new task essentially requires changing the model architecture. We address these challenges in our NatureLM-audio foundation model. Trained on a large and diverse audio-text dataset (> 29,000 hrs of audio) with > 40 tasks such as species classification, captioning, lifestage estimation, counting individuals etc., NatureLM-audio (Robinson et al 2024) is the first foundational audio-language model that can generate a natural language response to a natural language query on a reference audio. We show that the model is able to perform a number of bioacoustic evaluation tasks zero-shot (i.e. without any task specific examples) and generalizes to unseen taxonomic groups exhibiting significant knowledge transfer. Notably, our ablation experiments demonstrate positive transfer from human speech to animal vocalizations. However, a number of data-centric questions remain: a) How should the data be mixed / distributed across different taxonomic groups to maximize transfer to unseen or rarely recorded groups? b) Does augmentation with synthetic bioacoustic data help? and c) Can weak and/or strong annotations from sound detection models help improve data quality and encourage transfer? d) Can we benefit from including large, unlabelled passive acoustic monitoring datasets in a self-supervised learning setting? We present the results of experiments with self-supervised audio and audio-text embedding models to probe what matters most for large scale cross-taxa transfer.

Session: **6960773-3****7019725**

21/10/25 | 16:10

Room: Cauca

ORAL • EN

Integrating bioacoustic monitoring, AI, and occupancy models to assess black-and-white ruffed lemur (*Varecia variegata*) distribution in southeastern Madagascar

Presenter

Carly Batist

Authors

Carly Batist (Conservation International • United States)

Marconi Campos-Cerqueira (WildMon • Puerto Rico)

Nelson Buainain (WildMon • Brazil)

José Ribeiro Jr. (WildMon • Brazil)

Kris Harmon (WildMon • Puerto Rico)

Rija Rafamantanantsoa (University of Antananarivo • Madagascar)

Georges Razafindrakoto (Centre ValBio • Madagascar)

Mariah Donohue (University of Binghamton • United States)

Andrea Baden (CUNY Hunter College • United States)

Abstract

Black-and-white ruffed lemurs (*Varecia variegata*), a Critically Endangered primate, are keystone seed dispersers and pollinators in Madagascar's eastern rainforests. Their highly-frugivorous diet, sensitivity to disturbance, and unique reproductive traits make them particularly vulnerable to habitat loss and fragmentation. Despite their ecological importance, the species' current distribution in the Corridor Forestier d'Ambositra Vondrozo (COFAV)—a critical forest link between Ranomafana and Andringitra National Parks—remains poorly understood. To address this gap, we used passive acoustic monitoring (PAM) and machine learning (ML) to survey ruffed lemurs across the COFAV. We deployed autonomous recorders at 30 sites between December 2021 and June 2022, collecting over 550,000 minutes of audio. A subset of recordings was manually labeled for lemur call presence and absence. These data were then used to train a convolutional neural network (CNN) to automatically detect calls across the full dataset. We validated the positive detections from model outputs to remove false positives, and then used these detections alongside environmental variables in Bayesian spatial occupancy models. Ruffed lemurs were detected at just 10 sites, all located in the northern third of the corridor. No detections occurred south of Ambohimahamasina (halfway between the national parks), where a broad deforested area may now act as a dispersal barrier. We found that occupancy was positively associated with higher NDVI values, a proxy for vegetation health. Our study is among the first to apply an integrated PAM-ML-occupancy modeling pipeline for lemur conservation. It provides critical updated distribution data for a species difficult to survey by traditional means and highlights the utility of integrated technological stacks in conservation.

Session: 6960773-3**7020545**

21/10/25 | 16:20

Room: Cauca

ORAL • EN

Spyfish Aotearoa: streamlining and automating the marine reserve reporting pipeline - application of data-intensive science for policy implementation

Presenter

Kalindi Fonda

Authors

Kalindi Fonda (Wildlife.ai • New Zealand)

Abstract

How is tech changing the way rangers of the Department of Conservation in New Zealand (DOC) are doing marine reserve reporting? Come learn about what we built and the wins and opportunities created by Spyfish Aotearoa, a joint project by Wildlife.ai and DOC.

From standardized data input, along pipelines that streamline processes and tasks, to analyzing videos with machine learning and citizen science; it is changing the way marine reporting is done and the time it takes to do so.

On top of that, we'll share how we are collaborating with the University of Gothenburg, to make what we are building accessible to others. We are creating SUBSIM, an open source infrastructure that can be used by similar projects for underwater researchers.

Happy to chat with other speakers at the symposium, as I imagine we'll have some similarities in our talks, in order to focus on the most interesting/relevant part of this project.

Session: 6960773-3**7020060**

21/10/25 | 16:30

Room: Cauca

ORAL • EN

A user-friendly power analysis tool for confidently detecting biodiversity change

Presenter

Jake Lawlor

Authors

Jake Lawlor (McGill University • Canada)

Eden Tekwa (McGill University • Canada)

Jennifer Sunday (McGill University • Canada)

Abstract

Accurate monitoring programs are essential for detecting and attributing biodiversity change, but magnitudes of change will vary across space, requiring different sampling efforts and methods for confident detection. Here, we present an open-source simulation-based power analysis tool, which provides custom guidance for designing sampling schemes that confidently detect biodiversity change. First, we describe the method, which downsamples user-provided pilot data from any ecological system to assess the confidence with which biodiversity changes can be detected. Then, we showcase the implementation of the tool to answer a practical monitoring question: How many samples will we need in order to confidently detect changes in species richness within Canada's marine protected area network? We use model outputs of species' present and future distribution ranges to establish expectations of richness change across over 600 marine reserves, then, we apply our tool to empirical biodiversity data from eDNA metabarcoding pilot surveys in two distinct ocean regions to identify the number of eDNA samples needed to confidently detect the expected levels of biodiversity change regionally. We use these results to outline policy-relevant recommendations for effective monitoring. Finally, we demonstrate additional utilities of our tool for practitioners, including analyzing power of existing sampling schemes, identifying sampling effort necessary for confidently detecting thresholds of change that trigger policy actions, and comparing power and costs between sampling methods, and we discuss the transferability of our framework to monitoring schemes in other regions and systems.

Session: 6960773-3

7021015

21/10/25 | 16:40

Room: Cauca

LIGHTNING TALK • ES

Monitoreo Participativo en Humedales de La Mojana: Ciencia Viva para la Restauración

Presenter

Bibiana Gómez Valencia

Authors

- Bibiana Gómez Valencia (Instituto Humboldt • Colombia)
- Carlos Mario Gonzalez Charrasquiel (Instituto Humboldt • Colombia)
- Klaudia Cárdenas Botero (Instituto Humboldt • Colombia)
- Ana Carolina Santos Rocha (Instituto Humboldt • Colombia)
- Fabián Garzón (Instituto Humboldt • Colombia)
- Paola Isaacs (Instituto Humboldt • Colombia)
- Ronald Antonio Ayazo Toscano (Instituto Humboldt • Colombia)
- Alejandra Castaño (Instituto Humboldt • Colombia)
- Daniela Martínez (Instituto Humboldt • Colombia)

Abstract

Se evaluó el progreso de las acciones de restauración ecológica mediante indicadores estructurales, funcionales y socioecosistémicos del ecosistema de humedal en la Mojana. El monitoreo fue integrado desde la etapa de diseño hasta la implementación de las intervenciones, siguiendo principios de gestión adaptativa basada en datos. La evaluación periódica se estructuró con base en el marco metodológico de *Monitoreo de la biodiversidad del* Instituto Humboldt. Los indicadores monitoreados incluyeron: **Estructurales:** composición y cobertura vegetal. **Funcionales:** dinámica hidrológica y productividad ecosistémica. **Socioecosistémicos:** percepción comunitaria y generación de empleo local. Como resultado, se generaron **54 empleos locales**, de los cuales **el 70% fueron ocupados por mujeres**. Jóvenes y mujeres participaron activamente en la recolección de datos, el seguimiento y los procesos de toma de decisiones. El esquema también incorporó recomendaciones de expertos y saberes locales, fortaleciendo la apropiación comunitaria del monitoreo como una herramienta viva de gobernanza ambiental. Este caso constituye un modelo replicable de **monitoreo participativo e inclusivo**, donde los datos no solo informan: son co-producidos y movilizados por las comunidades. Destaca por su articulación entre ciencia, restauración ecológica y equidad de género, promoviendo datos que *viven* en las decisiones locales.

Session: 6960773-3**7020548**

21/10/25 | 16:50

Room: Cauca

ORAL • ES

Detección automatizada del roedor tuco-tuco (*Ctenomys magellanicus*) en imágenes de cámaras trampa mediante inteligencia artificial

Presenter

Darío Moreira

Authors

Javier Flores (Cienciambiental • Chile)

Jorge Homero Márquez Taffo (Chile)

Álvaro Ly (Cienciambiental • Chile)

Valentina Romero (Cienciambiental • Chile)

Darío Moreira (Cienciambiental • Chile)

Stephanie Orellana Bello (Cienciambiental • Chile)

Antonio Tironi (Cienciambiental • Chile)

Alex Oporto (Cienciambiental • Chile)

Sergio Moraga (Cienciambiental • Chile)

Rodrigo Ibaceta (Cienciambiental • Chile)

Abstract

La identificación eficiente de fauna en imágenes capturadas por cámaras trampa representa un desafío clave en los programas de monitoreo de biodiversidad, ya que una sola cámara trampa puede tomar más de 20 mil fotos en 1 mes, y se requiere personal calificado para su revisión y registro de las especies capturadas.

Este proyecto presenta el desarrollo de un modelo de inteligencia artificial para la revisión masiva de fotos basado en técnicas de deep learning y transfer learning para la detección del tuco-tuco (*Ctenomys magellanicus*), un roedor subterráneo nativo de la Patagonia.

Se utilizó el modelo YOLO (You Only Look Once) en su versión más reciente, entrenado con un conjunto de 300 imágenes etiquetadas manualmente que incluyen una amplia variedad de condiciones ambientales y lumínicas. También se incorporaron imágenes de fondo (sin presencia de la especie), para mejorar la capacidad del modelo de distinguir entre detección y ausencia. El entrenamiento fue realizado en Google Colab utilizando GPU, con técnicas de congelación de capas y data augmentation para optimizar la generalización del modelo.

Como resultado, se alcanzó una efectividad superior al 85% en la detección del tuco-tuco en el conjunto de validación, lo que disminuyó significativamente los tiempos de revisión de datos y entrega de resultados.

Este trabajo busca aportar una herramienta automatizada que reduzca significativamente el tiempo y esfuerzo requeridos para el análisis de imágenes por parte de especialistas ambientales. La iniciativa representa un avance concreto en la aplicación de inteligencia artificial al monitoreo ecológico, demostrando cómo los datos vivos pueden ser utilizados para fortalecer la conservación de la biodiversidad en contextos reales.

Session: 6960773-3**7021026**

21/10/25 | 16:55

Room: Cauca

ORAL VIRTUAL • EN

Upscaling the Connecting Landscapes (CoLa) decision support system with Earth observations (EO)

Presenter

Ivan Gonzalez

Authors

Ivan Gonzalez (Northern Arizona University • United States)

Jantz Patrick (Northern Arizona University • United States)

Abstract

Habitat loss is a significant issue for species since it threatens their survival. This panorama requires quick action in terms of conservation strategies and also an informed diagnosis of the spatial configuration of existing and remaining habitat. Landscape connectivity is essential because corridor designs might connect isolated habitats into a viable connected area. Detailed information about places that require particular management interventions, like conservation or restoration, facilitates the land managers' decisions. Recent experiences in decision-making workshops with participants from NGO's, academia, and governments invite us to develop Decision Support Systems (DSS), scientific tools suitable and accessible for local authorities and non-academic audiences. We provided the framework for developing suitability and resistance species data in a close-to-real-time way. These layers will be incorporated into CoLa DSS (Connecting Landscapes Decision Support System), leading to a posterior landscape connectivity analysis and summary. The system contains two modules: one for species distribution models and the second for landscape modelling. The species distribution model will be performed on Google Earth Engine to ensure processing capacity for the imagery and other Earth Observations products. We will use continuous change detection and classification (CCDC) and random forest as a predictor technique, as well as NASA imagery and GEDI products, among others, as predictors. This tool, presented as an R package and a web tool, allows users to generate spatially-explicit and updated landscape priority solutions for conserving populations under a rapidly changing world.



DATOS
VIVOS
2025

Day 2 - Wednesday, October 22

Día 2 - Miércoles 22 de octubre

Symposia & Panel Sessions

*Sesiones de
Simposios y Paneles*

Session

6798502-1

Symposium

22/10/25 | 10:45

Room: Ballroom A

Scaling AI For and Across Biodiversity: Data Collection and Curation in AI-Driven Biodiversity Research (Part 1)

Organizers

Sanson Poon

Arianna Salili-James

Ben Scott

Rukaya Johaadien

Michal Torma

Nicky Nicolson

Kit Lewers

Wouter Koch

David R. Williamson

Description

Artificial Intelligence (AI) is revolutionising the way biodiversity data are managed, studied, and preserved, offering groundbreaking possibilities for research, curation, conservation, policy-making and public engagement. Digital representations of organisms are central in biodiversity data collection, curation and use. It is these representations, rather than the physical organisms themselves, that are increasingly the basis for research. Digital representations allow the use of machine learning, AI, and computer vision to measure the physical properties of organisms and to classify them taxonomically and phenologically, on an unprecedented scale.

While AI-driven innovations are emerging across institutions and disciplines, a critical question remains: how can these advancements be successfully embedded and scaled to maximise impact? This session explores cutting-edge AI applications, from large-scale digitisation and automated species identification to advanced data management and predictive analytics. We will examine strategies for integrating AI across institutional frameworks, addressing challenges in adoption, collaboration, and sustainability. We welcome talks investigating the complexities of maintaining these services in the long term, addressing the financial burdens of API access and the rapid evolution of AI models and services that can quickly render solutions obsolete. By tracing the AI journey within our organisations, we aim to define best practices that unlock its full potential, as well as to understand what others are working on, and what we can learn from other domains. Finally, we are also interested in topics including:

- Novel data collection and analysis techniques or novel uses of established ones
- Data collection, digitization, standardization and curation for future applications
- Practical implications of AI use on data quality, interpretability, and legal aspects

Session: 6798502-1**7019753**

22/10/25 | 10:55

Room: Ballroom A

ORAL • EN

Next-generation AI workflows for the sensor data deluge

Presenter

Laurens Hogeweg

Authors

Laurens Hogeweg (Naturalis Biodiversity Center • Netherlands)

Rutger Vos (Netherlands)

Jacob Kamminga (Twente University • Netherlands)

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Dan Stowell (Netherlands)

Abstract

Continuous biodiversity monitoring through sensors (cameras, microphones, DNA-samplers) will shortly acquire data on the billion scale. These volumes of data cannot be handled through current AI methods easily, because of its sheer size and unknown or changing content. Therefore, we present a set of next-gen AI workflows, enabled through an integrated data analysis platform built on foundation models (FM), data exploration through vector spaces, data annotation using active learning (AL) and parameter efficient finetuning (PEFT) of FMs. AI-based data analysis allows users to leverage established FMs for biodiversity. Data exploration allows them to discover unknown concepts in their data (novel species), quality issues (blurry images, human sounds, ...), and non-stationarity (changes in time). AL will help users efficiently annotate the most critical data. This will shorten the development time of models for particular use cases from months to weeks. These short-cycle specialized models (SCSM) are an essential step in the acceptance of AI by end-users, including taxonomists and ecologists.

We will discuss particular workflows which apply data exploration concepts to particular tasks: (1) revision of existing datasets for detecting mislabeled samples, (2) exploration of multimodal data (image/DNA, video/sound, ...), and (3) annotation of time-series for ecological analysis, (4) development of models predicting quality of AI models, so called meta AI models.

We will demonstrate these concepts through a prototype on the million scale using DIOPSIS insect camera data, Audiomoth data, DNA sequences paired with images, and videos. We will also show how developed models can be easily evaluated, exported, and deployed to existing biodiversity infrastructures such as ARISE, DiSSCo, and eDentity.

Finally, we will discuss how these methods will start scaling to the billions. Here, novel concepts, workflows, and technologies are needed, as well as attention to the energy and material use of applying such models in practice.

Session: 6798502-1**7013244**

22/10/25 | 11:05

Room: Ballroom A

ORAL • EN

Navigating Nature Tech: AI-powered guidance for scalable conservation solutions

Presenter

Carly Batist

Authors

Carly Batist (Conservation International • United States)

Ali Swanson (Conservation International • United States)

Gilad Goren (Nature Tech Collective • Portugal)

Mikel Maron (Earth Genome • Costa Rica)

Abstract

Biodiversity technology solutions are rapidly proliferating, yet practitioners and stakeholders often struggle to identify suitable tools amid a fragmented and fast-evolving landscape. Despite a growing number of tools and platforms, many stakeholders face critical barriers such as fragmented information, limited validation data, and uncertainty around where to begin for their specific use cases. In response, Conservation International (CI) and the Nature Tech Collective (NTC) recently launched the Nature Tech for Biodiversity Sector Map to catalog available technologies and promote greater sector transparency. Building on this foundation, we are now partnering with Earth Genome developing a prototype AI agent designed to help users query this evolving landscape using natural-language prompts. Users will be guided to appropriate tools based on context-specific queries, bridging the gap between the vast solution space and on-the-ground conservation challenges. The agent will integrate multiple knowledge sources, enabling context-specific recommendations based on end-user needs and constraints. In this presentation, we will share progress on the prototype and discuss key implementation challenges. Our goal for this agentic tool is to lower the barrier to entry for tech adoption and help make sense of the nature tech space, so that conservationists can increase the speed, scale and efficiency of their vital work. Overall, we aim to demonstrate how AI-driven tools can accelerate the impact of technology in conservation and deliver transparent and credible decision-support systems.

Session: 6798502-1**7013595**

22/10/25 | 11:15

Room: Ballroom A

ORAL VIRTUAL • EN

OneStop4Wildlive: Turning Wildlife Monitoring Data into Shared Knowledge

Presenter

Daniel Bauer

Authors

Daniel Bauer (Senckenberg Society for Nature Research • Germany)**Rajapreethi Rajendran** (Senckenberg Society for Nature Research • Germany)**Jonas Grieb** (Senckenberg Society for Nature Research • Germany)**Alexander Wolodkin** (Senckenberg Society for Nature Research • Germany)**Maya Beukes** (Senckenberg Society for Nature Research • Germany)**Claus Weiland** (Senckenberg Society for Nature Research • Germany)**Martin Jansen** (Senckenberg Society for Nature Research • Germany)

Abstract

Today's wildlife monitoring systems collect audio and visual biodiversity data at an unprecedented scale. Yet, the majority of this data remains trapped on local storage devices, inaccessible to the broader research and conservation community. Turning this raw data into actionable and shared knowledge faces two key challenges: 1) the need for reliable machine assistance to annotate the vast amounts of automatically generated data, and 2) the need for friction-less data exchange that makes those annotations available in a FAIR (Findable, Accessible, Interoperable, Reusable) manner.

We present OneStop4WildLIVE, an in-development platform that addresses both these challenges by integrating AI-driven annotation with a Human-in-the-Loop (HITL) validation workflow and FAIR data sharing. Media uploaded to the platform first undergo semantic extraction by Convolutional Neural Networks that detect fauna, draw bounding boxes, and propose taxonomic labels for identified species. These machine-generated annotations are immediately made available as FAIR Digital Objects (FDOs) using our WildLIVE Monitoring Ontology (<https://wildlive.senckenberg.de/wlmo>).

Through the platform, domain experts and citizen scientists can interact with these AI-generated outputs to validate, refine, or extend the annotations. These evaluations are preserved as layered annotations linking back to the originating FDO, enabling future retraining of existing AI models with curated AI-ready datasets, thus closing the HITL cycle.

All artefacts generated along the annotation pipeline, from raw data to AI annotations and human refinements, are made available on our platform as machine-actionable, web-based FDOs. In alignment with community standards involving Camtrap DP, RO-Crate, and FAIR Signposting to ensure interoperability with emerging data spaces and across research domains.

By combining AI-powered assistance, citizen science participation, and FAIR data sharing principles, OneStop4WildLIVE aims to transform isolated wildlife monitoring projects into a unified and interoperable knowledge hub. In this talk, we present our platform's architecture and share early development outcomes.

Session: 6798502-1**7014083**

22/10/25 | 11:25

Room: Ballroom A

ORAL • EN

Better Together: Combining AI with Human Expertise to Enhance Species Identification

Presenter

Wouter Koch

Authors

Wouter Koch (Norwegian Biodiversity Information Centre • Norway)

Abstract

The landscape of AI-driven biodiversity research evolves rapidly, but few would argue that human expert knowledge is becoming less important, let alone being replaced by AI. While AI models demonstrate remarkable performance in automated classification tasks, the irreplaceable value of taxonomic expertise quickly becomes apparent when addressing the complexities of real-world biodiversity challenges.

This presentation explores practical ways to combine expert knowledge with AI for species identification. Rather than treating human expertise and machine learning as competing paradigms, we show how their integration produces better results than either approach alone.

We present two methods that exemplify this human-AI collaboration. The first approach demonstrates an integrated pipeline where AI-generated species candidates are used to guide users through a simplified identification key to confirm or refine the results. Users only need to answer a few targeted questions about visible features, making species identification faster and more accurate than either approach separately. The second method employs vision-language models to verify trait visibility in specimen images, generating textual explanations of the classification results for users.

These approaches address fundamental challenges in AI adoption for biodiversity applications, including model explainability, taxonomic accuracy, and user trust. Embedding human expertise in the identification process creates more reliable and educational identification systems, while end users experience how AI augments taxonomic expertise, rather than replacing it.

Our work demonstrates how the future of biodiversity informatics lies not in the displacement of human expertise by AI, but in thoughtful integration that leverages the strengths of both. Not only does this allow for better educational tools and engagement of the general public, it offers scalable solutions for biodiversity documentation while preserving the critical role of taxonomic specialists in an increasingly automated field.

Session: 6798502-1**7014902**

22/10/25 | 11:35

Room: Ballroom A

ORAL VIRTUAL • EN

Fine-Tuning Language Models for Structured Botanical Trait Extraction and Species Comparison

Presenter

Ayoub Nainia

Authors

Ayoub Nainia (Institut de Systématique, Evolution, Biodiversité (ISYEB), Sorbonne Université, Muséum National d'Histoire Naturelle • France)**Régine Vignes-Lebbe** (Institut de Systématique, Evolution, Biodiversité (ISYEB), Sorbonne Université, Muséum National d'Histoire Naturelle • France)**Hajar Mousannif** (Computer Science Department, LISI, Cadi Ayyad University • Morocco)**Jihad Zahir** (UMMISCO, IRD, Computer Science Department, LISI, CADI Ayyad University • Morocco)

Abstract

As AI becomes increasingly central to biodiversity research, transforming free-text morphological descriptions of species into structured data remains a major challenge, particularly in botany where identification keys and species descriptions are rich in detail but lack formal structure. In this work, we present a pipeline that fine-tunes large language models (LLMs) to extract standardized botanical traits from floristic texts and enable species-level comparison at scale.

To address this challenge, we developed a two-stage system based on the LLaMA architecture, trained on a curated corpus of French botanical descriptions. First, the system converts a predefined set of standardized botanical traits (such as leaf shape or flower color) into natural language questions tailored to each species description. Then, using these questions as extraction prompts, it processes the original morphological description to identify and extract the specific trait values. This approach acts as a specialized information extraction pipeline that transforms unstructured text into consistent character-state pairs. By applying identical trait extraction criteria across multiple species descriptions, the system builds a standardized, comparable trait database that supports systematic species comparison.

A key application of this work is the enrichment of descriptor-based systems like Xper- $\geq$, which rely on structured matrices to describe and differentiate taxa. By automating the extraction of traits from legacy floras, we aim to enable scalable descriptor population, enrich taxonomic knowledge bases, and facilitate the development of interactive identification tools.

Our initial results show that domain-specific LLM fine-tuning can bridge the gap between narrative botanical knowledge and structured trait data, offering a reproducible and scalable approach for structured information extraction in biodiversity science.

This research demonstrates how AI can be embedded into biodiversity workflows to accelerate data curation, promote interoperability across platforms, and directly support the current trajectory of scaling AI for biodiversity data collection, curation, and knowledge extraction.

Session: 6798502-1

7015018

22/10/25 | 11:45

Room: Ballroom A

ORAL • EN

Scaling AI Across the UK Culture and Heritage Sector: The NHM-DCMS AI Pilot Programme

Presenter

Sanson Poon

Authors

Sanson Poon (Natural History Museum • United Kingdom)

Arianna Salili-James (Natural History Museum • United Kingdom)

Chris Addis (Natural History Museum • United Kingdom)

Avellina Leong (Natural History Museum • United Kingdom)

Hester van Schalkwyk (Natural History Museum • United Kingdom)

Naifeng Zhang (Natural History Museum • United Kingdom)

Ben Scott (Natural History Museum • United Kingdom)

Abstract

From November 2024 to March 2025, the Natural History Museum, London (NHMUK), supported by the UK Department for Culture, Media and Sport (DCMS), led a national programme to explore a new model for deploying artificial intelligence (AI) across the UK cultural sector. The programme explored how AI support biodiversity research, collections management, accessibility, and public engagement, while addressing the practical realities of AI adoption, scalability, and sustainability.

Working with partners at the Zoological Society of London, Lyme Regis Museum, National Museums Liverpool, the Royal Agricultural University, and the Royal Botanic Garden Edinburgh, the programme delivered five AI pilot projects. Each developed an AI-driven solution to a critical challenge: automated species classification of illegally traded snake goods; automatic data extraction from index cards; AI-generated alt-text for digital collections; a conversational chatbot trained on herbarium data; and a herbarium digitisation quality-control tool, respectively.

Spanning institutions of varying scales, locations, and specialisms, the pilot projects provided a testbed for assessing how AI can be embedded in real-world museum and collection contexts. This talk reflects on the whole programme’s design and delivery, and shares insights gained about scaling AI across fragmented institutional landscapes. It addresses key themes including data standardisation, human-AI collaboration, infrastructure readiness, and the challenge of translating short-term prototypes into sustainable, long-term solutions in a rapidly evolving AI ecosystem.

The programme demonstrates that responsible, high-impact AI is achievable when projects are co-designed with institutional needs, grounded in local collections and practices, and developed with flexibility and potential for reuse. While the five pilot projects were distinct and tailored to their respective contexts, together they highlight a model for how the culture and heritage sectors can move from isolated experiments toward a more coordinated ecosystem of innovation. This approach ensures that AI delivers not just technological novelty, but public value and scientific insight.

Session: 6798502-1**7016344**

22/10/25 | 11:55

Room: Ballroom A

ORAL • EN

Determining the Scale of Herbarium Sheet Images via Ruler Detection

Presenter

Kenzo Milleville

Authors

Kenzo Milleville (IDLab, Ghent University • Belgium)

Dieter De Witte (IDLab, Ghent University • Belgium)

Maarten Trekels (Meise Botanic Garden • Belgium)

Quentin Groom (Meise Botanic Garden • Belgium)

Steven Verstockt (IDLab, Ghent University • Belgium)

Abstract

The digitization and online availability of herbarium specimens have increased the need for automated tools to extract specimen traits at scale. Quantitative trait data, such as leaf size or petal length, are critical for ecology, evolution, and climate change research. However, such image measurements need to be converted to standard units to be useful. Existing methods estimate this conversion factor (CF) by predicting the ruler tick locations and calculating the mean pixel distance between them. They typically require many annotated samples and often fail to generalize across diverse ruler types.

Therefore, we propose a generic pipeline that performs well with few labeled rulers. We constructed a dataset containing 220 ruler instances from over 25 institutions. Each ruler was annotated with its bounding polygon and tick mark locations. This allows the calculation of the CF for the ground truth set, which exhibits a human annotation error of 0.89%, calculated from the standard deviation of pixel distances between tick marks.

To predict the CF for a given image, we first segment the rulers on each herbarium sheet using a YOLOv11 object detection model. Second, these rulers are cropped and normalized, ensuring the longest side is horizontal. Third, CLIP embeddings are calculated to identify the most similar ruler types from our ground truth dataset. Next, the most similar ruler types are matched using the LightGLUE keypoint matching model. Finally, the matched keypoints define a homography to transform known tick mark locations and estimate the CF.

A leave-one-out cross-validation on our ground truth dataset resulted in a mean CF error of 1.40% using the best-matching ruler. 92.9% of rulers had a CF error of less than 2%. Seven rulers were not matched. We are actively increasing the dataset and improving our results, which can be found at: <https://github.com/kymillev/herbarium-rulers>

Session: 6798502-1**7018072**

22/10/25 | 12:05

Room: Ballroom A

ORAL • EN

The Utilisation of Robotics Systems and Cobots within Natural History Collections

Presenter

Jack Hollister

Authors

Jack Hollister (Natural History Museum, London • United Kingdom)**Arianna Salili-James** (Natural History Museum, London • United Kingdom)**Ben Scott** (Natural History Museum, London • United Kingdom)

Abstract

Natural history collections and museums worldwide are increasingly digitising their specimens to preserve fragile artefacts and improve global access to biodiversity data. This shift reduces the need for physical handling and travel, facilitating research and collaboration across institutions. However, the scale of these collections, often numbering in the millions, combined with the delicate nature of many specimens, presents significant logistical and practical challenges. Even with large and skilled teams, digitisation often remains a slow and resource-intensive process.

Here, we explore the application of cobots in the form of robotics arm systems paired with computer vision and artificial intelligence, as a means to enhance and assist in the speed, consistency, and scope of collection digitisation. Unlike conventional industrial settings where robotic systems operate in highly controlled environments, museum specimens are arranged by humans and vary in orientation and position. As such, we detail the design of a cobot system capable of performing more intuitive and adaptive pick-and-place operations. This includes the capturing of images, automated reading of existing specimen labels, and the attachment of new labels that conform to updated standards.

Beyond digitisation, we also propose additional applications in collection management. Through integration with AI systems, these cobot platforms can be used to identify and isolate potentially mislabelled, degraded, or damaged specimens. This capability supports curatorial tasks that are otherwise labour-intensive and error-prone, and helps institutions maintain more accurate and sustainable collections. This work will demonstrate the potential for robotics and AI not only to accelerate digitisation efforts but also to play an integral role in the long-term stewardship and curation of natural history collections.

Session: 6798502-1**7007451**

22/10/25 | 12:15

Room: Ballroom A

ORAL • EN

Predicting the number of Coleoptera species for a state province in Colombia using Deep Neural Networks and Open Data

Presenter

Esteban Marentes Herrera

Authors

Esteban Marentes Herrera (SiB Colombia • Colombia)

Abstract

Colombia is a mega biodiverse country, however the number of known species present in the country remains underestimated due to a lack of information, especially for understudied groups that are difficult to sample and identify, such as beetles (Coleoptera). It is not possible to obtain an exact number of species for this group using conventional methods, due to their diversity and lack of resources for taxonomic research. For this reason, a deep neural network model was built using occurrence records published through SiB Colombia and GBIF, checklists of various families and subfamilies compiled by experts of Coleoptera de Colombia, and relevant abiotic measurements available in open repositories, to make an indirect prediction of the number of species a particular state province (Antioquia), which has a large amount of available data and a variety of representative habitats.

To achieve this, a model was built using DNN an optimized using a hyperband for hyperparameters, it was evaluated using R^2 , Mean Absolute Error (MAE) and opinions of experts in several families from Colombia. For Antioquia it predicted a minimum of 2.007, a maximum of 9.381, and an average value of 4.410 species of Coleoptera. Additionally, an average value of 6.646 species was predicted for Colombia using the same model and compared to the last published checklist for Colombia which lists 6,170 species (Blackwelder 1945) and it is consistent with the number of species described since 1945.

However, the opinions of all experts was of underestimation or overestimation depending on each particular family, highlighting general uncertainty in species estimates and how AI models are also unreliable to predict a clear value, serving only as a starting point or providing a wide range to work with.

Session: 6798502-1**7012969**

22/10/25 | 12:25

Room: Ballroom A

ORAL • EN

AI for Wildlife Trafficking: Automated Species Identification of Snake Goods through a Computer Vision Pipeline

Presenter

Avellina Ming Yan Leong

Authors

Avellina Ming Yan Leong (The Natural History Museum • United Kingdom)

Chris Addis (The Natural History Museum • United Kingdom)

Arianna Salili-James (The Natural History Museum • United Kingdom)

Sanson Poon (The Natural History Museum • United Kingdom)

Louise Gibson (The Zoological Society of London • United Kingdom)

Victoria Luk (The Zoological Society of London • United Kingdom)

Abstract

The wildlife trade significantly contributes to the ongoing biodiversity crisis. Although charismatic taxa receive considerable attention, reptiles, which approximately 90% of the traded species are captured from the wild, are often overlooked. The challenge of curtailing the reptile trade begins with species identification, where enforcement officers at border control facilities often lack the necessary resources and access to herpetological expertise, thus hindering law enforcement efforts. However, with recent advances in artificial intelligence (AI), particularly in computer vision technology, interdisciplinary applications have emerged. This study introduces a proof-of-concept multi-model pipeline aiming to accurately identify illegal snake goods down to the species level. Our unique approach involves training segmentation and classification models to specifically classify species based on the distinct skin texture patterns captured from live snake imagery. With this pattern based classification approach, our trained model is subsequently generalised to recognise these same patterns in illegal snake goods. This method ensures that snake goods that have been processed artificially (e.g. dyed, reshaped or tanned) can still be classified despite losing typical taxonomically diagnostic features. On live snake imagery, the classification model achieved AUC-ROC scores ranging from 0.86 to 0.95 across 8 classes and an overall accuracy of 0.77. When generalised to classifying snake goods, the overall accuracy is maintained at 0.77. These findings highlight the potential of interdisciplinary AI applications to wildlife trade challenges, with this proof-of-concept pipeline offering promising scalability and adaptability into a time and cost efficient tool. This application could enhance enforcement effectiveness and increase the likelihood of successful prosecutions in cases of illegal reptile trade.

Session

6798479-1

Symposium

22/10/25 | 10:45

Room: Ballroom B1

Community Engagement and Capacity Building for Increased Biodiversity Data Accessibility (Part 1)

Organizers

Maheva Bagard Laursen**Katherine Tattersall****Elizabeth Lawrence****Mélanie Raymond**

Description

The critical importance of capacity building and globally accessible biodiversity knowledge in addressing the global biodiversity crisis is highlighted in the Kunming-Montreal Global Biodiversity Framework (GBF), particularly Targets 20 and 21. How are we taking action to address these priorities? What are the benefits of capacity development and organized biodiversity data on different scales from local communities to global networks?

For this session, we invite speakers to present approaches to community engagement, skills development, and knowledge-sharing for increased biodiversity data and information aggregation, sharing and use. We aim to inspire new ideas and partnerships that further support the knowledge needs of the global community.

Through compelling examples and success stories, we aim to showcase how empowering communities can result in enhanced data accessibility. We can also explore how we can nurture and strengthen collaborations to align efforts and share expertise for maximum impact.

Session: 6798479-1**7007114**

22/10/25 | 10:52

Room: Ballroom B1

ORAL • EN

BID picture thinking drives increased biodiversity capacity and data access

Presenter

Maheva Bagard Laursen

Authors

Maheva Bagard Laursen (Global Biodiversity Information Facility - GBIF • Denmark)**Mélanie Raymond** (Global Biodiversity Information Facility - GBIF • Denmark)**Laura Anne Russell** (Global Biodiversity Information Facility - GBIF • Denmark)**Sanja Novakovic** (Global Biodiversity Information Facility - GBIF • Denmark)**April Suen** (Global Biodiversity Information Facility - GBIF • Denmark)

Abstract

Open science and data accessibility are widely recognized as essential to addressing today's global challenges. At the core of GBIF's mission is the mobilization of the data, skills and technologies needed to enable access to comprehensive biodiversity information; demonstrated by the sharing of more than 3 billion occurrence records through its infrastructure.

However, the map of occurrence data accessible through GBIF still reveals important imbalances in the distribution of data, which often reflect gaps in capacity for data sharing. This disparity underscores the need to strengthen the ability of all to participate in and benefit from biodiversity data sharing as emphasised in Targets 20 and 21 of the Kunming-Montreal Global Biodiversity Framework.

GBIF's approach to capacity development seeks to respond to this challenge and is demonstrated through the EU-funded Biodiversity Information for Development (BID) programme. Focusing on developing capacities from individual to regional levels, the BID programme aims to empower communities of practice to actively engage in data mobilization activities aligned with identified regional or national priorities and needs.

This presentation will highlight opportunities to contribute to the BID programme and participate in its activities and future development. It will explore how capacity development activities are embedded within competitive calls for proposals, how scientific and technical cooperation is promoted through training and mentoring, and how knowledge-sharing within and across regions supports the growth of communities of practice among data publishers and users.

Session: 6798479-1**7012684**

22/10/25 | 11:07

Room: Ballroom B1

LIGHTNING TALK • EN

Harnessing Regional Support Teams to Empower GBIF Networks in the Global South for Increased Data Mobilization and Use

Presenter

Leonardo Buitrago

Authors

Leonardo Buitrago (Global Biodiversity Information Facility • Colombia)

Anabela Plos (Universidad Nacional de Colombia • Argentina)

Laban Musinguzi (Global Biodiversity Information Facility • Uganda)

Tsiky Rabetrano (Museo Argentino de Ciencias Naturales “Bernardino Rivadavia” MACN-CONICET • Madagascar)

Abstract

Regional support teams play a vital role in expanding and sustaining engagement across the GBIF network. Functioning as regional connectors between the GBIF Secretariat, data holders and national nodes, these professionals lead outreach, build technical capacity, and foster long-term collaboration in biodiversity data publishing—especially in countries without an established GBIF node.

Contracted by GBIF, as part of the overall Biodiversity Information for Development (BID) programme, the regional support teams in Africa, Latin America & the Caribbean and Pacific provide distributed technical helpdesk services in multiple languages, guiding institutions through GBIF tools and standards, supporting data quality improvement, and delivering training and mentorship tailored to regional needs. This ongoing support ensures that both new and experienced participants can contribute high-quality data and remain active within the network.

A key strength of the regional support model is its emphasis on peer exchange. The teams help connect communities of practice, enabling the transfer of experiences and solutions across countries and regions. In this way, lessons from BID-funded projects or data mobilization efforts can benefit many others.

While the calls for proposals launched under the BID programme help catalyze initial engagement, the sustained efforts of the regional support teams support the strengthening of regional communities of practice, leading to long-term impact. Their focus on working directly with institutions, including those in countries not yet formally part of the GBIF network, helps close gaps and build inclusive participation in global biodiversity data sharing.

This talk will showcase, through lessons learned and examples, how these efforts are shaping a more connected, capable, and resilient GBIF community. We will also outline opportunities to connect with and participate in these regional activities for increased data mobilization and use, including how individuals and institutions can engage with their regional support teams to receive guidance, training, and collaboration opportunities.

Session: 6798479-1**7020199**

22/10/25 | 11:28

Room: Ballroom B1

ORAL • EN

OBIS Capacity Development Initiatives in light of the OBIS-GBIF Strategy

Presenter

Elizabeth Lawrence

Authors

Elizabeth Lawrence (UNESCO | IOC Project Office for IODE Ocean Biodiversity Information System • Canada)**Ana Carolina Peralta** (University of South Florida | MBON | Caribbean OBIS • United States)

Abstract

Capacity development (CD) is at the heart of OBIS' mission to enhance marine biodiversity data mobilization, accessibility, and application. As part of Priority Area 1, OBIS is committed to fostering partnerships with observing programs and developing tools and guidelines to empower contributors worldwide. The OBIS network leverages a suite of tools to enhance CD, including the OBIS Manual, online and in person courses, how-to videos, code example notebooks, and data mobilization workshops. These efforts are often community-led, exemplified by initiatives like the newly established OBIS Latin America and Caribbean regional group for peer-to-peer mentoring. A cornerstone of OBIS' success is its network of individuals who share and co-develop resources tailored to local communities.

Through its thematic, national, and regional nodes, OBIS delivers both virtual and hands-on training combining technical skills with open science principles. Collaborations with OceanTeacher Global Academy (OTGA) amplify these efforts by offering certified courses through a global network of Regional Training Centres. OBIS also partners with other ocean observation initiatives such as MBON, SeagrassNet and OBPS to deliver training focused on articulating the data value chain into best practices for both data collection and data sharing. OBIS requires at least one representative from each node to successfully complete the OBIS/OTGA training course, underscoring its commitment to capacity development.

As Darwin Core evolves towards a new data model, OBIS is planning future CD efforts to support this transition for data providers. Joint initiatives within the OBIS-GBIF Strategy, such as harmonized training sessions, will further strengthen global marine biodiversity data mobilization. This presentation will showcase current OBIS CD resources, highlight regional success stories, and outline future plans to ensure the community adapts to new data standards and continues to thrive in a rapidly changing landscape.

Session: 6798479-1**7019904**

22/10/25 | 11:43

Room: Ballroom B1

LIGHTNING TALK • EN

EurOBIS & EMODnet Biology as two of the driving forces behind marine biodiversity data capacity building within Europe

Presenter

Leen Vandepitte

Authors**Ruben Perez Perez** (GBIF Spain (CSIC) • Spain)**Cyril Radermecker** (Flanders Marine Institute (VLIZ) • Belgium)**Lynn Delgat** (Flanders Marine Institute (VLIZ) • Belgium)**Joana Beja** (Flanders Marine Institute (VLIZ) • Belgium)**Leen Vandepitte** (Flanders Marine Institute (VLIZ) • Belgium)**Abstract**

The European Ocean Biodiversity Information System (EurOBIS) was launched in 2004, as part of the OBIS-network. Its main goal is to centralize the largely scattered biogeographic data on marine species collected by European institutions and to make these data freely available and easily accessible. All data goes through a number of quality control procedures before they are made available online, assuring a minimum level of quality necessary to put the data to good use. Since 2009, the data infrastructure behind EurOBIS was also adopted by the biological lot of the European Marine Observation and Data Network (EMODnet Biology), a European Union service for marine in situ marine biodiversity data. EurOBIS is also part of the LifeWatch Species Information Backbone, which is embedded in the Flemish contribution to the LifeWatch European Research Infrastructure Consortium (LW-ERIC).

Within the framework of EMODnet Biology, the Data Management Team has engaged in several training activities, all aimed at increasing the accessibility to and quality of European marine biodiversity data. These activities include in-person and online training courses, regular online meetings ('Data laundry sessions') where several partners of marine European projects can ask questions on the ins and outs of marine data management and receive support on all marine data management related topics. The Data Management Team has also contributes to global online training courses on Ocean Data Management (ODM) and Biological Data Management (BDM), available through the Ocean Teacher Global Academy (OTGA) platform, managed under the UNESCO-IODE umbrella. All of these activities contributed to a wider, global availability of high-quality marine biodiversity data that is also available in other biodiversity initiatives through EurOBIS, a dedicated data provider to the overall Ocean Biodiversity Information System (OBIS), as well as the Global Biodiversity Information Facility (GBIF).

Session: 6798479-1**7013618**

22/10/25 | 11:47

Room: Ballroom B1

LIGHTNING TALK • EN

Towards developing regional platform for Global Biodiversity Observing System in the Asia and Pacific -Asia-Pacific Biodiversity Observation Network (APBON)

Presenter

Hiroyuki Muraoka

Authors

Hiroyuki Muraoka (The University of Tokyo | National Institute for Environmental Studies • Japan)

Yayoi Takeuchi (National Institute for Environmental Studies | Osaka Metropolitan University • Japan)

Masahiro Nakaoka (Hokkaido University • Japan)

Takehisa Yamakita (Japan Agency for Marine-Earth Science and Technology • Japan)

Alice Hughes (University of Melbourne • Australia)

Christian Elloran (ASEAN Centre for Biodiversity • Philippines)

Yongyut Trisurat (Kasetsart University • Thailand)

Runi Anak Sylvester Pungga (Forest Department Sarawak • Malaysia)

Ryo Mabuchi (Biodiversity Center of Japan • Japan)

Abstract

Asia-Oceania region is characterized by many biodiversity hotspots, complex geographical characteristics and climatic zones, diverse cultures based on diversity in nature, increasing impacts of climate change, rapid changes in usage of land, coasts and ocean, APBON will further convene the existing biodiversity data and knowledge in the region.

APBON (est. 2009) is a network for observations and assessment of biodiversity, and a platform for science-policy engagement to contribute to effective biodiversity conservation and sustainable use of biodiversity at the national, regional and global scales. APBON has developed networks, facilitated communication for sharing knowledge, and built the capacity of researchers and stakeholders through workshops/webinars/publications.

APBON will further develop the network for addressing local, national and regional biodiversity issues with particular attention to the impacts of changes in climate and society. The planned activities include, launching ‘super-sites’ for long-term and multiple monitoring; promoting interdisciplinary research and problem-solving approaches with filling observational and knowledge gaps by integrating technologies and platforms; promoting data sharing and data accessibility by networking the observation networks and collaboration with partner organizations; delivering information and knowledge through stakeholder engagement at local, national, and regional scales. These collective efforts are expected to develop further the concept of building regional platform for the Global Biodiversity Observing System (GBIOS) which was proposed by the Group on Earth Observations Biodiversity Observation Network (GEO BON). Since we are challenged to observe and assess the biodiversity integrity under the changing climate and then to deliver necessary data and knowledge to the society, this paper will attempt to discuss the ongoing efforts and way forward on multidisciplinary observations by different research networks as well as to integrate in-situ and remote sensing observations.

Session: 6798479-1**7014999**

22/10/25 | 12:03

Room: Ballroom B1

ORAL • EN

Engaging Communities and Improving Accessibility: Natural History Collections as Catalysts for Biodiversity Knowledge Sharing

Presenter

Vanessa Pitusi

Authors

Vanessa Pitusi (The Arctic University Museum of Norway - UiT • Norway)

Andreas Altenburger (The Arctic University Museum of Norway - UiT • Norway)

Abstract

Natural history collections are invaluable libraries of biodiversity knowledge. By displaying historical occurrences of taxa, these collections can be extremely helpful in addressing the global biodiversity crisis. However, natural history collections often remain underutilized due to their limited visibility, funding, and engagement with non-academics.

This presentation highlights our approach to addressing these challenges by publishing natural history collections FAIR through the Global Biodiversity Information Facility (GBIF) and Ocean Biodiversity Information System (OBIS), at the Arctic University Museum of Norway.

Through our partnership with GBIF, we have made 495,203 museum records available via a hosted portal (<https://specimens.tromsomuseum.no/en>), covering both botanical and zoological collections.

Original label information and, when available, specimen photos are included with every record, making them an invaluable tool for research, education, and policy-making.

In addition to increasing the visibility of our collections, our digitization and open access initiatives have promoted cooperation among regional, national, and international networks. To date, 1,334 publications have used the occurrence data from our natural history collections and cited them, illustrating the positive impact of disseminating biodiversity knowledge. We hope to encourage increased participation and capacity building by involving communities in the use and access of these resources, guaranteeing that biodiversity data can guide conservation and policy initiatives at all levels.

The significance of freely disseminating natural history collections and, by extension, biodiversity knowledge is highlighted by various case studies in this presentation. We present examples of how sharing biodiversity data has sparked interaction with scientists, journalists, and students. To tackle the global biodiversity crisis, we have to work together more effectively, exchange knowledge, and make the most of biodiversity data.

Session: 6798479-1**7018481**

22/10/25 | 12:17

Room: Ballroom B1

LIGHTNING TALK • EN

Scaling Digital Fluency for Unlocking Biodiversity data - Lessons Learnt from Organisation-Wide Data Management Training

Presenter

Olivia Mitrovits

Authors

Olivia Mitrovits (Royal Botanic Gardens, Kew • United Kingdom)

Sidrah Ikram (Royal Botanic Gardens, Kew • United Kingdom)

Reinis Rozkalns (Royal Botanic Gardens, Kew • United Kingdom)

Richard Dodd (Royal Botanic Gardens, Kew • United Kingdom)

Udayangani Liu (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

The Royal Botanic Gardens, Kew holds the largest and most diverse botanical and mycological collections in the world, comprising over 8.5 million objects and representing approximately 95% of vascular plant genera and 60% of fungal genera. The continued relevance of these collections and their associated data in the context of global biodiversity loss cannot be overstated. Since 2020 Kew's collections have been moving to a new data management system shared across the organisation; the Integrated Collection Management System (ICMS), supported by EarthCape OY software.

ICMS enables harmonisation of data and workflows across Kew's varied collections through core functionalities: the implementation of shared vocabularies, protocols, and standards; managed plant and fungi taxonomic backbones; linkages between related materials and their derivatives; and the tracking of legal agreements, transactions, and varying curatorial tasks.

A critical component of this transition has been the organisation-wide training, to enable staff to adopt ICMS effectively, and ultimately to enhance data accessibility and drive research. This includes training staff across a wide range of disciplines and with varying levels of technical literacy, through a blend of approaches, balancing planned rollouts with the need for flexibility and responsive support. Delivering technical training at this scale has presented several challenges, including varying user needs, staff expectations, and limited training resources. We present the evolving strategy employed to deliver this training, covering the initial approach, lessons learned, and adaptations made in response to practical constraints and user feedback. By sharing Kew's experience, we aim to support other organisations navigating similar digital transformations and foster discussion on scalable, sustainable strategies for enabling access to biodiversity data.

Session: 6798479-1**7014701**

22/10/25 | 12:23

Room: Ballroom B1

LIGHTNING TALK • EN

Developing an Educational Game - The Benefit Sharing Compass

Presenter

Katie Lee Riddle

Authors**Katie Lee Riddle** (Te Kotahi Research Institute • New Zealand)**Tim Coltman** (Independent Researcher, Sydney Australia • Australia)**Finley Power** (Geo AR, Auckland New Zealand • New Zealand)**Maui Hudson** (Te Kotahi Research Institute • New Zealand)**Abstract**

Fair and equitable sharing of benefits arising from utilisation of genetic sequence data and other types of biological data, known as Digital Sequence Information (DSI) has been a topic of recent international discussion. Ensuring fair and equitable benefit sharing from use of DSI allows Indigenous Peoples and Local Communities (IP & LCs) to derive better economic and social outcomes. Central to discussions has been the development of a suitable governance mechanism to ensure benefits derived from DSI are shared with provider countries, as well as IP and LCs. However, benefit sharing is the outcome of a commercialisation process, occurring at the end of a much longer sequence of research and development. Ideally, appropriate consultation with IP and LCs starts with negotiations around access and developing mutually agreed terms throughout the research phase, including commitments towards non-monetary benefits. Yet, benefit sharing initiatives differ in their ability to deliver results for IP and LCs, as individuals seeking to access and use DSI often lack insights on how to navigate different benefit sharing scenarios.

In this session, we present an educational game designed to: support researchers in building a practice-oriented understanding of the context of benefit sharing with IP and LCs, and provide individual players with scores for Fairness, Equity and Relationship building. The game allows users to explore different scenarios, represented by varying communities, research budgets and outcomes. Participants navigate discussions with IP and LCs, and allocate budget to various benefits to balance the best outcomes. Feedback in the game provides a deeper appreciation for how benefit sharing decisions across the R&D spectrum contribute to their social license to operate with IP and LCs, and how initiatives differ in their ability to deliver results for them. The game thus provides a safe practice environment for researchers to prepare for real-life negotiations.

Session **6799056-1**

Symposium

22/10/25 | 10:45

Room: Ballroom B2

Overcoming challenges in biodiversity modelling (Part 1)

Organizers
Natalie Briscoe
Santiago Velazco
Mark Urban
Greta Bocedi
Damaris Zurell

Description
The availability of biodiversity and environmental data is rapidly increasing. Yet to address global challenges, support informed decision-making, and plan effective mitigation, we also need models that can integrate these data to identify the drivers underpinning species and ecosystem responses to environmental changes and reliably forecast future impacts. This is no small task: biodiversity data are often patchy and geographically and taxonomically biased; including biological mechanisms can improve accuracy, but these mechanisms are often complex and poorly understood; and models need to be applied to varying spatial extents, time periods, divergent climate and management scenarios, and millions of species. While many promising modelling frameworks exist to support management and policy, the wider use of models to assess and project environmental change impacts on biodiversity is hampered by data and methodological challenges and limited coordination of modelling efforts. We aim to explore recent advances to overcome these challenges including (i) emerging approaches and data integration methods to incorporate mechanisms into models for many species; (ii) methods to scale results across different spatial extents and time periods; and (iii) how to coordinate efforts and compare modelling frameworks to advance knowledge and protect nature.

Session: 6799056-1**7016159**

22/10/25 | 10:45

Room: Ballroom B2**ORAL • EN**

Overcoming challenges in biodiversity modelling: data, mechanisms, scale and model intercomparisons

Presenter

Natalie Briscoe

Authors

Natalie Briscoe (The University of Melbourne • Australia)**Mark Urban** (University of Connecticut • United States)**Damaris Zurell** (University of Potsdam • Germany)**Santiago Velazco** (San Diego State University • United States)**Greta Bocedi** (University of Aberdeen • United Kingdom)**Jane Elith** (The University of Melbourne • Australia)**Gurutzeta Guillera-Arroita** (The University of Melbourne • Australia)

Abstract

Effective action to halt biodiversity decline will require models that can reliably project future changes and inform policy and management decisions. While many promising modelling frameworks exist to support management and policy, wider use of models to assess and project environmental change impacts on biodiversity is hampered by patchy and biased biodiversity data, challenges incorporating mechanisms and scaling outputs, and limited coordination of modelling efforts. In this talk, we briefly review current data and methodological challenges to biodiversity models and highlight emerging advances that aim to address them, including key topics that will be explored in this session. We also emphasise pathways for greater international coordination and knowledge sharing. Climate model intercomparison projects were pivotal for rapidly advancing the mechanistic understanding of climate change and increasing confidence in climate models. We argue that biodiversity model intercomparisons could play a similar role, identifying ‘fit-for-purpose’ modelling tools that should be a priority for development, efficiently tackling methodological challenges, and enhancing trust in model projections. Yet to date, very few biodiversity model intercomparisons have been conducted. Drawing on a case study from our own work testing different biodiversity models using simulated data, we illustrate some of the benefits and challenges of evaluating and comparing models that capture species responses to environmental change in fundamentally different ways. We found that the performance of different models depended strongly on the simulated dynamics of the species and aspect of model projection being evaluated (e.g. identifying spatial locations of key habitat, forecasting extinction risk), with no model consistently outperforming all others. In addition, decisions about model parameterisation had large impacts on performance for some modelling frameworks. These results highlight the benefits of a coordinated and ongoing effort to iteratively and methodically address key uncertainties and refine methods, data inputs and priority research gaps.

Session: 6799056-1**7019911****22/10/25** | 11:00**Room:** Ballroom B2**ORAL • EN**

More Than Heat: Mapping Climatic Constraints on Global Biodiversity

Presenter

Dirk Nikolaus Karger

Authors

Dirk Nikolaus Karger (Swiss Federal Research Institute WSL, • Switzerland)**Fabienne Baumgartner** (Wyss Academy for Nature • Switzerland)**Edouard Davin** (Wyss Academy for Nature • Switzerland)**Damaris Zurell** (University of Potsdam • Switzerland)

Abstract

Species differ in the climatic conditions that constrain their geographic distributions, some are limited by temperature, others by water-related factors such as precipitation and relative humidity. Yet climate change alters these drivers unevenly: while global temperatures rise steadily, shifts in water availability are more variable, nonlinear, and spatially heterogeneous. Anticipating biodiversity responses requires identifying which climatic dimensions are ecologically limiting, and how their changes intersect with species' realized niches. We use an ensemble of species distribution models (SDMs)—including Generalized Linear Models (GLMs), Generalized Additive Models (GAMs), and Random Forests (RFs)—to quantify climate sensitivities across over 20,000 terrestrial vertebrate species. All models follow a harmonized, protocol-driven pipeline based on the Inter-Sectoral Impact Model Intercomparison Project phase 3 (ISIMIP3) climate inputs. Climatic predictors include temperature means and seasonality, annual and seasonal precipitation, relative humidity, and site water balance. Variable importance is derived from each model type and synthesized across the ensemble to map the relative strength of climate constraints across species and regions. Our results reveal consistent spatial patterns: species in boreal and arctic regions are primarily limited by temperature, while in tropical ecosystems, temperature seasonality is often more influential. In many subtropical and montane regions, however, humidity and precipitation—particularly relative humidity—emerge as the dominant constraints on species distributions. These findings indicate that in large parts of the world, ecological impacts under climate change may be driven more by shifts in water-related variables than by warming alone. By applying a unified modelling framework to globally harmonized biodiversity and climate data, we provide a robust foundation for identifying key climatic drivers of biodiversity change across taxa, regions, and future scenarios.

Session: 6799056-1**7020354**

22/10/25 | 11:15

Room: Ballroom B2**ORAL • EN**

From Complex Models to Scalable Forecasts: Emulators in the Age of Living Data

Presenter

Justin Travis

Authors**Justin Travis** (University of Aberdeen • United Kingdom)**Tamsin Woodman** (University of Edinburgh • United Kingdom)**Greta Bocedi** (University of Aberdeen • United Kingdom)**Job Aben** (University of Paris Saclay • France)**Roslyn Henry** (University of Aberdeen • United Kingdom)**Abstract**

The rapid growth of biodiversity and environmental data—so-called Living Data—opens new opportunities for understanding and forecasting species and ecosystem responses to environmental change. Yet making full use of these data requires models that can capture key ecological mechanisms, integrate diverse datasets, and scale to large spatial and temporal extents. A fundamental challenge has been the trade-off between biological realism and computational scalability. In this talk, I explore how *emulators*—statistical or machine learning surrogates trained on outputs from complex models—can help *relax* this trade-off.

Emulators are already central to fields like weather and climate science, where they enable fast, flexible exploration of computationally expensive models. I will introduce the concept of emulation and demonstrate its application to biodiversity forecasting using RangeShifter, an individual-based, process-rich modelling platform. By training emulators on outputs from RangeShifter, we can scale up ecological forecasting while preserving core biological processes such as dispersal, demography, and evolution.

This approach allows us to embed detailed ecological understanding within forecasting pipelines while expanding spatial, temporal, and taxonomic coverage. Crucially, it also enhances our ability to integrate rich biodiversity data—including species distributions, population densities, and genetic structure—into model calibration and validation. Emulators open the door to inverse fitting of complex models, making them more responsive to real-world data and more useful for guiding decision-making.

Through a series of case studies, I will show how emulators provide a scalable, data-integrated framework for biodiversity modelling—enabling forecasts that are both mechanistically grounded and practically useful in addressing global environmental challenges.

Session: 6799056-1**7012846**

22/10/25 | 11:30

Room: Ballroom B2**ORAL • EN**

Attributing bird occupancy dynamics to past climate and land use change in North America

Presenter

Damaris Zurell

Authors

Katrin Schifferle (University of Potsdam • Germany)

Natalie Briscoe (The University of Melbourne • Australia)

Mark Urban (University of Connecticut • United States)

Damaris Zurell (University of Potsdam • Germany)

Abstract

Species respond dynamically to global environmental change, yet the relative contribution of different global change drivers on colonisation and local extinctions remains poorly understood. In this study, we leverage dynamic occupancy models to simulate metapopulation dynamics to explicitly attribute observed changes in occupancy to climate and land use. Using 25 years (1995–2019) of occurrence data for 159 bird species from the North American Breeding Bird Survey we assess the impact of climate and land use change on site-level colonisation and extinction rates within a Bayesian approach. Our framework incorporates spatial and temporal block cross-validation to ensure robust evaluation of predicted occupancy dynamics. To disentangle the specific effects of climate and land use, we employ counterfactual scenarios, comparing observed dynamics to those expected under detrended climate conditions and constant 1995 land use. This approach allows us to quantify the relative contribution of each driver to observed occupancy trends. By explicitly linking species range dynamics to their underlying drivers, our study offers critical insights for species management and conservation in the face of ongoing environmental change, representing a significant step towards mechanistically attributing observed range changes to global change pressures.

Session: 6799056-1**7015965**

22/10/25 | 11:45

Room: Ballroom B2**ORAL • EN**

Neural Dynamic N-mixture model: a deep learning framework to infer demographic rates from abundance data

Presenter

Francois Leroy

Authors

Francois Leroy (The Ohio State University • United States)

Marta Jarzyna (The Ohio State University • United States)

Abstract

Temporal changes of abundance arise from the difference between recruitment rate (*i.e.* proportion of new individuals entering the population through birth or immigration) and loss rate (*i.e.* proportion of individuals removed from the population by death or emigration). The interplay between these vital rates and how they change through time at large spatio-temporal scales remains largely unexplored, mainly given the cost of gathering such mark-recapture data. Bridging this knowledge gap would provide deeper insights into the mechanisms of the ongoing biodiversity crisis and help shape effective conservation strategies.

Here, we combine advances in Hidden Markov Models with Neural Hierarchical Models and develop a *Neural Dynamic N-mixture model*, to infer latent recruitment and survival (and thus loss) from repeated abundance data. Our approach combines decades of development in *N*-mixture models for ecological datasets with the predictive power and flexibility of neural networks to capture complex and non-linear relationships from high-dimensional datasets.

We optimize a custom loss function (namely negative log-likelihood) that integrates transition matrices and the forward algorithm to enable gradient-based learning. We then validate the model through simulations and demonstrate the ability of our model to infer cross-level, nonlinear relationships. We also compare its performance with traditional Bayesian implementations of dynamic *N*-mixture models.

Our results show that leveraging the relevance of *N*-mixture models for ecological datasets within a deep learning framework is a promising avenue for inferring demographic parameters. While the architecture of our Neural Network is, so far, a Multilayer Perceptron, this framework could be easily extensible to multi-modal data and more complex network architectures, such as Convolutional Neural Networks, to infer demographic rates from satellite imagery, camera trap and/or audio loggers.

Session: 6799056-1**7020242**

22/10/25 | 12:00

Room: Ballroom B2

ORAL • EN

Leveraging Deep Learning Joint Species Distribution Models and Participatory Science Data for Scalable Biodiversity Modeling

Presenter

Courtney Davis

Authors

Courtney Davis (Cornell University • United States)

Abstract

Our ability to measure the status and trends of biodiversity at actionable scales, across large areas, and for entire ecological communities has been limited by a lack of sufficient, high-quality data across species' ranges. In recent years, participatory science programs have shown remarkable potential to fill these data gaps, contributing vast numbers of species observations across diverse geographies and taxa. However, the opportunistic and non-systematic nature of data collection creates challenges for biodiversity modeling, particularly in terms of spatiotemporal sampling bias and uneven data coverage. To address these challenges, we present a novel deep learning joint species distribution model (DL-JSDM) designed to harness the rich and growing biodiversity data streams from participatory science. Our model can extract complex ecological signals from noisy and biased data by explicitly accounting for spatiotemporal variation in sampling effort, while modeling key processes that shape ecological communities. This approach generates robust, landscape-level biodiversity metrics at continental scales, including year-round predictions of species occurrence, relative abundance, community composition, and diversity at high spatial (3km x 3km) and temporal (weekly) resolutions. By leveraging state-of-the-art deep learning technologies, our DL-JSDM can efficiently scale to accommodate thousands of species, hundreds of environmental predictors across diverse data modalities, and capture multiple ecological processes—including disentangling the independent effects of land use and climate to better understand the effects of alternative climate and management scenarios. To demonstrate the real-world utility of this approach, we highlight several applications to participatory science data from eBird across North, Central, and South America – each describing how our model can support ecological forecasting, conservation planning, and biodiversity monitoring across biogeographic contexts. In doing so, we show how emerging technologies combined with participatory data can overcome key limitations in biodiversity assessment and contribute to a more coordinated, global response to environmental change.

Session: 6799056-1

7012980

22/10/25 | 12:15

Room: Ballroom B2

ORAL • EN

An early warning system for biodiversity

Presenter

Josep M Serra-Diaz

Authors

- Josep M Serra-Diaz (Botanical Insitute of Barcelona • Spain)
- Lauren Andrews (Global Modeling and Assimilation Office, NASA Goddard Space Flight Center • United States)
- Brian Maitner (Department of Integrative Biology, University of South Florida • United States)
- Gonzalo E Pinilla-Buitrago (Institute of Ecology, National Autonomous University of Mexico • Mexico)
- Andreas Meyer (Climate Risk Lab, African Climate and Development Initiative • South Africa)
- Alex L Pigot (Centre for Biodiversity and Environment Research, Department of Genetics, Evolution and Environment, University College London. • United Kingdom)
- Christopher H Trisos (Climate Risk Lab, African Climate and Development Initiative, University of Cape Town • South Africa)
- Adam Wilson (Department of Geography, University at Buffalo • United States)
- Mark C Urban (Center of Biological Risk, University of Connecticut • United States)
- Cory Merow (Eversource Energy Center • United States)

Abstract

Effective biodiversity conservation during periods of rapid environmental change requires identifying the species and regions at greatest risk. However, most predictions focus on biodiversity shifts several decades ahead, offering limited guidance for immediate conservation action. Here, we develop an early warning system for biodiversity based on 9-month seasonal weather forecasts combined with species-specific historical temperature limits. In May 2024, we predicted that >3,500 vertebrate species (out of 30,585 species), including >1,250 species of conservation concern, would be substantially exposed to extreme temperatures 1-2 months in advance. Mexico, sub-Saharan Africa, and the Himalayas were predicted to face the highest threats during this forecast period. Emerging evidence suggests that these regions did experience extreme temperatures which were associated with population declines. Such advance notice enables rapid actions to monitor and mitigate these extreme events for sensitive species and regions.

Session: 6799056-1**7020010**

22/10/25 | 12:30

Room: Ballroom B2**ORAL • EN**

Galaxy-Ecology a forgotten potential framework who can help in biodiversity modelling

Presenter

Yvan Le Bras

Authors

Coline Royaux (MNHN Data Terra PNDB Biodiversity Data Hub • France)

Pauline Segumineau (MNHN Data Terra PNDB Biodiversity Data Hub • France)

Claire Bissery (France)

Romain Lorrilliere (MNHN • France)

Yves Bas (MNHN • France)

Alexis Martin (MNHN • France)

Dominique Pelletier (IFREMER • France)

Jean-Baptiste Mihoub (Sorbonne Université • France)

Yvan Le Bras (MNHN Data Terra PNDB Biodiversity Data Hub UAR 2047 DoHNÉE • France)

Abstract

Galaxy platform is a web solution originally developed 16 years ago to facilitate high performance computing access and computational workflows creation by life science researchers. During last 10 years, evolutions of the Galaxy platform made it notably possible 1/ to attain high degree of FAIRness for a computational point of view thanks to conda, containers orientations, 2/ to create Galaxy training network and related infrastructure, 3/ to address needs of new communities as “Climate”, “Ecology” and more recently “Earth Science” 4/ to propose innovative ways of integrating synchronous and asynchronous scientific workflows and 5/ to integrate state of the art approaches notably on modeling and artificial intelligence domains.

Thanks to Galaxy Ecology initiative, we started in 2018 to test the use of the platform to propose generic modeling tools allowing to facilitate reconfiguration of models for others taxonomic, geographic and/or temporal extent. Seven years later, we can now demonstrate how Galaxy platform can be a candidate existing solution to integrate diverse modeling types including statistical and mechanistic biological models and earth systems models for biodiversity communities providing high level of FAIRness, transparency and reproducibility.

Particularly, we will showcase the relevance of the “atomization-generalization framework” designed for Galaxy Ecology platform. <https://doi.org/10.1093/gigascience/giae122> to allow reusing modeling tools in different taxonomic, spatial and temporal extents.

Session

6798638-1

Symposium

22/10/25 | 10:45

Room: Tolima

Beyond 2030: Building the Data Foundations for Biodiversity Action to support the KMGBF (Part 1)

Organizers

Andrew Rodrigues

Lina Estupinan Suarez

Description

With the Kunming-Montreal Global Biodiversity Framework setting ambitious targets to halt biodiversity loss by 2030, the pressure is on to ensure that effective monitoring systems are in place—not just for 2030, but for the long-term future of biodiversity governance.

Are we ready? Do we have the capacity, technology, and data infrastructure to track progress, measure policy effectiveness, and support biodiversity action beyond 2030? This session explores how different regions, sectors, and organizations are addressing these challenges—developing new data products, tools, and systems to meet growing policy demands.

We invite researchers, practitioners, and decision-makers to share innovative approaches to biodiversity monitoring, data synthesis, and reporting. By fostering discussion and bringing together global expertise, we aim to identify best practices and pathways for building a stronger, more connected biodiversity data ecosystem for the decades ahead. Join us as we explore how to transform biodiversity commitments into long-term, measurable success.

Session: 6798638-1**7020899**

22/10/25 | 10:50

Room: Tolima

ORAL • EN

Mapping What Matters: Foundational Ecosystem Data for the GBF and Beyond

Presenter

David Patterson

Authors

Lela Gomersall (Group on Earth Observations (GEO) • Switzerland)

David Patterson (Group on Earth Observations (GEO) • Switzerland)

Abstract

Meeting the ambitions of the GBF requires an unprecedented scale-up of reliable, and policy-relevant ecosystem data. At the core of this is ecosystem extent data, a foundational layer underpinning numerous indicators across the GBF, including those related to Target 1, 2, and 3. Robust data on where ecosystems occur and how they are changing provides the essential baseline for measuring progress, informing national biodiversity strategies, enabling ecosystem accounting, and supporting both public and private sector decisionmaking.

The Atlas is an initiative convened by the Group on Earth Observations (GEO), in collaboration with the CBD Secretariat, IUCN, and a growing network of partners. Its aim is to close critical knowledge gaps on the state of the world's ecosystems by producing the first comprehensive, global map of all ecosystems on Earth. The Atlas brings together high-quality global, regional, and national ecosystem maps, and aligning them to the internationally recognized IUCN GET. In areas where ecosystem maps are lacking, the Atlas will accelerate production using AI technologies to generate new, wall-to-wall ecosystem maps.

The Atlas not only delivers foundational ecosystem data but also provides the means to generate it, through a collaborative platform that will offer open training datasets, AI models, and tools to produce nationally validated maps. This effort democratizes access to spatial ecosystem data and enables a wide range of actors, including governments, Indigenous Peoples and Local Communities, researchers, and the private sector, to contribute to and benefit from the evolving ecosystem data infrastructure.

This presentation will explore how the Atlas is advancing spatial ecosystem mapping tools that are accessible and usable across a wide range of contexts. The presentation will focus on how these tools can support implementation and monitoring of the GBF, while enabling alignment between local knowledge, national priorities and long-term global biodiversity goals.

Session: 6798638-1**7021008**

22/10/25 | 11:05

Room: Tolima

ORAL VIRTUAL • EN

Applying continuous community-level biodiversity indicators for CBD reporting

Presenter

Mathew Vickers

Authors

Mathew Vickers (CSIRO • Australia)

Abstract

Through the Kunming-Montreal Global Biodiversity Framework (KM-GBF), member countries acknowledged the importance of conserving biodiversity and committed to act, monitor and report on their progress toward KM-GBF goals and targets. The indicators selected in the monitoring framework for the KM-GBF vary in ease of use and interpretation, but also in the degree to which rigorous quantitative biodiversity data are applied in their derivation and application, and the consistency with which they can be applied across different countries. This variation poses significant challenges for global-level analysis and reporting on progress toward achieving biodiversity goals.

To address this, CSIRO has developed four quantitative, objective indices, accepted as component indicators under the KM-GBF, that are well positioned to facilitate consistent quantitative assessment for countries and the world. The BERI (Biodiversity Ecosystem Resilience Index), BHI (Biodiversity Habitat Index), and two PARC (Protected Area Representativeness and Connectedness) indices rely on free and open data, and were designed to assess change in the expected persistence of species-level biodiversity as a function of observed or predicted changes in the integrity and spatial configuration of natural ecosystems, as well as to measure the representativeness and connectivity of protected area systems. These indices are spatially explicit, operate at a fine resolution, are easy to use, and are straightforward to interpret.

Here I briefly describe how these indicators are derived, synthesising large amounts of biodiversity and environmental data to quantify key aspects of change in the capacity of biodiversity to persist. I demonstrate how these indicators can be used to report against the KM-GBF Goal A and Targets 1, 2, 3, and 8, and how they can also be used to inform decision making by estimating the expected impact of proposed actions on biodiversity. Lastly, I introduce a resource that makes country-level results freely available via a simple web interface.

Session: 6798638-1**7019859**

22/10/25 | 11:20

Room: Tolima

ORAL • EN

Bridging Biodiversity Knowledge Gaps: Unlocking Botanical and Mycological Collections at Royal Botanic Gardens, Kew

Presenter

Sidrah Ikram

Authors

Sidrah Ikram (Royal Botanical Gardens, Kew • United Kingdom)

Olivia Mitrovits (Royal Botanical Gardens, Kew • United Kingdom)

Sarah Cheseldine (Royal Botanical Gardens, Kew • United Kingdom)

Udayangani Liu (Royal Botanical Gardens, Kew • United Kingdom)

Robert Turner (Royal Botanical Gardens, Kew • United Kingdom)

Abstract

Understanding biodiversity and the threat to its survival is crucial for tackling global challenges in biodiversity and climate crises, as well as food insecurity. Target 21 of the Kunming-Montreal Global Biodiversity Framework (KMGBF) focusses on utilizing the best available data, information, and knowledge, and ensuring their accessibility to decision makers, practitioners, and the public to support effective management of biodiversity. However, much of the information describing biodiversity remains highly fragmented. While diverse collections of fungal and plant materials are housed in organisations worldwide, most of their valuable information has not been digitized. Large-scale digitisation is key to unlocking the wealth of information within these collections, enabling virtual access to images and data. This process not only contributes to KMGBF but also opens doors to large-scale data mining and analysis, enabling scientific discovery.

We present how the Royal Botanic Gardens, Kew is prioritising the digitisation of its extensive living and preserved plant and fungal collections at the heart of its scientific work. In this context, we share our experience, insights, best practices, and learnings from this four- year project. This includes the imaging and transcribing of over 8.5 million specimens. The development of our new Integrated Collection Management System (ICMS) supported by EarthCape software to manage data across 12 distinct collections (Plant DNA, Tissue, Herbarium, Spirit, Fungi DNA, Fungarium, Seeds, Economic Botany, Illustrations and Artefacts, Living Plants, In-vitro, and Microscopy).

How we have standardized and migrated data from isolated and outdated databases to ICMS, as well as incorporated the latest plant and fungal taxonomy. We have also launched an open data portal for the global sharing of this collection data, ensuring these digital assets are accessible to researchers and policymakers worldwide. By harnessing the power of data, we can strengthen our efforts for safeguarding the future of biodiversity for generations to come.

Session: 6798638-1**7011296**

22/10/25 | 11:35

Room: Tolima

ORAL VIRTUAL • EN

Window to the Wild: The Smithsonian's Global Biodiversity Data Collection

Presenter

Sarah E. Huebner

Authors

Sarah E. Huebner (Smithsonian's National Zoo and Conservation Biology Institute • United States)**William McShea** (Smithsonian's National Zoo and Conservation Biology Institute • United States)**Alexander E. White** (Smithsonian's Office of Digital Transformation • United States)**Peter Leimgruber** (Smithsonian's National Zoo and Conservation Biology Institute • United States)**Brigit Rooney** (Smithsonian's National Zoo and Conservation Biology Institute • United States)

Abstract

Accurate and robust data are mission critical for conservation. Wildlife images from camera traps are among the most detailed data available and have accumulated on a massive scale. However, the quality and availability of these datasets vary, and specific types of labeled images—such as those with behavioral annotations—are often difficult to find and access. Long-term trend analyses and global synthetic studies of biodiversity require standardized datasets that are expert-verified, preserved in perpetuity, and updated as technology advances.

The Smithsonian is building its first 'born-digital' biodiversity collection, composed entirely of labeled wildlife images curated for quality and designed to facilitate regional and global analytics. This collection promotes open science, encourages interdisciplinary collaboration, and strengthens scientific reproducibility.

Camera trap images collected by Smithsonian scientists via the Snapshot USA monitoring network and other projects, along with those contributed by global partners, have been curated to serve multiple audiences. For conservation and ecology researchers, the collection can be freely accessed and queried to download relevant metadata. In the field of machine learning, researchers can improve their models using the Smithsonian's targeted training datasets, which include labeled images that are otherwise difficult to obtain, such as cryptic species and interspecies interactions. Educators and the public benefit from outreach resources that enhance understanding of and engagement with biodiversity conservation.

The cyberinfrastructure developed to support this collection includes platform linkages that enable the rapid and reliable transmission of large-scale image datasets, including publication on the Global Biodiversity Information Facility (GBIF) for maximum discoverability. This digital collection and its supporting infrastructure will significantly enhance data accessibility and promote collaborative research, accelerating progress in wildlife conservation and ecological understanding.

In pursuit of advancing digital biodiversity data infrastructure, the Smithsonian aspires to collaborate with peer institutions globally to replicate and integrate born-digital biorepositories.

Session: 6798638-1**7031438**

22/10/25 | 11:50

Room: Tolima

ORAL • EN

Gaps on Biodiversity Indicators for Ecosystem Restoration Monitoring

Presenter

Adelola Temitope

Authors

Carmen Morales

Adelola Temitope

Abstract

Ecosystem restoration has emerged as a global priority, recognized for its potential to address the interconnected challenges of biodiversity loss, land degradation, and climate change. The United Nations Decade on Ecosystem Restoration (2021–2030) and Target 2 of the Kunming–Montreal Global Biodiversity Framework call for the effective restoration of at least 30% of degraded ecosystems by 2030 and underscore the need for accelerated restoration actions and robust systems to monitor progress. As the custodian agency for the Target 2 headline indicator, “area under restoration,” the Food and Agriculture Organization (FAO) developed the Framework for Ecosystem Restoration Monitoring (FERM) to monitor global restoration progress and indicators.

Target 2 qualifiers of restoration include biodiversity enhancement, ecosystem functions and services, ecological integrity, and connectivity. The indicators to monitor global progress include area under restoration, proportion of land that is degraded over total land area, Global Ecosystem Restoration Index and Proportion of key biodiversity areas in favorable condition. These indicators can support monitoring restoration outcomes, particularly in relation to biodiversity status and ecosystem health. However, methodology and guidance are lacking for some of these indicators, resulting in a lack of quantitative data on these indicators. Additionally, indicators measuring ecosystem function and services, ecological integrity and connectivity are lacking, and socio-economic indicators demonstrate that restoration benefits both people and nature. To address these gaps, there is a need to recommend additional biodiversity indicators that reflect ecological processes at the site level and socio-economic indicators, while remaining compatible with national and global reporting frameworks.

Strengthening the link between remotely sensed data and field-based biodiversity metrics could enhance the ability to evaluate restoration outcomes. This study reviews biodiversity indicator gaps across multiple scales, drawing from peer-reviewed literature and FERM submissions, and proposes recommendations to improve national and global monitoring to ensure measurable contributions and global restoration targets

Session: 6798638-1**7020809**

22/10/25 | 12:05

Room: Tolima

ORAL • EN

RegRed: an effort to collate data on species' red list assessments at the national level

Presenter

Florescia Grattarola

Authors

Florescia Grattarola (Czech University of Life Sciences Prague • Czechia)**Adam Uličný** (Czech University of Life Sciences Prague • Czechia)**Ivo Kadlec** (Czech University of Life Sciences Prague • Czechia)**Petr Keil** (Czech University of Life Sciences Prague • Czechia)

Abstract

Effective conservation biology relies on robust assessments of threats to species. While global evaluations are conducted through initiatives like the IUCN Red List, many countries and regions also produce their own threat assessments, often compiled into national or regional red lists. RegRed is a project dedicated to developing a comprehensive, accessible database of these localised assessments and associated sources that document threatened or extinct species at the national level. Our first phase, “RegRed metadata”, involved a systematic search and compilation of relevant sources worldwide (https://github.com/petrkeil/RegRed_metadata). This effort yielded 2,093 sources from 172 countries, encompassing threat data across 487 broad taxonomic groups. The second phase, “RegRed data”, focuses on digitising the data, starting with the tetrapods group. We aim to extract species-level threat information from diverse conservation literature using a semi-automated workflow, including large language models (LLMs). The ultimate goal of RegRed is to create a standardised, per-species database of national and regional threat assessments to support research, policy, and conservation action. We invite collaboration to scale this initiative, promote decentralisation, and ensure broad participation in advancing global conservation knowledge.

Session

6788879-1

Symposium

22/10/25 | 10:45

Room: Caldas

Long Live Biodiversity Data: Knowledge Transfer and Continuity across Research Projects (Part 1)

Organizers

Christos Arvanitidis

Niels Raes

Lyubomir Penev

Peter Bozakov

Nikol Yovcheva

Description

Research projects transcend disciplines and national borders to pursue tomorrow's scientific insights. However, their duration is limited and the question arises: How can the data they generate remain impactful for future endeavours? In the context of open science and its principles, securing the legacy of research results is essential for fostering lasting collaboration and innovation.

This session will showcase how a continuous knowledge transfer over time can be ensured by open data and effective science communication across research projects. Representatives of several such international initiatives will reveal how the longevity of their work is guaranteed with success stories of tools, information hubs and workflows enabling exchanges that truly consolidate the global biodiversity data space.

The presentation of this multi-level approach to information sharing and continuity will also demonstrate the potential impact of sustainable research on decision-making. In that context, the session will explore how targeted communication can help transform science results into actionable knowledge by raising awareness among agenda-setters. Thereby, methods bridging the gap between science and policy in relation to an increasingly ambitious global environmental agenda will be discussed.

Session: 6788879-1**7015644**

22/10/25 | 10:50

Room: Caldas

ORAL • EN

Biodiversity Knowledge Hub: Bridging Research Infrastructures, Aggregators, and Communities - Past, Present, and Future

Presenter

Christos Arvanitidis

Authors

Christos Arvanitidis (LifeWatch ERIC • Spain)**Joaquin López Lérída** (Spain)**Cristina Isabel Huertas Olivares** (Spain)**Alberto Basset** (Italy)**Sara Montinaro** (Italy)**Lucia Vaira** (Italy)**Nikos Minadakis** (HCMR • Greece)**Michalis Griniezakis** (HCMR • Greece)**Julio López Paneque** (LifeWatch ERIC • Spain)**Niels Raes** (Netherlands)**Lyubomir Penev** (Pensoft Publishers • Bulgaria)

Abstract

Between 2021 and 2024, the Horizon-funded project Biodiversity Community Integrated Knowledge Library (BiCIKL) demonstrated the transformative impact of interdisciplinary collaboration in addressing biodiversity research challenges. By providing centralized access to a wide range of information sources, tools, and services, BiCIKL integrated FAIR-compliant biodiversity data from research infrastructures, scientific repositories, and expert communities. In doing so, it bridged the gap between fragmented knowledge systems and the need for actionable insights in biological conservation and ecological resilience.

One of BiCIKL's key achievements is the creation of the Biodiversity Knowledge Hub (BKH), an innovative platform that offers seamless access to biodiversity data, tools, and workflows. The BKH promotes interoperability across diverse resources, empowering researchers, policymakers, and practitioners to make informed, data-driven decisions. Grounded in open-science principles, the BKH supports long-term, scalable solutions that foster ongoing collaboration, innovation, and resilience in biodiversity research and management.

Building on BiCIKL's legacy, the newly launched Biodiversity Meets Data (BMD) project advances the BKH by integrating high-throughput biodiversity tools, AI-powered species identification, and direct connections to global infrastructures like GBIF (Global Biodiversity Information Facility). Central to BMD is the standardization of data across space, time, and taxonomy, crucial for harmonized and interoperable outputs.

Furthermore, BMD actively promotes the mobilization of historical baseline data from literature and reports, enabling robust trend analyses and the formulation of biodiversity restoration targets across terrestrial, freshwater, and marine ecosystems—from local to national scales. These functionalities will converge in the BMD Single Access Point, which will eventually become an integrated service within the BKH ecosystem.

Session: 6788879-1**7008032**

22/10/25 | 11:01

Room: Caldas

ORAL • EN

How Open Science Builds Enduring Value for Biodiversity Research

Presenter

Quentin Groom

Authors

Quentin Groom (Meise Botanic Garden • Belgium)

Tim Adriaens (Research Institute for Nature and Forest (INBO) • Belgium)

Amy J. S. Davis (University of Konstanz • Germany)

Peter Desmet (Research Institute for Nature and Forest (INBO) • Belgium)

Damiano Oldoni (Research Institute for Nature and Forest (INBO) • Belgium)

Diederik Strubbe (Research Institute for Nature and Forest (INBO) • Belgium)

Lien Reyserhove (Research Institute for Nature and Forest (INBO) • Belgium)

Sonia Vanderhoeven (Belgian Biodiversity Platform • Belgium)

Abstract

Most research projects are, by their nature, short-lived. They often emerge from specific questions, institutional strategies, funding opportunities, and policy or management needs. But once finished, what becomes of the data, tools, and insights they created? Drawing on experiences from the Belgian TriAS project (Tracking Invasive Alien Species) and recent European projects, such as B-Cubed, RiparIAS and OneSTOP, we reflect on how we can build something that endures: infrastructure, workflows, and collaborative communities that continue to support science and policy long after the project ends.

In practice, research rarely follows a neatly planned trajectory. The process is inherently messy, shaped by shifting priorities, new collaborations, and the pressures of delivery. And yet, by deliberately building a solid foundation, documenting, sharing openly, aligning with standards, and using platforms like GBIF, Zenodo, GitHub, and Wikidata, we can protect the progress we've made and create common understanding and lasting value. Open standards developed by TDWG and other communities provide the semantic and technical glue that ensures data from one project can be reused, reinterpreted, and integrated into the next.

The direction of our work has not only been driven by scientific curiosity but also by policy at levels spanning from institutional to global. Through these projects, we've come to see science communication not as an afterthought but as a mechanism for durability: engaging with stakeholders, framing outputs in ways that resonate beyond the scientific community, and supporting the science-policy interface in a meaningful way.

This talk will present concrete examples of tools, data pipelines, and communication strategies that have helped ensure the long-term utility of research. It makes the case that while we cannot fully predict the future, we can prepare for it, by investing in openness, interoperability, and relevance from the start.

Session: **6788879-1****7019849**

22/10/25 | 11:14

Room: Caldas

ORAL • EN

Bringing nomenclature back into the lamplight

Presenter

Patricia Mergen

Authors

Saliba Elie (Muséum National d'Histoire Naturelle • France)**Patricia Mergen** (Meise Botanic Garden and Royal Museum for Central Africa • Belgium)**Thomas Pape** (Natural History Museum Denmark, University of Copenhagen • Denmark)**Richard Pyle** (Center for the Exploration of Coral Reef Ecosystems, Bernice P. Bishop Museum • United States)

Abstract

Taxonomy sensu lato has found its prominent place back in many biodiversity information-related activities and projects. However, this is less the case for α -taxonomy, which is focused on describing new species or performing revisions. The so-called taxonomic impediment remains acute, with fewer and fewer experts available for a wide range of taxa. When describing a new species or revising a taxon, respecting the naming conventions governed by the nomenclatural Codes is essential. However, the complexity of the Codes and the long learning curve can act as a barrier, discouraging young scientists from engaging in α -taxonomy. Modernising or introducing changes to the existing Codes also involves very strict and relatively lengthy procedures, making it difficult to keep up with the technological changes. To overcome these issues and find common ground, TDWG (with the support of the Partnerships and Fundraising Sub-Committee) and the ICZN (International Commission on Zoological Nomenclature) signed a Memorandum of Understanding.

This presentation will showcase the MoU as an example of collaboration with a nomenclatural body, before expanding it to other Codes. The ultimate goal is to correctly implement nomenclature into TDWG standards with the appropriate controlled vocabularies and definitions. It also intends to explore how nomenclature, alongside taxonomy, can be incorporated into biodiversity informatics research projects to attract a new generation of α -taxonomists. This should involve developing tools and applications, such as the use of software and AI, to support new species descriptions and revisions that comply with the nomenclature Codes. It should also involve organising dedicated training sessions and encouraging enriched taxonomic publications while maintaining the necessary human involvement in the process.

Session: 6788879-1**7019925**

22/10/25 | 11:26

Room: Caldas

ORAL • EN

Retrieving information about taxonomic expertise from specimen data and the importance of data quality for effective data reuse

Presenter

David Fichtmueller

Authors

David Fichtmueller (Freie Universität Berlin, Botanic Garden and Botanical Museum • Germany)

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Abstract

Understanding the current landscape of taxonomic expertise is crucial for addressing the growing challenges in biodiversity research, conservation, and data management. There remains a lack of comprehensive insight into who the active taxonomists are, where they work and which taxon groups they specialize in. Within the European TETTRIs project (Transforming European Taxonomy through Training, Research and Innovations, <https://tettris.eu/>) we aim to fill that gap by systematically identifying taxonomic expertise in Europe, using different sources. The approach for the expertise from taxonomic publications has already been presented during TDWG 2023 (De Nolf et al, 2023, <https://doi.org/10.3897/biss.7.111534>).

This presentation focuses on the approach to retrieve taxonomic expertise from specimen data and will show the steps necessary to produce a result dataset that is compatible with the outcome of the publication approach. The core data are around 20 million specimen records (<https://doi.org/10.15468/dl.2jyxx8>) retrieved from GBIF via the new SQL-API. From that dataset, the names of the researchers were extracted, cleaned and matched to external identifiers, then the institutional affiliations were added as well as country information for both the person and the institution. In the process, data from multiple other sources were used, processed and integrated with the specimen data, namely Bionomia, Wikidata, ORCID, ROR and GRSciColl as well as some intermediate data products from the publication approach.

Despite this process only relying on recent data from the past 10 years, one of the major obstacles in integrating the data in an easy and reproducible way was the lack of data quality, consistency and use of identifiers for both people and institutions. These issues highlight how the lack of high-quality data hinders data reuse and integration even within our community.

Session: 6788879-1**7020780**

22/10/25 | 11:37

Room: Caldas

ORAL • EN

Towards a Biodiversity Genomics FAIR data foundation: perspectives from Biodiversity Genomics Europe

Presenter

Joana Paupério

Authors

Joana Paupério (EMBL-EBI - European Bioinformatics Institute • United Kingdom)**Astrid Böhne** (Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn • Germany)**Christian de Guttry** (SIB Swiss Institute of Bioinformatics • Switzerland)**Sharif Islam** (Naturalis Biodiversity Center • Netherlands)**Nick Juty** (Department of Computer Science, University of Manchester • United Kingdom)**Camila Mazzoni** (Leibniz Institute for Zoo and Wildlife Research • Germany)**Felix Shaw** (Earlham Institute • United Kingdom)**Tom Brown** (Leibniz Institute for Zoo and Wildlife Research • Germany)**Rutger Vos** (Naturalis Biodiversity Center • Netherlands)**Robert Waterhouse** (SIB Swiss Institute of Bioinformatics • Switzerland)

Abstract

Biodiversity genomics is a powerful approach that leverages genomics to monitor, describe, and understand biodiversity and provide guidance to prevent biodiversity loss. This approach uses two main methodologies: DNA barcoding and metabarcoding based on standardised genetic markers for monitoring, and generation of reference genomes, using genome assembly and annotation. In Europe, there are two prominent communities driving each methodology: iBOL Europe, which connects national barcoding initiatives and researchers working on DNA barcoding and metabarcoding, and the European Reference Genome Atlas (ERGA), an initiative to coordinate the production of high-quality reference genomes.

The Biodiversity Genomics Europe (BGE) project brings these two networks together to establish and pilot a framework for coordinating biodiversity genomics efforts across Europe. As these networks have traditionally followed specific technical paths, their integration requires careful coordination of data management practices, computational pipelines, and data and infrastructure integration and interoperability. We will discuss the challenges identified and present the work that is being developed in BGE to build a FAIR (Findable, Accessible, Interoperable, and Reusable) biodiversity data ecosystem. Overall, work progressed through collaborating with existing data infrastructures to improve standards, facilitate data brokering, and enhance data accessibility and interoperability. Mapping and harmonising metadata across both networks and alignment with international biodiversity and genomics standards initiatives (DwC, GSC, INSDC) has been a main focus of the work. Significant advances were also made in integrating bioinformatics tools (bio.tools) and infrastructures within BGE workflows, and making these available through WorkflowHub. RO-Crate has been adopted as a lightweight solution to capture complex data structures, together with metadata and provenance (using JSON-LD). An initial biosample RO-Crate profile successfully integrated into the COPO data management and sharing platform.

Overall, these efforts constitute a step forward in creating a FAIR data foundation to enhance the use of genomic data in biodiversity applications.

Session: 6788879-1**7014911**

22/10/25 | 11:50

Room: Caldas

ORAL • EN

The role of the ERGA community in securing the legacy of research results from reference genomes for European biodiversity

Presenter

Robert Waterhouse

Authors

Robert Waterhouse (SIB Swiss Institute of Bioinformatics • Switzerland)

Abstract

The European Reference Genome Atlas (ERGA) initiative plays a pivotal role in securing the legacy of biodiversity genomics by generating high-quality, openly accessible reference genomes for Europe's biodiversity. By producing gold-standard genomic data across a broad range of species, ERGA contributes to long-term scientific, conservation, and policy-related goals. These reference genomes serve as foundational resources for future research, enabling deeper understanding of species biology, adaptation, and evolution, as well as informing conservation strategies in the face of climate change and biodiversity loss. A key strength of ERGA lies in its commitment to open data sharing and adherence to FAIR (Findable, Accessible, Interoperable, Reusable) principles. This ensures that genomic data produced today remains accessible and usable for future generations of researchers, even as analytical methods and scientific questions evolve.

Furthermore, ERGA actively collaborates with global efforts, such as the Earth BioGenome Project, amplifying its impact and helping to standardise approaches across the international genomics landscape. Beyond data generation, ERGA invests in capacity-building and the development of best practices in ethical, legal, and social dimensions of biodiversity genomics, ensuring that genomic resources are used responsibly and inclusively. This holistic approach strengthens the sustainability and relevance of ERGA's outputs. By aligning cutting-edge science with long-term stewardship of biodiversity data, ERGA not only advances immediate research but also ensures that the knowledge and resources it generates remain impactful: supporting future scientific, conservation, and societal endeavours across Europe and beyond.

Session: 6788879-1

7014546

22/10/25 | 12:01

Room: Caldas

ORAL • EN

From local alerts to European policy impact: toward faster detection and communication of invasive species threats

Presenter

Damiano Oldoni

Authors

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Lien Reyserhove (Research Institute for Nature and Forest (INBO) • Belgium)

Damiano Oldoni (Research Institute for Nature and Forest (INBO) • Belgium)

Abstract

It is universally recognised that early detection of invasive alien species (IAS) incursions is the most cost-effective way to prevent invasion once they have been introduced. At the TDWG 2022 annual conference we presented an early alert tool (<https://alert.riparias.be/>), an open- source system designed to send e-mail alerts to researchers and managers of IAS based on GBIF (Global Biodiversity Information Facility) occurrence data (<https://doi.org/10.3897/biss.6.93879>). The tool was developed by the LIFE RIPARIAS project and it was initially tailored to a specific project area and thirty target species. However, the importance of the tool transcended the project, as other actors within the Belgian IAS landscape were interested in using it. Adding some specific areas of interest and extending the taxonomic scope were relatively easy improvements with a high positive impact.

The software consists of two independent elements: the tool core functionality, or engine, and the configuration setup, which specifies the areas and species of interest, the text elements and the general web appearance. The engine, called **GBIF Alert**, is an open source software (<https://github.com/riparias/gbif-alert>) to use in combination with a configuration setup to create an alert tool based on Darwin Core Archive and tailored to the specific target community, and so transcending the initial Belgian IAS community. This flexibility was not only awarded with winning the 2023 Ebbe Nielsen Challenge, but is also leading to further development in the context of two European Horizon projects started in 2025: GuardIAS (<https://guardias.eu/>) and OneSTOP (<https://onestop-project.eu/>). Thanks to the collaboration with the European Alien Species Information Network (EASIN, <https://easin.jrc.ec.europa.eu/easin>), the tool is evolving to become a European initiative with potential for direct impact on decision-making.

Session: 6788879-1**7010333**

22/10/25 | 12:13

Room: Caldas

ORAL • EN

Collaborative authoring, peer review and publication of data-rich documents with the new ARPHA Writing Tool 2.0

Presenter

Teodor Georgiev

Authors

Lyubomir Penev (Pensoft Publishers • Bulgaria)

Teodor Metodiev (Pensoft Publishers • Bulgaria)

Teodor Georgiev (Pensoft Publishers • Bulgaria)

Nikolay Mehandzhiyski (Pensoft Publishers • Bulgaria)

Iva Boyadzhieva (Pensoft Publishers • Bulgaria)

Peter Bozakov (Bulgaria)

Abstract

ARPHA Writing Tool (AWT) is an XML-first authoring tool, which allows researchers to collaborate with co-authors, editors, reviewers, proofreaders and others, to prepare a ready-to-submit manuscript in a shared online environment before publishing it in any scientific journal or platform.

Being the very first authoring tool to provide ontology-linked and domain-specific semantic tagging, AWT 2.0 also supports import of structured data from external resources (e.g. DwC data from GBIF, iDigBio, BOLD) and semantic enhancements during the writing process (e.g. citation intent based on the Citation Typing Ontology - CiTO or automated links for taxon names to trusted online resources).

Amongst the most notable benefits designed for the domain of biodiversity science are various biodiversity-specific data import and export features and bi-directional links with leading biodiversity data aggregators (e.g. GBIF, BOLD, Catalogue of Life, ChecklistBank, TreatmentBank, Biodiversity Literature Repository at Zenodo, ENA, OpenBiodiv).

Originally designed for the Biodiversity Data Journal and later integrated in other journals published on the ARPHA platform, in its 2.0 version, the authoring environment is now also available as a fully collaborative editing tool. As such, it allows users to export manuscripts in either PDF or JATS-XML format, before submitting them to any scientific journal or platform. Thus, the AWT 2.0 prompts wider use of XML-born and FAIR scientific publications.

AWT 2.0 can also be used for collaborative authoring, community review, editing and publication of documents for institutions or international organisations. The publications are automatically available in semantically enriched HTML, well-designed PDFs and machine-readable JATS XML. This is how, for example, the collaborative SOLO platform allows the Soils for Europe project community to create and share documents before inviting reviews from hundreds of stakeholders. Those publications serve to address knowledge gaps relevant to the EU Soil Mission and guide funding priorities.

Session

6787919

Symposium

22/10/25 | 10:45

Room: Valle

Wikimedia and Biodiversity Data: A Mutualistic Relationship in the Open Knowledge Ecosystem

Organizers

Tiago Lubiana

Anabela Plos

Description

This session explores the intersection of Wikimedia projects (Wikipedia, Wikidata, and Commons) with global biodiversity infrastructures like GBIF, iNaturalist, and the Biodiversity Heritage Library (BHL), emphasizing their alignment for data mobilization, standardization, and public engagement and knowledge dissemination. Additionally, it will examine how the sociotechnical aspects of Wikimedia may support connecting specimen data, literature, and multimedia resources towards a linked biodiversity knowledge graph.

Through a combination of presentations and panels, we hope to discuss the interface of Wikimedia and Biodiversity Informatics, including:

- Wikidata as a hub for persistent identifiers
- The role of Wikipedia in biodiversity informatics technology and dissemination
- Structured Data on Wikimedia Commons to represent details of biodiversity images
- iNaturalist-Wikimedia roundtripping of images and articles
- Wikibase & Wikidata for Digital Extended Specimen networks

This session will offer a space for discussing the links of biodiversity data with Wikimedia platforms, ensuring that biodiversity knowledge is openly available, structured, and widely accessible to researchers, policymakers, and the public.

Session: 6787919**7020796**

22/10/25 | 10:50

Room: Valle

ORAL • EN

Open knowledge for all: connecting initiatives with diverse audiences

Presenter

Anabela Plos

Authors

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Abstract

Open data initiatives allow (almost) unrestricted access. But this doesn't mean they're accessible to everyone... Often, a lack of knowledge about where and how to access them hinders widespread access.

In Argentina, since 2020, a group/team of people (some of whom are long-time Wikimedians) with the support of Wikimedia Argentina and various institutions, have undertaken the goal of supporting and facilitating access to open knowledge. We have led and collaborated on various editatons and training sessions for university students and professors, as well as the public.

Editatons such as “Adopt a Ladybug” arose from the need to complete the information on species (taken from Wikipedia) on the iNaturalist platform. We also uploaded images from iNaturalist to Wikimedia Commons so we could add images to the articles. This event was held jointly with the “Ladybug Project” team, whose members belong to the Instituto de Investigaciones en Biodiversidad y Medioambiente (INIBIOMA) and study native and exotic ladybugs.

Another experience involved completing information on the Wikipedia biographies of women in science: either virtually since 2020 (Museo de La Plata) or in person (Museo Argentino de Ciencias Naturales, Instituto Darwinion). In addition to completing and improving the biographies on Wikipedia and adding relevant images to Wikimedia Commons, These activities have made it possible to complete the necessary information to link these articles to the Bionomia initiative. Bionomia allows for attribution of collected and identified specimens available in the Global Biodiversity Information Facility, with the Q numbers belonging to the profiles of deceased individuals, facilitating the location of specimens in natural history collections around the world.

The cumulative experience of these initiatives provide feedback that we use to design and adjust new activities and tools, obtain better results, and promote the satisfaction and engagement of the diverse categories of participants.

Session: 6787919**7020811**

22/10/25 | 11:00

Room: Valle

ORAL • EN

Variety is the spice of life: Leveraging Wikidata for interoperable subspecies nutritional biodiversity data

Presenter

Sarah Brinkley

Authors

Sarah Brinkley (Colombia)

Jenny J. Gallo-Franco (The Alliance of Bioversity-CIAT • Colombia)

Marie-Angélique Laporte (The Alliance of Bioversity-CIAT • France)

Damion Dooley (Simon Fraser University • Canada)

Anoosha Sehar (Simon Fraser University • Canada)

Kai Blumberg (Oak Ridge Institute for Science and Education • United States)

Katherine Thornton (WikiData, Yale University • United States)

Abstract

The Periodic Table of Food Initiative (PTFI)® is a global, open-science effort generating high-resolution multi-omics data on the biochemical composition of the world's edible biodiversity. A core objective is building an interoperable database connecting nutritional, taxonomic, environmental, and cultural data through community-driven ontologies. While current taxonomic systems are robust at the species level, they often lack the granularity to capture intra-species diversity (e.g., cultivar, variety, breed). Common names vary locally, further complicating classification. These distinctions are essential to understanding agricultural biodiversity, food composition, and ecological interactions.

PTFI uses FoodOn for food entities (Uniform Resource Identifiers, or URIs) from sample metadata and NCBI taxon IDs for species-level classification. However, limited NCBI coverage below subspecies level challenges the representation of biodiversity nuances critical to nutritional variation. Subspecies of the same food can differ significantly in nutrient and metabolite profiles, yet most systems lack structured representation below species level.

To address this, PTFI is integrating Wikidata as a complementary taxonomic resource—a living, collaborative, machine-readable platform documenting cultivar-, variety-, and breed-level identifiers. Wikidata models cultivars as instances or subclasses of species-specific cultivar groups (e.g., “tomato cultivar”) and provides persistent, multilingual IRIs. These are now linked to FoodOn terms in the PTFI metadata model, enabling hierarchical classification and richer semantic annotation of food samples. This establishes a mutualistic relationship: Wikidata contributes structured cultivar identifiers and metadata, while FoodOn provides a formal framework for interoperability.

By linking both, PTFI enables finer resolution in describing nutritional variation across genetic diversity and enhances access to standardized food composition data. This work shows how open knowledge infrastructures can collaborate to fill biodiversity data gaps. It underscores the importance of cultivars as a vital yet overlooked layer of agrobiodiversity that must be visible in digital ecosystems to inform nutrition, conservation, and sustainable food systems.

Session: 6787919**7020500**

22/10/25 | 11:10

Room: Valle

ORAL • EN

Wikibase to the rescue? Exploring the use of Wikibase to extend the Sherwin Carlquist Digital Extended Specimen Network

Presenter

Jason Best

Authors

Jason Best (Botanical Research Institute of Texas • United States)**Sam Ekberg** (Botanical Research Institute of Texas • United States)**Mare Nazaire** (California Botanic Garden • United States)**Ana Niño** (Botanical Research Institute of Texas • United States)**Krishna Shenoy** (Botanical Research Institute of Texas • United States)

Abstract

The Digital Extended Specimen Network concept incorporates diverse objects and data types often distributed across multiple management platforms, standards, formats, and protocols. These diverse components often create silos that impede the core vision of an integrated network where specimens, derivatives, and associated data connect seamlessly.

We present exploratory work using Wikibase (the platform underpinning Wikidata.org) to link research outputs of botanist Dr. Sherwin Carlquist including field photographs and notes housed at the Botanical Research Institute of Texas (BRIT) and specimens housed at California Botanic Garden (RSA).

Connecting these disparate objects between BRIT's archival data repository and CalBG's biological collection management system presented several challenges. Despite established metadata standards, the archival repository lacked flexibility to apply the most relevant metadata terms and had limited ability to represent relationships with external objects. Similarly, the biological collection management system (Symbiota) initially couldn't add relationships to external archival records, though we collaborated with the Symbiota team to implement this feature. While we created a functional Carlquist ESN with available platforms, compromises were necessary.

Wikibase provides a promising opportunity to enhance this network by serving as a flexible integration layer where items and relationships can be defined using its item and property model. By creating Wikibase entries for specimens and archival materials, we established connections impossible in the source platforms alone. Our experimental Carlquist ESN demonstrates how Wikibase can serve as a parallel and complementary extension to our core Carlquist ESN built within the project's archival and biological collection platforms.

Our experience demonstrates that Wikibase can effectively bridge existing data ecosystems while allowing institutions to maintain their specialized platforms. We share technical and organizational lessons to benefit similar integration efforts and seek partners to continue exploring Wikibase as a solution for creating Digital Extended Specimen Networks.

Funded by NSF Award Numbers 2133561 and 2133562

Session: 6787919**7014694**

22/10/25 | 11:20

Room: Valle

ORAL • EN

From Specimens to Statements: Connecting Biodiversity Collections to the Linked Open Data Cloud with LUX and Wikidata

Presenter

Gary Motz

Authors

Gary Motz (Yale Peabody Museum • United States)

Jessica Utrup (Yale Peabody Museum • United States)

Abstract

As biodiversity institutions strive to make their data more accessible, discoverable, and interoperable, linked open data (LOD) technologies offer transformative potential. This presentation explores how Yale University is leveraging the LUX cross-collections discovery platform to unify access to cultural and scientific holdings across the university, with a special focus on its application to natural history collections at the Yale Peabody Museum (YPM).

Built on modern, semantic web-friendly infrastructure, LUX (<https://lux.collections.yale.edu/>) draws on persistent identifiers, shared vocabularies, and linked data principles to bridge traditionally siloed data ecosystems. As YPM prepares to launch a new public access platform using the LUX infrastructure (<https://github.com/project-lux>), we are embedding LOD practices at the core of the museum's digital strategy—aligning specimen records, party records, multimedia, literature, and taxonomic information to Wikidata entities, GBIF records, Wikimedia, and their physical specimens in the Peabody Museum's holdings.

We will highlight examples where Wikidata serves as a lightweight authority hub, enabling reconciliation across collection records, taxonomic references, and people/entities. The talk will also explore workflows and challenges in aligning internal identifiers with external persistent identifiers (PIDs) like Wikidata QIDs, ORCiDs, and DOIs, as well as opportunities for engaging with other external datasets for representing rich biodiversity media.

Ultimately, we advocate for a sociotechnical approach that treats Wikimedia platforms not just as dissemination tools but as collaborative infrastructures for data stewardship. The Yale LUX and YPM integration provides a scalable, standards-driven case study in building a linked biodiversity knowledge graph that is not only interoperable, but public-facing and standards-driven.

Session: 6787919**7010239**

22/10/25 | 11:30

Room: Valle

ORAL • EN

Botanical cross-border connections unveiled through linked data

Presenter

Giulia Micai

Authors

Giulia Micai (Natural History Museum Vienna • Austria)**Heimo Rainer** (Natural History Museum Vienna • Austria)

Abstract

In botany, supplementary material, such as the personal correspondence of scientists, holds a great potential: it might be the only documentation of a scientist's thought processes, ideas and observations, and it often helps filling in gaps on missing or poorly documented collection objects, e.g. herbarium specimens.

Starting from a collection of more than 700 letters received by the Austrian botanist Eduard Hackel between 1870 and 1932, we implemented:

- The use of AI for the transcription of handwritten text into machine-readable and searchable texts
- The use of crowdsourcing for finalising and polishing the transcriptions
- The joint use of the Transkribus platform for text recognition in combination with Goobi Workflow tool for the management and display of digitisation projects
- The linkage of biographical data on Wikidata and Bionomia with specimen data on **JACQ** and GBIF

Furthermore, because of the intense scientific exchanges between Italy and Austria in the 19th and first half of 20th centuries, we created a sub-project focusing on the cross-border connections between Hackel and 17 Italian botanists.

The outcomes of this projects will be publicly accessible as:

- an online exhibition on the Europeana platform
- the curated stories of these scientists on the Sciencestories website, that links their biographical data from Wikipedia, Wikidata and Bionomia and visuals from Wikimedia

This contribution will provide an insight on the possibilities for extracting data from natural history collection and interlinking them to implement their usability and accessibility for research institutions and the general public.

Session: 6787919**7011372**

22/10/25 | 11:40

Room: Valle

ORAL VIRTUAL • EN

Integrating research expedition data from the Biodiversity Heritage Library into the Wikiverse

Presenter

SIOBHAN LEACHMAN

Authors

SIOBHAN LEACHMAN (WIKIMEDIA AOTEAROA NEW ZEALAND • New Zealand)

Abstract

Extracting biodiversity related data from publications can be technically challenging and undertaking such work may be daunting to those who recognise the need but do not feel they have the technical expertise to assist with such efforts. The aim of this presentation is to illustrate a simple workflow empowering anyone interested to contribute to the work of extracting and reusing biodiversity data from literature.

Using research expeditions as an example, this presentation will outline a simple method for extracting data from publications contained in the Biodiversity Heritage Library (BHL), the subsequent organising of that data following a schema recommended by the TDWG expeditions working group, and the transforming of that data into linked open data by reconciling it against and then ingesting it into Wikidata. This workflow uses tools many in the biodiversity community are familiar with including Google Sheets, OpenRefine and Wikidata.

It will then discuss further digital linking work that can be undertaken, including connecting research expedition participants to the specimens they have collected during that expedition via the tool Bionomia.net. It will outline how the information provided by the newly created or enriched Wikidata expedition items can assist in improving the accuracy of this attribution work.

Finally, the presentation will explain how the Wikidata expedition item can then be linked to other items in Wikidata, including items for expedition participants as well as publications by and about the expedition. Further information will also be provided on how the existence of a Wikidata item for a research expedition can ensure that expedition is linked to and can assist in enriching other areas of the Wikiverse, such as images held in Wikimedia Commons and Wikipedia articles in various languages, thus facilitating access to and the reuse of a wide variety of biodiversity related knowledge.

Session: 6787919**7020451**

22/10/25 | 11:50

Room: Valle

ORAL • EN

Towards a Museum Knowledge Graph: Measuring the Impact of Linked Open Collection Data for the Museum für Naturkunde Berlin

Presenter

Sabine von Mering

Authors

Sabine von Mering (Museum für Naturkunde Berlin • Germany)

Abstract

As part of the so-called Future Plan the Museum für Naturkunde Berlin (MfN) is digitally cataloguing and digitizing its vast natural history collection of approximately 30 million objects. Within the transformation process towards an integrated research museum, it is developing an open knowledge infrastructure for all.

The collaborative and multilingual knowledge base Wikidata serves as a central hub for Linked Open Data (LOD) related to the museum and its collection. The evolving museum knowledge graph will comprise data on entities such as taxa, specimen, people, places, publications, and events. Currently, the focus is on collection agents with different roles working at the museum and/or contributing to the collection, publications dealing with the collection (e.g. accession catalogues or catalogues of type specimens) or the institutional history, and research expeditions commissioned or organised by the museum.

Persistent identifiers for collections and collection objects enable linking with many other entities. For example, subcollections like the archive or the entomological and ornithological collection are connected to the Wikidata item of the museum. Significant events can be added to visualise the history of the museum in a timeline. People are linked as (former or current) employees, as suppliers or collectors of specimens or via archival material held at the museum.

Measuring these linked entities and relationships helps quantifying institutional impact and also highlights a wide range of contributions to the collection and knowledge production. In the larger LOD ecosystem, different initiatives and websites are reusing Wikidata identifiers (e.g., GBIF, Bionomia, Expeditia). Thus, creating identifiers and integrating them in the Collection Management System also helps the larger biodiversity community. The example of the MfN is used to demonstrate the value of Wikidata for unlocking, connecting and contextualising information about natural history collections (and the specimens they are housing) in a museum knowledge graph.

Session: 6787919**7020185**

22/10/25 | 12:00

Room: Valle

ORAL • EN

Linking Biodiversity Literature and Data: Persistent Identifier Exchange Between BHL and Wikidata

Presenter

Mike Lichtenberg

Authors

Mike Lichtenberg (Biodiversity Heritage Library • United States)

Abstract

The Biodiversity Heritage Library (BHL) is a global consortium of natural history and botanical institutions that cooperate to digitize and share biodiversity literature. Wikidata, a free, collaborative, multilingual knowledge base, has become a central hub for persistent identifiers (PIDs) across diverse domains, many of which link directly to BHL resources.

BHL is now leveraging the structured data curated by Wikidata contributors to enhance its own metadata. This presentation will describe an automated pipeline developed to extract and align PIDs from Wikidata with existing BHL records. The process involves tailored queries, automated scripts, and data formats designed for reliable integration. These tools are open, adaptable, and intended to support similar efforts by other organizations seeking to enrich their data with PIDs extracted from Wikidata.

Equally important is the bi-directional flow of information: BHL also contributes structured metadata back to Wikidata volunteers, closing the loop and enabling a collaborative exchange of biodiversity knowledge. This round-tripping of data strengthens the overall biodiversity knowledge graph by connecting literature and associated identifiers across platforms.

Sharing identifiers between BHL and Wikidata offers multiple benefits. It enhances the discoverability of biodiversity literature, improves entity disambiguation, and builds stronger links between BHL and other infrastructures that rely on shared identifiers. It also reinforces Wikidata's role as a PID hub within the global biodiversity informatics landscape.

This talk will highlight how the BHL-Wikidata collaboration demonstrates the utility of Wikidata as a source of persistent identifiers, and we hope to encourage use of Wikidata as a tool for connecting biodiversity infrastructures and making knowledge more open, structured, and accessible.

Session: 6787919**7010913**

22/10/25 | 12:10

Room: Valle

ORAL • EN

Using links from wikis to help discover content in the Biodiversity Heritage Library (BHL)

Presenter

Roderic Page

Authors

Roderic Page (University of Glasgow • United Kingdom)

Abstract

The Biodiversity Heritage Library (BHL) has over 63 million pages of content, which presents a major challenge: how do we discover content in these millions of pages? To date, discovery has relied on indexing BHL text for taxonomic names (e.g., Global Names) and segmenting scanned volumes into articles (e.g., BioStor). Name indexing enables finding pages that mention a taxonomic name.

Segmenting BHL makes it easier to find relevant articles within journals. But these searches give little clue as to the relative importance of the (sometimes thousands) of results. One approach to ranking results is to count the number of incoming links to individual BHL pages, akin to Google's PageRank method. The main source of these links are likely to be from Wikipedia, Wikispecies, and Wikidata. Whereas most work on Wikimedia and BHL has focused on getting BHL content into these wikis (with the notable exception of BHL adopting Wikidata Q numbers for authors), here I flip that relationship and count the number of links coming from the wikis to individual BHL pages. These links can be supplemented by links from taxonomic databases, such as those being aggregated by the Catalogue of Life. The number of these links could be used to rank the importance of a search result (the more links the more likely that the page is relevant). This talk will discuss this approach and show examples based on the "BHL-Light" test bed for exploring new interfaces to BHL.

Session: 6787919**7013309**

22/10/25 | 12:20

Room: Valle

ORAL • EN

The impact of the BHL-Wiki working group in making biodiversity heritage knowledge accessible to all

Presenter

Giovanna Fontenelle

Authors

Giovanna Fontenelle (Wikimedia Foundation • Brazil)**Tiago Lubiana** (Biodiversity Heritage Library • Brazil)

Abstract

In 2023, the Biodiversity Heritage Library (BHL) started a Wikimedia engagement by organizing a working group and publishing a whitepaper about the value of unifying biodiversity knowledge on the Wikimedia projects for a sustainable planet (available here: <https://bhl.pubpub.org/pub/bhlwiki/release/6>). In 2024, these activities led to the hiring of a Wikimedian in Residence to model and enhance structured metadata on images from BHL collections available on Wikimedia Commons, Wikimedia's multimedia platform. In particular, the use of Wikidata for entity recognition meant linking BHL images to core biodiversity informatics identifiers, including those provided by GBIF and the Catalogue of Life.

In the meantime, BHL and the Wikimedia Foundation partnered to test two ideas for the Product and Tech section of the Foundation's annual plan: adding descriptive metadata to BHL files related to Africa and South America available on Commons and organizing events to encourage their usage on Spanish, French, and Portuguese Wikipedia.

This session aims to present the case of BHL's Wikimedian in Residence role and work with the Wikimedia Foundation from a linked open data perspective. It will present the outcomes of the residentsip, including a metadata model for biodiversity illustrations and tools to explore the semantically-enriched BHL collection on Wikimedia Commons. It will also mention community engagement via BHL's Wikimedia working group and demonstrate how structured (linked) open data can be integrated throughout Wikimedia projects and generate impact worldwide by illustrating Wikipedia articles in different languages.

Finally, the last few minutes will also be dedicated to reflecting on the challenges of organizing diversity-related events (both biodiversity and diversity in terms of target audience, languages, etc.) in a challenging, politically charged moment (between January and April 2025) and the resilience strategies for continuing to work with open data, diversity, and biodiversity.

Session

6799422-1

Symposium

22/10/25 | 10:45

Room: Cauca

Indigenous Data Provenance, Local Contexts and the CARE Principles for Indigenous Data Governance (Part 1)

Organizers

Jane Anderson

Maui Hudson

Description

The provenance of Indigenous data is a key issue in the biodiversity data community particularly in the context of data governance and the establishment of a Multilateral Mechanism for sharing the benefits of DSI. Implementation activities for the CARE Principles for Indigenous Data Governance are under development providing guidance for researchers, repositories and publishers including appropriate attribution for both biocultural resources and associated traditional knowledge. Local Contexts (<https://localcontexts.org/>) is a global non-profit that provides Indigenous communities, institutions, and researchers with tools to support Indigenous data sovereignty and recognise cultural authority in collections and data - both in legacy collections as well as new and emerging biodiversity, environmental monitoring and cultural projects. In this session, the Local Contexts team and users of Local Contexts across GBIF, ODIS and TDWG will discuss and show examples of their implementation of Local Contexts and how this tool supports the operationalization of the CARE Principles of Indigenous Data Governance.

Session: 6799422-1**7009119**

22/10/25 | 11:00

Room: Cauca

ORAL • EN

The CARE Data Maturity Model

Presenter

Cas Sedran-Price

Authors

Cas Sedran-Price (University Centre for Rural Health, University of Sydney • Australia)**Riley Taitingfong** (Native Nations Institute, Udall Center for Studies in Public Policy, University of Arizona, • United States)**Lydia Jennings** (Department of Environmental Studies, Dartmouth College • United States)**Maui Hudson** (Te Kotahi Research Institute, University of Waikato • New Zealand)**Stephanie Russo Carroll** (Native Nations Institute, Udall Center for Studies in Public Policy, University of Arizona • United States)

Abstract

Since their publication in 2019, the CARE Principles have become a leading resource guiding the development of policies and practices for the governance of Indigenous data. The CARE Principles have informed national and international policies around the world, such as the Australian Institute of Aboriginal and Torres Strait Islander Studies (AIATSIS) Code of Ethics for Aboriginal and Torres Strait Islander Research, the United Nations Educational, Scientific, and Cultural Organization (UNESCO) Recommendation on Open Science, and the Policy Partnership on Science, Technology, and Innovation (PPSTI) Statement on Open Science. As universities, repositories, governments, and other data-holding institutions increasingly acknowledge and endorse the CARE Principles, and mandate their application within their organizational policies, new tools are needed to guide, assess, monitor, and ensure that CARE implementation adheres to the rights, interests, and protocols of the Indigenous Peoples and communities from which data derive.

The CARE Data Maturity Model (CARE DMM) will meet this need, serving as a tool to iteratively assess and improve the strength of CARE implementation in data ecosystems and infrastructures. After the release of CARE, RDA International IDSov IG members collaborated with FAIR Data Maturity Model WG members to plan the development of a CARE DMM. The CARE DMM core team will present progress on the CARE DMM, including criteria and indicators (i.e., measurable actions for the governance of Indigenous data) to evaluate an organization or project's policies, practices, relationships, and data infrastructure for alignment to the CARE Principles. Feedback will be sought on the applicability of the CARE DMM to data practitioners' contexts, the scope of the criteria and indicators, and how to translate the indicators into a user-friendly, web-based tool. Finally, progress on the application and endorsement of the tool will also be shared, for instance, in the American Geophysical Union's CARE Publishing and Authors Guidelines. As

Session: 6799422-1**7020838**

22/10/25 | 11:15

Room: Cauca

ORAL • EN

Implementing mechanisms to assert Indigenous provenance across the globally federated Ocean Data and Information System (ODIS)

Presenter

Pier Luigi Buttigieg

Authors

Pier Luigi Buttigieg (Alfred Wegener Institute • Germany)

Ashley Rojas (Local Contexts • United States)

Abstract

In this contribution, we describe the initial phase of implementing the CARE Principles in the Ocean Data and Information System (ODIS; <https://odis.org>), a federation of globally distributed, independent data systems coordinated by the International Oceanographic Data and Information Exchange (IODE) of UNESCO's Intergovernmental Oceanographic Commission (IOC). ODIS mediates an active, interoperable (meta)data layer that spans across all ocean data, including biodiversity data from systems such as the Ocean Biodiversity Information System (OBIS). Together with Local Contexts, the ODIS coordination team has co-developed an expression of the Traditional Knowledge (TK), Biocultural (BC) Labels, and Notices (<https://localcontexts.org/labels/>) in the widely adopted and domain-neutral semantic context of schema.org, and templated their serialisation in JSON-LD. This implementation supports digital exchanges based on linked open data (LOD), the natural modality for data on the Web and ODIS. Further, the associated specifications are being incorporated into the ODIS Book: an UNESCO-IOC resource that sets global norms for oceanographic data exchange across the entire ODIS Federation.

This focused effort is of considerable consequence, fusing 1) the Provenance, Protocol, and Permission Labels and Notices which Local Contexts has developed through sustained partnership with multiple, globally distributed Indigenous communities and 2) the core technical specifications of the ODIS Architecture that are federating ocean data systems from continental-scale hubs to single-team initiatives across sectors. The result is a concrete mechanism for Indigenous communities to assert the provenance of digital assets, the conditions for using and sharing them, as well as acceptable modes of engagement that result from digital interactions. While comprehensively implementing the CARE Principles across global-to-local contexts will be a multi-decadal effort, these efforts represent a significant step in their realisation, which we hope will inspire and support similar implementations.

Session: 6799422-1**7016074**

22/10/25 | 11:30

Room: Cauca

ORAL • EN

Learnings about Data Governance of fungal environmental DNA from Indigenous territories in South America

Presenter

Adriana Corrales

Authors

Adriana Corrales (SPUN • United States)

Bethan Manley (SPUN • United States)

Sujai Kumar (SPUN • United States)

Daniela Soto-Hernandez (Chile)

Michael Van Nuland (SPUN • United States)

Toby Kiers (SPUN • Netherlands)

Abstract

Although Indigenous peoples only account for 5% of the world's population, their territories contain around 80% of the world's remaining biodiversity, therefore they play a fundamental role in any strategy towards conservation as well as their cosmologies and practices. SPUN, the Society for the Protection of Underground Networks is a science based non-profit organization that has as its mission to protect and harness the fungal networks that regulate the Earth's climate and ecosystems. Therefore, engaging Indigenous communities constitutes a key effort toward recognizing their leadership in conservation, as well as offering sovereignty and new tools to defend their biodiversity, cultures and territories.

SPUN develops expeditions to underexplored areas around the world to produce scientific data on mycorrhizal fungal communities based on sequencing of environmental DNA to help increase our understanding of the ecology of mycorrhizal fungi around the world, while also helping to improve local collaborations and scientific capacities. In collaboration with the More Than Human Life (MOTH) program and Local Contexts we are currently developing protocols for scientific expeditions and post-expedition data management on Indigenous territories based on CARE Principles for Indigenous Data Governance. In this way, we have developed two expeditions to ancestral Indigenous territories, one to Sarayaku territory (Ecuador) and one to the Atacama desert (Chile) which have been co-constructed with the local Indigenous scientists and communities. In this talk we would like to share our experiences working with Indigenous communities in South America and our learnings about the recognition of what it means to carry out scientific work in collaboration with Indigenous scientists and communities in their ancestral Indigenous territories and the importance of safekeeping their biological data.

Session: 6799422-1**7018880**

22/10/25 | 11:45

Room: Cauca

ORAL VIRTUAL • EN

Integrating Biocultural Labels and Notices into the Nationally Significant Biological Collections at Manaaki Whenua -- Landcare Research

Presenter

Meredith McKay

Authors

Aaron Wilton (Manaaki Whenua - Landcare Research • New Zealand)

Holden Hohaia (Manaaki Whenua - Landcare Research • New Zealand)

Hone Kapa (Manaaki Whenua - Landcare Research • New Zealand)

Bevan Weir (Manaaki Whenua - Landcare Research • New Zealand)

Meredith McKay (Environment Canterbury • New Zealand)

Abstract

Manaaki Whenua – Landcare Research is the custodian of five of New Zealand’s nationally significant biological collections. These encompass preserved specimens in the Allan Herbarium (CHR), Fungal Herbarium (PDD), and New Zealand Arthropod Collection (NZAC), as well as living collections in the National New Zealand Flax Collection (*Phormium* spp.) and the International Collection of Microorganisms from Plants (ICMP). Together, these collections contain material dating from the 1700s to the present day, with a primary focus on Aotearoa New Zealand but also including significant global representation.

In 2022, we participated in a collaborative project with five iwi – Te Roroa, Taranaki Iwi, Whakatōhea and Ngāti Maru – to implement Biocultural Labels and Notices across these collections. Through this partnership, Notices have been systematically applied to all biological objects in these collections. In parallel, iwi partners have applied Local Contexts Labels to specimens collected within their respective rohe (territories). As part of the project we established automated processes to ensure new digital records are integrated into the Local Contexts projects.

In this presentation, we will share key insights, challenges, and outcomes from this kaupapa (project). We will briefly outline some of our subsequent and ongoing work.

Session: 6799422-1**7013795**

22/10/25 | 12:00

Room: Cauca

ORAL • EN

Reconnecting New York Botanical Gardens Herbarium specimen records back to Country

Presenter

Rose Barrowcliffe

Authors

Rose Barrowcliffe (Centre of Critical Indigenous Studies, Macquarie University • Australia)

Dakota Feirer (Australia)

Abstract

One of the biggest challenges to implementing the CARE principles is finding Indigenous data and reconnecting it with the Indigenous knowledge authorities to whom it relates. On a visit to New York Botanical Gardens (NYBG), we were surprised to discover that the NYBG Herbarium holds over twenty thousand botanical specimens that were collected from around Australia across the course of colonisation. As Aboriginal people, our first question was, “Whose Country were these specimens collected from?”, so we embarked on a project to answer that question. In this ENRICH-funded project, we explored different ways to correlate NYBG Herbarium specimen records to the Aboriginal and Torres Strait Islander Countries from which the specimens were collected. The Indigenous provenance of data held in collecting institutions is often hidden behind metadata and systems that preference non-Indigenous worldviews and descriptors. In the first stage of the project, we developed a process using GBIF datasets and data analysis to correlate geolocation metadata to Aboriginal and Torres Strait Islander Country. The process gave NYBG an understanding of whose Indigenous data they are holding. In the second stage of the project, we are working with NYBG and Local Contexts to have BC Notices applied to the Australian specimen records. In this presentation, we discuss the stepped process for identifying Country and for reconnecting the specimen records back to Country. More importantly, we share the considerations throughout the process for how to embed the CARE principles in the reconnection process to support Indigenous data governance in NYBG Herbarium records now and into the future.

Session: 6799422-1**7020640**

22/10/25 | 12:15

Room: Cauca

ORAL • EN

From FAIR to CARE: Supporting Indigenous cultural authority by integrating Local Contexts in GBIF hosted portals

Presenter

Kyle Copas

Authors

Kyle Copas (GBIF Secretariat • Denmark)

Mélianie Raymond (GBIF Secretariat • Denmark)

Federico Mendez (GBIF Secretariat • Denmark)

Corrie Roe (Local Contexts • United States)

Ashley Rojas (Local Contexts • United States)

Maui Hudson (Local Contexts • New Zealand)

Jane Anderson (Local Contexts • United States)

Lydia L. Jennings (Dartmouth College • United States)

Erin Robinson (Metadata Game Changers • United States)

Abstract

In late 2024 and early 2025, GBIF began recruiting the members of a task group on Indigenous data governance. Along with its other activities, this group has a remit to guide a pilot project to enhance the GBIF infrastructure's capabilities to support Indigenous data sovereignty and recognize cultural authority in collections and data. Developed through a collaboration between three Indigenous communities—the Whakatōhea (New Zealand), the Pueblo Kichwa de Sarayaku (Ecuador) and Te Ora Fenua (French Polynesia)—Local Contexts (LC), and the GBIF Secretariat and nodes, these proofs-of-concept will explore the viability of adopting LC labels within the GBIF infrastructure. This work is intended both to demonstrate potential methods for operationalizing the CARE Principles of Indigenous Data Governance within GBIF and to provide signals developing standards for implementing labels and notices across both community and global scales.

Each of the three Indigenous communities involved have experience applying LC labels, and customized versions of the GBIF's hosted portal service will offer platform for integrating them within species occurrence records from dataset targeted as relevant to each community. The initial display will leverage the flexibility of the Darwin Core dynamicProperties term, demonstrating possible approaches for developing standardized terms and/or extensions to support more programmatic display of Indigenous-related information.

The targeted datasets present a useful mix of consistency and diversity, representing a natural history collection, a long-term marine eDNA monitoring project, and born-digital eDNA soil samples. Each will appear hosted portals customized to display LC label information integrated in individual occurrence records, both at community level and at global scale where the results might be compared and contrasted. Their connections in DNA barcoding will also provide a testbed for aligning with the Convention on Biological Diversity's recent decisions on the use of digital sequence information (DI) on genetic resources.

Session

6786653

Symposium

22/10/25 | 14:00

Room: Ballroom A

Data model for global implementation of open Digital Specimen & the status of specimen digitization

Organizers

Wouter Addink

Sharif Islam

Sam Leeftang

Anton Güntsch

Claus Weiland

Elspeth Haston

Mathias Dillen

Ben Norton

Cat Chapman

Description

The open Digital Specimen (openDS) framework provides a standardized data model for digitally representing physical specimens and derived data, enabling seamless data sharing, integration, and reuse across global research infrastructures. This session will present key aspects of the openDS data model, highlighting its role in supporting the FAIR principles (Findable, Accessible, Interoperable, Reusable), persistent identifiers and biodiversity information standards.

A walkthrough and demonstration of the practical implementation of the openDS data model will be provided. The session will cover the integration of controlled vocabularies via a dedicated Vocabulary Server, ensuring semantic consistency and interoperability. Attendees will gain insights into how openDS can be leveraged for robust, scalable, and interoperable specimen data management, fostering a globally connected digital specimen network.

The session will also present the Minimum Information about a Digital Specimen (MIDS) specification. The digitisation of the world's natural science collections is expanding massively and providing a unique global resource for answering some of the most fundamental bio- and geodiversity questions. The ability to measure and monitor the level of digitisation of each individual specimen, in each collection within each country has never been more important. MIDS, along with the implementations to calculate the MIDS score of specimens and collections, provides users with tools to help develop a digitisation strategy, and plan and manage a digitisation programme, including prioritisation and data enhancement.

The session will show how MIDS, Darwin Core and ABCD (Access to Biological Collection Data) standards align with openDS, facilitating compatibility with existing biodiversity and earth science data infrastructures.

By addressing vocabulary semantics and their role in data harmonization, this session will highlight the importance of standardized terminology in earth and natural sciences.

Session: 6786653**7018482**

22/10/25 | 14:05

Room: Ballroom A

ORAL VIRTUAL • EN

Towards a Common Language for Digital Specimens: Exploring the openDS Data Model

Presenter

Sam Leeflang

Authors

Sam Leeflang (Naturalis Biodiversity Center • Netherlands)

Soulaine Theocharides (Naturalis Biodiversity Center • Netherlands)

Abstract

With the rapid decline of biodiversity, it is essential to scale up our knowledge of the life around us. Natural history collections play a vital role in this effort, providing reliable, traceable and historical information about the species on the planet. However, most of the specimen information is still locked in the collections. Combining our knowledge, resources, and expertise is essential to accelerate the digitisation process. To facilitate this collaboration on a European level, the Distributed System for Scientific Collections (DiSSCo) is being founded.

Within DiSSCo we will provide a platform where machines and humans can collectively work on enhancing and curating specimen data. The tools for this platform will be built by a diverse group of service providers. To ensure that all providers use a common language and understanding of the specimen metadata, we need an all encompassing, extensible data model. Not only will this data model need to provide the option to handle any specimen related metadata, it also needs to ensure the data will follow the latest FAIR Digital Object principles. We call this new data model, the open Digital Specimen (openDS).

openDS has been developed by building on existing TDWG standards such as Darwin Core, Audiovisual Core and Chronometric Age as well as broader standards such as Schema.org, W3C Web Annotation and Prov-Ontology. It can be seen as an implementation of the Darwin Core Conceptual Model and will ensure lossless data transfer to and from a Darwin Core Data Package (DwC-DP). In 2024 openDS was publicly reviewed and since December 2024 it is the backbone of DiSSCo's Core infrastructure.

During this session, we will guide the audience through the data model. With its 7 top level classes, a range of generic nested classes and hundreds of terms, this can be a daunting effort for anybody.

Session: 6786653**7016607**

22/10/25 | 14:20

Room: Ballroom A

ORAL VIRTUAL • EN

Building and Serving FAIR Terms and Vocabularies for open Digital Specimen

Presenter

Sharif Islam

Authors

Sharif Islam (Naturalis Biodiversity Center • Netherlands)

Abstract

This presentation introduces the vocabulary infrastructure under development in DiSSCo for the openDS (open Digital Specimen) framework, focusing on the management of terms and controlled vocabularies as FAIR (Findable, Accessible, Interoperable, and Reusable) Digital Objects (FDOs) to support semantic interoperability and machine-actionable data.

The vocabulary service defines terms within the “ods” namespace, used throughout the openDS schema. Following TDWG guidance, a term in openDS is defined as an entity representing a class, property, or concept, identified by an IRI and accompanied by human-readable labels and definitions. A vocabulary is a curated collection of such standardised terms.

This implementation also enables constraints on literal values and establishes relationships among terms through controlled values. For instance, disciplinary metadata (e.g., ods:topicDiscipline) and origin metadata (e.g., ods:topicOrigin) are governed by predefined properties (e.g., values like Botany, Geology, Zoology, Natural, Human-made), ensuring standardised representation and consistent usage across collections. Each value (such as “Botany”) is itself treated as a FDO, with a persistent identifier, metadata, and machine-readable representation. These values could also be linked using `rdfs:isDefinedBy`, which references the authoritative source where the term is formally described or `skos:inScheme`, which places the concept within a SKOS-compliant concept scheme. Together, these properties provide both structural and semantic context for each term.

The talk will demonstrate how this vocabulary implementation integrates with the openDS and the MIDS (Minimum Information about a Digital Specimen) specification and other existing standards. These alignments are essential for harmonising term usage across infrastructures such as GBIF, ENA, BOLD, LifeWatch, and eLTER. This presentation makes the case for domain-specific vocabulary infrastructure that is rooted in open standards but tailored for federated biodiversity data systems. By managing terms as FDOs, the openDS vocabulary service enables scalable, interoperable, and semantically robust data workflows across infrastructures and institutions.

Session: 6786653**7020574**

22/10/25 | 14:30

Room: Ballroom A

ORAL • EN

What is the status of global digitisation? MIDS as an institutional & global digitisation standard

Presenter

Elspeth Haston

Authors

Elspeth Haston (Royal Botanic Garden Edinburgh • United Kingdom)

Cat Chapman (United States)

Ben Norton (Independent • United States)

Stefan Seifert (Bavarian State Collections of Natural History (SNSB) • Germany)

Wouter Addink (Naturalis • Netherlands)

Marie Briggs (Royal Botanic Garden Edinburgh • United Kingdom)

Sam Leeflang (Naturalis • Netherlands)

Mathias Dillen (Meise Botanic Garden • Belgium)

Abstract

The digitisation of the world's natural science collections is expanding massively and providing a unique global resource for answering some of the most fundamental bio- and geodiversity questions. However, digitisation at this scale can only be done in stages. The ability to measure and monitor the level of digitisation of each individual specimen, each collection within each country on a global scale has never been more important. The Minimum Information about a Digital Specimen (MIDS) specification along with implementations which can calculate the MIDS score of specimens and, by extension, datasets, provide users with tools to help develop a digitisation strategy as well as plan, manage and monitor a digitisation programme, including prioritisation and data enhancement. For researchers, the MIDS score of published specimens gives information about the expected amount of associated data for intended analyses, including geographic coordinates and identifiers.

The MIDS website (<https://tdwg.github.io/mids/>) provides access to the current draft. The four MIDS levels are described and a detailed schema for the information elements includes the label, definition, purpose and examples as well as the disciplines for which each element is required. The website explains how the Simple Standard for Sharing Ontology Mappings (SSSOM) is being used to map MIDS to DwC and ABCD terms and provides a tabulated quick reference of MIDS mappings. Links to tools are provided for users to calculate MIDS scores for DwC and ABCD datasets, including the MIDS Calculator (<https://github.com/AgentschapPlantentuinMeise/MIDSCalculator>) and a reference implementation as part of the open Digital Specimen model with the Distributed System of Scientific Collections (DiSSCo) where the MIDS level is calculated for each digital specimen.

Session: 6786653**7012924**

22/10/25 | 14:45

Room: Ballroom A

ORAL VIRTUAL • EN

MIDS in practice: Comparing specimen digitisation levels

Presenter

Mathias Dillen

Authors

Mathias Dillen (Meise Botanic Garden • Belgium)

Ben Norton (United States)

Cat Chapman (United States)

Elsbeth Haston (Royal Botanic Garden Edinburgh • United Kingdom)

Marie Briggs (Royal Botanic Garden Edinburgh • United Kingdom)

Abstract

The MIDS standard aims to indicate the digitisation level of natural history specimens on a simple scale. Much progress has been made over the past year to standardise this process for optimal reusability and scalability. The Simple Standard for Sharing Ontological Mappings (SSSOM) framework has been adopted by the MIDS task group for this purpose and mappings are now available for Darwin Core archives and ABCD. The use of SSSOM mapping sets should facilitate the assessment of digitisation status over time, for different kinds of specimens and for different data standards and their serialisation.

In this presentation, we will show the results of calculating MIDS levels for those different use cases when applied to several datasets, using the MIDSCalculator and the GBIF MIDS Checker tools. We will determine the reasons why MIDS levels were (not) met, highlighting the impact of MIDS information element definitions and, in particular, their mappings to different standards and the stability of their implementation in different kinds of software. These results should show the feasibility of enabling MIDS across different infrastructures and promote implementation of the MIDS standard.

Session: 6786653**7001210**

22/10/25 | 14:55

Room: Ballroom A

ORAL VIRTUAL • EN

Compound Specimen Model

Presenter

Ben Norton

Authors

Ben Norton (Independent • United States)

Abstract

The Traditional, Simple Model

In biological collections, most specimens are identified by a singular Linnaean taxonomic classification, referred to as the “determination.” A classification may change over time, while the singular identity remains. From a modeling perspective, this is represented by a one-to-one relationship between specimen and determination. This relationship is fundamental to the Simple Specimen Model, a conceptual model for the digital representation of physical specimens identified by a singular determination. This flat paradigm is effective for most collections and has been embraced by almost all current collections management systems and data publication standards.

A Compound Solution

The Simple Specimen Model is not without shortcomings. The most notable case involves specimens defined by several determinations. Here, the Simple Specimen Model does not support the one-to-many relationship between a specimen and its determinations. For instance, *Chelonibia testudinaria*, a barnacle species, is commonly found attached to the shells of *Caretta caretta*. The sea turtle and the barnacle are separate organisms physically conjoined as a single object. These are especially pronounced in geological collections where most specimens are aggregates of multiple earth materials. Examples include a limestone containing coral and brachiopod fossils and a specimen containing an equal proportion of apophyllite and stilbite. We refer to these as Compound Specimens.

Extended specimen network connections are impeded, and substantial information loss occurs when compound specimen data is stored using the Simple Specimen Model. To address these issues, we created a new conceptual data model that makes compound specimen data meaningful and discoverable. We call this model the Compound Specimen Model. In this presentation, we will introduce the Compound Specimen Model, summarize its structure compared to its Simple Specimen Model counterpart,

and describe its significance in ongoing initiatives, including the TDWG Mineralogy Extension and the upcoming Darwin Core Data Package.

Session: 6786653**7022567**

22/10/25 | 15:05

Room: Ballroom A

LIGHTNING TALK VIRTUAL • EN

Scaling Data Extraction from Natural History Records with Automated LLM-Based Methods.

Presenter

Minerva Singh

Authors

Minerva Singh (NHM • United Kingdom)

Ben Scott (NHM • United Kingdom)

Arianna James (United Kingdom)

Ken Norris (United Kingdom)

Abstract

Biodiversity institutions have documented collections using handwritten or typed index cards, accession records, and other structured documents. These often serve as the primary record of when, where, and how a specimen was collected, identified, and curated, and are essential for understanding the scientific and historical context of collections. However, the format and structure of these records vary widely, not only between institutions but within collections, reflecting changes in curatorial practices over time. We present a scalable pipeline that uses Large Language Models (LLMs) and task orchestration frameworks to extract, clean, and validate information from these diverse records. We began by collating a dataset of digitised index cards and labels from the diverse collection at the Natural History Museum, UK (NHMUK). These datasets were different in their own ways, many of which feature front-and-back content, challenging handwriting, and inconsistent field placements, and more.

This project was a generalised expansion of previous projects developed at NHMUK which focused on the automatic data extraction from specimen cards, beginning with the collection of egg index cards from the vast bird collection at NHM Tring. To generalise across formats and handle scale, we implemented Luigi-based task orchestration, allowing asynchronous processing of thousands of cards. YAML templates were used to define expected fields and map card types to prompt structures—ensuring transparency and modularity. A fundamental aspect of this is being able to use generic rather than card specific prompts (thus enabling the addition of other disparate card types without prompt modification). Multiple LLMs such as Claude and GPT were tested, and the modular approach of the workflow enables the inclusion of other LLMs.

Beyond data extraction, we are now building workflows to correct and validate outputs using existing biodiversity data repositories. As part of this, we reflect on lessons

Session: 6786653**7022902**

22/10/25 | 15:10

Room: Ballroom A

LIGHTNING TALK • EN

Contributions to biodiversity data in the Global South: Digitization progress and open data through the SiBBr at Museu Nacional|UFRJ

Presenter

Cristiana Silveira Serejo

Authors**Cristiana Serejo** (Museu Nacional|Universidade Federal do Rio de Janeiro • Brazil)**Mariane Targino** (Museu Nacional|Universidade Federal do Rio de Janeiro • Brazil)**Fernanda Amaral** (Museu Nacional|Universidade Federal do Rio de Janeiro • Brazil)**Marcus Vinicius de Almeida** (Museu Nacional|Universidade Federal do Rio de Janeiro • Brazil)**Aluf Elias** (Museu Nacional|Universidade Federal do Rio de Janeiro • Brazil)**Abstract**

In 2022, the ColBio Project was launched, together with the establishment of the Col-Digi Laboratory, a hub for digital infrastructure development and planning. New photograph stations, esteroscopic equipments, together with digitization protocols were implemented. Also, longtime databases runned in spreadsheet are being transfered to the collection management program Specify 7.0. This is as a first institutional initiative regarding a mass digitization of its biological collections. Main focus was to digitize initially rare, historical, and type material. Four major áreas of natural history collections are being worked out: Entomology, Invertebrates, Vertebrates and Botany. By December 2024, a total of 22,081 images had been captured, representing 4,544 specimens across 3,743 species. Among these, 3,805 images correspond to nomenclatural types, comprising 783 specimens and 645 species. Final image editing was also performed, including images captured under the SiBBr (Brazilian Biodiversity Information System) and ColBio projects, and individual initiatives. Nearly three thousand entomological type material images captured in the SiBBr Project were crucial for the digital preservation of part of the collection, since almost all physical specimens were destroyed in the 2018 fire. For the time being, 13 Museu Nacional biological collections databases (with few photos) are available at the SiBBr, a node of the GBIF plataforma. Organization to make available the photos herein mentioned is in progress. While integration into the SiBBr represents a nationally consolidated option, the feasibility of a dedicated institutional platform to promote collections data is also being considered. Such a platform would provide greater autonomy and visibility for the Museum's collections.

Session: 6786653**7012673**

22/10/25 | 15:15

Room: Ballroom A

LIGHTNING TALK • EN

Anarchy Unveiled: The Current State of “Standards” in Morphometric Data from Neotropical Lizards

Presenter

Juan Manuel Daza

Authors

Juan Manuel Daza (Instituto de Biología, Universidad de Antioquia • Colombia)

Katerine Rodriguez-Salazar (Instituto de Biología, Universidad de Antioquia • Colombia)

Abstract

Since the inception of biodiversity informatics, data standards (e.g. Darwin Core) have primarily focused on mobilizing primary biodiversity data derived from biological collections. In recent years, however, there has been growing interest in extending standardization efforts to encompass emerging data types, including ecoacoustic recordings, mark-recapture datasets, population monitoring, and environmental DNA (eDNA). Simultaneously, new technologies have enabled the generation of high-resolution 3D images from biological specimens. Yet, despite these advances, there remains a critical gap: the absence of widely adopted standards for morphometric data. Key issues include the lack of controlled vocabularies, inconsistent terminology, and a general anarchy in the definition and measurement of characters and their homologies. We investigated this issue using the lizard genus *Anolis*, the most species-rich lizard genus in the Americas and a widely used model in studies of biogeography, ecomorphology, trait evolution, and speciation. We reviewed over 80 scientific publications to evaluate how meristic and linear morphometric characters have been applied. Our analysis revealed substantial inconsistencies in trait nomenclature, differences in the identification and use of homologous landmarks, and broad variability in the application of morphometric measurements across studies. We further assessed these findings through the lens of the FAIR principles. We demonstrate that addressing this morphometric anarchy is essential for ensuring interoperability, reproducibility, and the long-term value of morphological data in biodiversity science.

Session: 6786653**7018655**

22/10/25 | 15:20

Room: Ballroom A

LIGHTNING TALK • EN

Quality Assurance in Large-Scale Herbarium Transcription: Standards, Methods and Lessons Learnt

Presenter

Olive Adams

Authors

Olive Adams (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

The Royal Botanic Gardens, Kew houses one of the world's largest and most comprehensive botanical collections, with over 6.4 million herbarium specimens and 1.1 million fungarium specimens. As part of its commitment to increasing access to scientific data, Kew is nearing the end of a four-year Science Collections Digitisation project. The project aims to produce high-resolution images and accurate transcriptions, alongside associated metadata. To achieve this, a dual approach was adopted: standard herbarium specimens were digitised by an external supplier, while an in-house team focused on more complex and bulky material.

Delivering high-quality transcriptions at scale presents challenges, particularly in balancing the rapid processing of large volumes of material with the need for accurate, consistent and reusable data that can support future research. To address this, a comprehensive quality assurance (QA) workflow was developed to monitor outputs, manage errors and ensure transcriptions were standardised across the project to support FAIR principles and Minimal Information about a Digital Specimen (Level 2) requirements.

Focusing on the in-house team, this presentation will outline key elements of the QA workflow, including the role of curatorial support, training requirements for a team of over 25 digitisation officers and data cleaning of transcription outputs prior to import into a new integrated collections management system. It will also explore the challenges of adapting workflows, responding to changing priorities and maintaining consistency both pre- and post-transcription. Finally, the presentation will share lessons learnt and reflections that may support other institutions undertaking large-scale transcription projects.

Session

6799373

Symposium

22/10/25 | 14:00

Room: Ballroom B1

Leveraging partnerships across data providers to facilitate synthesis of biodiversity data

Organizers

Eric Sokol

Chandra Earl

Kate Ingenloff

Greg Maurer

Marty Downs

Description

Environmental data science is rapidly changing as increasing data availability and recent advances in technology, including AI/ML-based tools, reconfigure the field. Biodiversity data providers and data users both face a new landscape of opportunities and challenges. Data users have unprecedented opportunities to synthesize data to address global challenges, but face an ever growing diversity of data sources and standards. Many data providers and aggregators, including the National Ecological Observatory Network (NEON) in the US, the US Long Term Ecological Research (US LTER) program, and the Global Biodiversity Information Facility (GBIF), are trying to understand the needs of data users and how to leverage partnerships to increase data interoperability and compatibility with new technologies (e.g., AI/ML tools) and to build tools to facilitate synthesis work. We invite biodiversity data providers, data aggregators, and data users to present on their experiences in lightning talks and then join a panel discussion about opportunities to leverage partnerships in this space to lower barriers in the synthesis of biodiversity data.

Session: 6799373**7020523**

22/10/25 | 14:05

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

The road to interoperability: finding common ground among biological data providers

Presenter

Kelsey Huelsman

Authors**Kelsey Huelsman** (NASA | GESTAR-II | Earth Resources Technology • United States)**Stephen Formel** (Formel Data Services • United States)**Shawn Serbin** (NASA Goddard Space Flight Center • United States)**Kristen “Kit” Lewers** (NASA Goddard Space Flight Center | University of Colorado Boulder • United States)**Abstract**

We highlight existing findable and accessible “bottom-up” (on-the-ground) data that are available from providers, including the Global Biodiversity Information Facility (GBIF), U.S. Forest Service (USFS), the Long-Term Ecological Research (LTER) Network, and the National Ecological Observatory Network (NEON). Although these data are generally findable and accessible, they are not inherently interoperable, due to differences in database organization and labeling schemes. As a case study, we created a workflow to promote the interoperability of GBIF and NEON vegetation occurrences by applying the DarwinCore biological data standard used by GBIF to NEON’s vegetation survey data. We then examine the potential of additional data aggregation from other providers that would complement and augment biodiversity synthesis via interoperability. We highlight the importance of FAIR (Findable, Accessible, Interoperable, and Reproducible) data and demonstrate the relative ease with which biological data standards, such as DarwinCore (DwC), can be applied to make data interoperable. Interoperability is a crucial component in the holistic analysis of biodiversity across space and time. We close by highlighting how these data can be further leveraged, by pairing them with available “top-down” hyperspectral aerial imagery in preparation for NASA’s Surface Biology and Geology (SBG) satellite mission, and additional opportunities to facilitate the synthesis of biodiversity data.

Session: 6799373**7020534**

22/10/25 | 14:10

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

Harmonising systematic survey Observations : Applications of the TERN Ontology in Ecology

Presenter

Siddeswara Guru

Authors

Siddeswara Guru (University of Queensland • Australia)

Junrong Yu (University Of Queensland • Australia)

javier Sanchez Gonzalez (University Of Queensland • Australia)

Abstract

Terrestrial Ecosystem Research Network (TERN) is Australia's national collaborative research infrastructure that facilitates the collection, collation, curation, and publication of terrestrial ecosystem data. TERN collects ecological data from survey plots across Australia using standard protocols. Several agencies across different jurisdictions conduct site-based systematic surveys to make ecological observations. Although the observed properties are similar, these systematic surveys use varying methods and procedures. Therefore, these data can only be analysed within the jurisdiction where they are collected.

However, integration of these datasets is critical for cross-jurisdiction analysis and synthesis.

TERN Ontology is a semantic framework developed to support the standardised representation of site-based systematic surveys and associated artefacts for data integration and exchange. The ontology provides a shared set of vocabularies to describe core concepts of sites, site visits, activities during the site visits, features of interest and related observations. The phenomenon measured is captured as a result of observations of the feature, and each observation relates to one observable property. The Ontology has core classes and additional controlled vocabularies to describe domain feature types, observable properties, attributes, methods and Units of Measurement. The ontology facilitates interoperability across heterogeneous datasets and enables linking thematic, spatial and temporal information across ecological sites, systematic surveys and long-term ecological research programs.

The TERN Ontology is aligned with W3C Semantic standards, particularly Semantic Sensor Network and Sensor, Observation, Sample, and Actuator (SOSA) ontologies and dependencies on Dublin core, Darwin core and GeoSPARQL. The ontology is implemented in TERN EcoPlots, the data integration platform for site-based system surveys, enabling users to search and integrate ecological surveys across disparate data sources.

The presentation will introduce the structure and representation of the TERN Ontology and highlight its application to integrate systematic survey data across multiple data sources.

Session: 6799373**7010101**

22/10/25 | 14:15

Room: Ballroom B1**LIGHTNING TALK • EN**

Mapping Your Neighbourhood Avifauna (MYNA): Empowering Biodiversity Conservation through Citizen Science in India

Presenter

Sanjeev Menon

Authors

Praveen J (Nature Conservation Foundation • India)

Sanjeev Menon (State of India's Birds • India)

Ashwin Viswanathan (Nature Conservation Foundation • India)

Pradeep Koulgi (India)

Abstract

The Mapping Your Neighbourhood Avifauna (MYNA) web tool, developed under the State of India's Birds (SoIB) initiative, exemplifies the transformative potential of citizen science in biodiversity monitoring and conservation. MYNA enables users to generate localized bird checklists and conservation assessments by selecting any geographic area—be it a district, wetland, or village—on an interactive map. This tool democratizes access to avian data, fostering community engagement and facilitating data-driven conservation actions.

MYNA's integration of extensive citizen-contributed data from platforms like eBird allows for deferred visualization of species distributions and trends. By aligning with FAIR (Findable, Accessible, Interoperable, Reusable) data principles, MYNA ensures that biodiversity information is accessible and actionable for researchers, policymakers, and local communities alike.

The platform has already demonstrated tangible conservation impacts. In Tamil Nadu, MYNA data was instrumental in halting the felling of over 2,000 trees at Elathur Lake, a critical avian habitat. Similarly, in Kancheepuram, the tool aided in protecting nesting sites of cormorants and egrets at Damal Lake. On the other hand in Andhra Pradesh, the MYNA report strengthened the Gudem-Marripakala biodiversity data report in its proposal to be a biosphere reserve with a core and buffer zone encouraging tribal rights. Also, in Telangana, MYNA reports were used to support conservation of Tiger corridors, proposals for new wildlife sanctuaries and to correct Environment Impact Assessments in urban areas to stop deforestation. These instances underscore MYNA's role in translating data into conservation outcomes.

By facilitating localized biodiversity assessments, MYNA exemplifies how open-access data platforms can bridge the gap between citizen observations and policy interventions, promoting inclusive and effective biodiversity conservation strategies.

This presentation will delve into MYNA's development, functionalities, and its role in empowering communities to participate in biodiversity monitoring. It will also discuss the platform's alignment with global biodiversity data standards and its potential as a model for similar initiatives worldwide.

Session: **6799373****7020425**

22/10/25 | 14:20

Room: Ballroom B1

LIGHTNING TALK • EN

Ship to shelf: Scripps Oceanography's Pelagic Invertebrate Collection, supporting sample collection, marine biodiversity data production and storage for global users

Presenter

Linsey M. Sala

Authors

Linsey M. Sala (Scripps Institution of Oceanography at UC San Diego • United States)**Moira Décima** (Scripps Institution of Oceanography at UC San Diego • United States)**Mark D. Ohman** (Scripps Institution of Oceanography at UC San Diego • United States)

Abstract

The Scripps Pelagic Invertebrate Collection (SIO-PIC) works in close partnership with the *California Current Ecosystem* Long Term Ecological Research (CCE-LTER) and California Cooperative Oceanic Fisheries Investigations (CalCOFI) programs to produce and store physical samples, specimens, and data. In 2020, we joined a consortium of 18 other institutions across the United States to establish a Thematic Collection Network (TCN) through the NSF-supported Advancing Digitization in Biodiversity Collections (ADBC) program. This TCN, *Documenting Marine Biodiversity through Digitization of Invertebrate Collections (DigIn)* set out to digitize and mobilize 835K lots, representing 7.5 million specimens - with SIO-PIC digitizing ~34,500 lots, available through Global Biodiversity Information Facility (GBIF) and Integrated Digitized Biocollections (iDigBio). The collaborative network built through DigIn helped provide the scaffolding for our collection to serve voucher specimen data from our archives and collaborating program sample sets, while supporting FAIR principles (Findable, Accessible, Interoperable, Reusable) on a global scale. We assembled diverse investigators' voucher collections and specimens from our collection over the last hundred years, under one standardized umbrella within our collection management system. This significantly improves the way we track and share our materials, including adopting biodiversity information standards (i.e. Darwin Core (DwC), World Registry of Marine Species (WoRMs) taxonomy), persistent identifiers, and vocabulary semantics. These data serve diverse research activities, as well as teaching, training, and supporting the next generation of students, scientists, leaders, and public service professionals to find solutions to environmental challenges. We look forward to sharing this recent chapter of our collection's evolution and exploring opportunities towards emerging data services and applications.

Session: 6799373**7015839**

22/10/25 | 14:25

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

Translating ecological data to advance biodiversity data synthesis and partnerships through the U.S. National Ecological Observatory Network (NEON) Biorepository

Presenter

Kelsey Yule

Authors**Kelsey Yule** (NEON Biorepository, Arizona State University • United States)**Chandra Earl** (NEON Biorepository, Arizona State University • United States)**Edward Gilbert** (NEON Biorepository, Arizona State University • United States)**Abstract**

The U.S. National Ecological Observatory Network (NEON) is a continental-scale observatory providing open-access data to support research on environmental change. In addition to more than 180 data products arising from field observations, automated instruments, and airborne remote sensing, NEON collects samples from all 81 field sites that are archived by the NEON Biorepository and published via a customized, Symbiota-based data portal. While NEON field protocols are highly internally standardized across space and time, their ecologically-focused data structures are not necessarily aligned across taxonomic groups or research objectives. The NEON Biorepository works within the broader NEON ecosystem to essentially serve as a mid-level data aggregator, transforming disparate ecological data products into a single source of biodiversity occurrence data following Darwin Core standards. Doing so relies on API-assisted data translation efforts that pull from multiple NEON data products to create integrated occurrence records and extend specimens by automating the linkages between associated sample records and to NEON- and researcher-derived genetic, genomic, and trait data. Ultimately, these translations increase the actionability of NEON biodiversity-centric data for users through contributions to global aggregators (e.g. the Global Biodiversity Information Facility). Additionally, they allow us to serve as an exemplar for advancements in biodiversity data standards, such as the Humboldt Extension for Ecological Inventories and Darwin Core Data Package, through partnerships with Biodiversity Information Standards (TDWG). To reach new research communities, we partner with Earth Science Information Partners (ESIP) to evaluate the readiness of our data for AI/ML applications. We continuously undertake highly customized on-the-ground collections management and bioinformatics efforts to support projects led by various institutes (e.g. Imageomics) and hundreds of individual research teams. Moving forward, we seek input from potential users to understand the extensions and improvements that will most immediately lower barriers to use and facilitate novel research.

Session: 6799373

7020088

22/10/25 | 14:30

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

Tracking Year-over-Year Forest Dynamics at SJER Using Multimodal and Multiplatform Data

Presenter

Kristen (Kit) Lewers

Authors

Kit Lewers (NASA Goddard Space Flight Center and University of Colorado Boulder • United States)

Abstract

Understanding annual shifts in forest structure and species composition is key to monitoring ecological resilience. In this lightning talk, I introduce an algorithmic pipeline under development that integrates LiDAR, hyperspectral, RGB, and ground truth data from the NEON site at San Joaquin Experimental Range (SJER), California. By aligning repeated airborne observations with field plot data, the workflow aims to enable year-over-year tracking of individual trees and canopy-level biodiversity change. This approach combines crown delineation, species classification, and vertical structure from LiDAR to detect turnover and growth dynamics. The goal is to generate standardized biodiversity outputs that can be mobilized to platforms like GBIF, creating a replicable model for cross-year ecological monitoring.

Session: 6799373**7007581**

22/10/25 | 14:35

Room: Ballroom B1

LIGHTNING TALK • EN

Beyond spatial bias: Understanding the colonial legacies and contemporary social forces shaping biodiversity data

Presenter

Melissa Chapman

Authors

Melissa Chapman (ETH Zürich • Switzerland)

Hilary Faxon (University of Montana • United States)

Abstract

With over 2 billion observations of species from across the earth, the Global Biodiversity Information Facility (GBIF) has become an influential repository of information for not only ecologists, but also conservation scientists and policy makers. Yet biodiversity data reveal more than species distributions. They reflect colonial histories, economic inequities, and cultural differences. In this talk, we summarize a recent article that argues for moving beyond ideas of “spatial bias” in conservation science to highlight the colonial legacies and contemporary social forces that shape biodiversity data. Drawing on interviews with the GBIF staff and data publishers as well as critical mapping of GBIF data patterns, we visualize and analyze how and why colonial patterns persist and shift in this global biodiversity data. To explain diverse trajectories of postcolonial production of data, we identify three social forces—colonial legacies of collecting, infrastructures of international development, and contemporary data cultures—that structure biodiversity observation distributions and data ownership and availability. Together, these findings demonstrate how colonial and postcolonial practices and politics continue to shape what we know about the natural world, providing a foundation for considering opportunities for improved synthesis of biodiversity data.

Session: 6799373**7018527**

22/10/25 | 14:40

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

Connecting Sound and Life: Integrating Noise and Cetacean Databases for Marine Ecosystem Understanding

Presenter

Carlos Pinto

Authors

Carlos Pinto (ICES • Denmark)

Maria Makri (ICES • Denmark)

Joana Ribeiro (ICES • Denmark)

Neil Holdsworth (ICES • Denmark)

Abstract

Since 2015, ICES has developed several key databases to support marine environmental assessments. The Impulsive Noise Registry (<https://underwaternoise.ices.dk/impulsive/>), established for HELCOM and OSPAR, documents short-lived, high-energy sound events such as pile driving and underwater explosions.

Later, ICES launched the Continuous Noise Database (<https://underwaternoise.ices.dk/continuous/>), which required the development of data standards and QC to unify distinct projects data. This database supports HELCOM's underwater (continuous) noise indicator for the Baltic Sea Action Plan (BSAP), the draft Regional Action Plan on Underwater Noise and the third HELCOM Holistic assessment (HOLAS III), as well the indicators for the OSPAR Ambient Noise Monitoring Strategy. It currently includes data from 54 offshore monitoring stations (Baltic and North Sea).

In 2019, ICES created the Joint Cetacean Data Programme (JC DP) portal (<https://cetaceans.ices.dk/>), funded by the UK's DEFRA, to collect Cetacean data, to help to better understand their distribution and abundance.

In 2022, ICES participated in the EU-funded European Catalog of Sound Signatures project (<https://ecoss.ctnaval.com/>), aimed at creating an open, curated, and expanding repository of underwater sound signatures from shallow seas.

Though developed independently, these initiatives present a valuable opportunity for integration. Member countries could be encouraged to label continuous noise data prior to submission (using the open catalogue of sound signatures library develop during the project) . If the European expert group TG-Noise recommends this to EN-Noise and ICG-Noise, the continuous noise database could be adapted to support labelled data, allowing linkage with biological datasets like JC DP.

Such integration would significantly enhance our ability to analyse marine ecosystems holistically. Each dataset is a piece of a larger puzzle; and together, they reveal a clearer picture of the underwater environment and how that can affect marine life. The Descriptor 11 of the Marine Strategy Framework Directive (https://environment.ec.europa.eu/topics/marine-environment/descriptors-under-marine-strategy-framework-directive_en) has been central to these efforts.

Session

6802499

Symposium

22/10/25 | 14:00

Room: Ballroom B2

Disentis Roadmap: A decadal roadmap for liberating global biodiversity knowledge from literature

Organizers

Donat Agosti

Laurence Bénichou

Description

Published research and underlying observations of biodiversity – ranging from species descriptions and traits to distributions, interactions and insights on drivers of change – are too often locked in inaccessible literature and electronic resources. This represents a key roadblock to scientific progress, and ultimately to informed policy and decisions. Opening up what is known about biodiversity through a network of connected, curated, and digitally accessible knowledge bases is a fundamental challenge, and an exciting opportunity, for the global research and policy communities.

The Disentis Roadmap is the outcome of a symposium held in Disentis, Switzerland in August 2024 to analyse the impact of the 2014 Bouchout Declaration of Open Biodiversity Knowledge Management, and to identify priorities for the next decade. In this symposium we will introduce the vision behind the roadmap, and a blueprint for how its ambitious goals can be achieved from a technical and organizational point of view. We will demonstrate existing, highly-automated workflows for conversion and semantic enhancement of articles, including the standards used, to make the underlying data findable, accessible, interoperable and reusable. We invite submissions from Living Data participants to demonstrate how their work supports momentum in the community towards the Disentis Roadmap vision.

Session: 6802499**7020711**

22/10/25 | 14:00

Room: Ballroom B2**ORAL • EN**

The Disentis Roadmap: A decadal roadmap for liberating global biodiversity knowledge from scientific literature

Presenter

Donat Agosti

Authors

Donat Agosti (Plazi • Switzerland)**Laurence Bénichou** (Muséum National d'Histoire Naturelle • France)**Tim Hirsch** (Tim Hirsch Consulting • United Kingdom)

Abstract

Published biodiversity research—ranging from species descriptions and traits to distributions, interactions, and drivers of change—remains largely locked in inaccessible literature and electronic resources. This constitutes a major barrier to scientific progress and evidence-based policy. Making biodiversity knowledge openly available through connected, curated, and digitally accessible knowledge bases is both a pressing challenge and a critical opportunity for the global research and policy communities.

The Disentis Roadmap emerged from a symposium held in Disentis, Switzerland, in August 2024, which assessed the impact of the 2014 Bouchout Declaration on Open Biodiversity Knowledge Management and identified strategic priorities for the coming decade. As of May 25, 2025, the Roadmap has been signed by 97 individuals and institutions.

Discussions were grounded in existing workflows for data liberation, involving a collaborative effort among key stakeholders: publishers (CETAF, Muséum national d'Histoire naturelle Paris, Pensoft), Plazi, the Biodiversity Literature Repository at Zenodo, the Global Biodiversity Information Facility (GBIF), ChecklistBank, and the Biodiversity PubMedCentral hosted by the Swiss Institute of Bioinformatics Library Services (SiBILS). These efforts include the automated conversion and reuse of 198 biodiversity journals, resulting in substantial outputs from 95,000 publications such as Open Findable, Accessible, Interactionable, and Reusable (FAIR) 760,000 taxonomic treatments, 630,000 figures, and 1,7 million material citations. Additional input has been the extensive digitization of the Biodiversity Heritage Library (BHL) and a large number of individual scientists and research groups. Use cases have informed the process, including literature reuse for Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) reporting, mining of biotic interactions at Biodiversity PMC, the Global Mountain Biodiversity Assessment, and the expansion of ChecklistBank at GBIF.

This presentation introduces the Disentis Roadmap and concludes with a blueprint outlining how its ambitious goals can be achieved through technical innovation and coordinated organizational action.

Session: 6802499**7016784**

22/10/25 | 14:10

Room: Ballroom B2**ORAL • EN**

Biodiversity literature after Disentis: FAIR, AI-assisted, XML-first publishing workflows

Presenter

Laurence Bénichou

Authors

Laurence Bénichou (Museum national d'Histoire naturelle • France)

Penev Lyubomir (Pensoft • Bulgaria)

Abstract

For over a decade a lot of effort has been put into making millions of pages and taxonomic treatments available online. Yet, too often, biodiversity knowledge remains locked in hardly accessible and non-machine-readable literature and electronic resources. Indeed, most prospective publications are still produced in an “old-fashioned” way (PDF), thereby posing a risk of following a pattern we have seen with legacy literature from the past centuries.

Even though access barriers can be demolished using retroconversion, it is far more efficient to have author- and editor-vetted annotations and semantic enhancements to the texts and data ready ahead of publication. Doing so avoids discrepancies, and ensures earlier and rapid dissemination and re-use of data.

Making data within publication findable, accessible, interoperable, and reusable (FAIR) implies text structuration, semantic annotations, and standardization. Furthermore, to link data, information and knowledge contained in literature and other electronic resources to uniquely-identifiable components (images, tables, references, taxonomic treatments) means that those would be re-usable in research and policy covering biodiversity and other domains. Ultimately, this enables immediate re-use of the data, and the integration of publications into a comprehensive global biodiversity knowledge graph.

Following the vision of the Disentis roadmap, this presentation will outline and demonstrate the value of advanced methods for scholarly publishing, production and FAIR-isation of biodiversity data during the journal production process. We will describe the latest developments in the scientific publishing industry and – more specifically – how to publish linked and semantically enhanced research outcomes. The presentation will clarify the concepts that are relevant within the publication for semantic enhancement. Highly-automated, XML-first, AI-assisted existing workflows for semantic enhancement of articles will be introduced, including the related standards, all dedicated to making published data FAIR. In the second part of the presentation, the potential reuse of data will be discussed and showcased.

Session: 6802499**7002409**

22/10/25 | 14:20

Room: Ballroom B2**ORAL • EN**

Evidence Mapping in Support of a Global Assessment of Mountain Biodiversity

Presenter

Davnah Urbach

Authors

Mark A. Snethlage (Global Mountain Biodiversity Assessment • Switzerland)**Davnah Urbach** (Global Mountain Biodiversity Assessment • Switzerland)

Abstract

Scientific assessments of current knowledge about the Earth System and its components have become essential for planning, implementing, and evaluating environmental policies such as the Global Biodiversity Framework. However, to date no such assessment exists for mountains. With the increasing availability and accessibility of biodiversity data and knowledge, this gap in our knowledge of the state of and trends in mountain biodiversity research, species, and ecosystems can now be filled following an approach similar to that adopted by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES).

Here and as part of a first-of-its-kind global assessment of mountain biodiversity, we present a novel approach for systematically mapping scientific literature on mountain biodiversity. Our method integrates text mining, pattern recognition, heuristic algorithms, and an expert-validated vocabulary to enrich publications metadata with spatial, taxonomic, and topical information. This approach enables the creation of a richly annotated database, serving as a foundation for both evidence mapping and a global assessment of mountain biodiversity.

While the current workflow remains labour-intensive, requiring expert validation to ensure accuracy, it also lays the groundwork for AI-driven literature mining, content recognition, and meaning extraction. Specifically, our validated database will be used to train machine learning models in the process of creating a first ever Knowledge Graph for Mountain Biodiversity (MoBiKo) and enhancing automated knowledge extraction and synthesis.

By developing this structured, curated, and digitally accessible knowledge base for re-use across scientific disciplines and policy applications, we aim to support scientific research and inform policy, conservation efforts, as well as financial investments for biodiversity in mountains worldwide. We contribute to “opening up what is known about biodiversity” in the specific case of mountains and support the Disentis Roadmap 2024 vision to fully “leverage the power of biodiversity knowledge from research publications within an open science framework”.

Session: 6802499

7020784

22/10/25 | 14:30

Room: Ballroom B2

LIGHTNING TALK • EN

From Dust to Data: Mobilizing Biodiversity Data from Natural History Museum Archives

Presenter

Britt Andermann

Authors

Britt Andermann (Museum of Evolution, Uppsala University • Sweden)

Mats Eriksson (Museum of Evolution, Uppsala University • Sweden)

Paco Cardenas (Museum of Evolution, Uppsala University • Sweden)

Tobias Andermann (Uppsala University • Sweden)

Abstract

Natural history museums are recognized for the scientific value of their specimen collections, but a vast and often overlooked source of biodiversity knowledge lies hidden in their archives. These archival materials—field notes, journals, registers, and excursion reports— contain unique, time-stamped data that can significantly enrich our understanding of biodiversity change over time and space.

At the Museum of Evolution at Uppsala University, one of the oldest natural history collections in Europe, the archives stretch back to the time of Carl Linnaeus. Among these records are the *Kullenberg Excursion Journals*, an extraordinary series documenting over 30 years of biodiversity observations between 1948 – 1979 from sites around Uppsala, Sweden. These volumes contain typed pages of detailed species inventories of insects and other taxa representing approximately 100,000 occurrence records. Inventories are accompanied by rich metadata on weather and site conditions, offering an exceptional resource for studying long-term trends such as local insect diversity decline.

In collaboration with the Biodiversity Data Lab at Uppsala University, we are transcribing and structuring these historical records into interoperable biodiversity datasets. While initial work has involved manual transcription, we aim to develop and implement automated workflows for extracting biodiversity data from archival materials at scale, enabling large-scale conversion of analog records into FAIR-compliant biodiversity data.

Our work not only supports the recovery of local biodiversity baselines but also contributes to a broader vision: unlocking biodiversity knowledge from institutional archives worldwide. By demonstrating how hidden data can be systematically mobilized, structured, and connected to global biodiversity knowledge frameworks, this project directly aligns with the ambitions of the Disentis Roadmap and highlights the critical role of natural history museum archives in the digital biodiversity infrastructure of the future.

Through this work, we call attention to archives not as static repositories of the past, but as dynamic frontiers for biodiversity discovery.

Session: 6802499**7014440**

22/10/25 | 14:35

Room: Ballroom B2**LIGHTNING TALK • EN**

From literature to biodiversity data: mining arthropod organismal and ecological traits with machine learning

Presenter

Robert Waterhouse

Authors**Joseph Cornelius** (Universita della Svizzera Italiana • Switzerland)**Harald Detering** (University of Lausanne • Switzerland)**Oscar Lithgow-Serrano** (Universita della Svizzera Italiana • Switzerland)**Donat Agosti** (Plazi • Switzerland)**Fabio Rinaldi** (Universita della Svizzera Italiana • Switzerland)**Robert Waterhouse** (SIB Swiss Institute of Bioinformatics • Switzerland)**Abstract**

The fields of taxonomy and biodiversity research have witnessed an exponential growth in published literature. This vast corpus of articles holds information on the diverse biological traits of organisms and their ecologies. However, access to and extraction of relevant data from this extensive resource remain challenging. Advances in text and data mining (TDM) and Natural Language Processing (NLP) techniques offer new opportunities for liberating such information from the literature. Testing and using such approaches to annotate articles in machine actionable formats is therefore necessary to enable the exploitation of existing knowledge in new biology, ecology, and evolution research. Here we explore the potential of these methods to annotate and extract organismal and ecological trait data for the most diverse animal group on Earth, the arthropods. The article processing workflow uses manually curated trait dictionaries with trained NLP models to perform labelling of entities and relationships of thousands of articles. A subset of manually annotated documents facilitated the formal evaluation of the performance of the workflow in terms of entity recognition and normalisation, and relationship extraction, highlighting several important technical challenges. The results are made available to the scientific community through an interactive web tool and queryable resource, the ArTraDB Arthropod Trait Database. These methodological explorations provide a framework that could be extended beyond the arthropods, where TDM and NLP approaches applied to the taxonomy and biodiversity literature will greatly facilitate data synthesis studies and literature reviews, the identification of knowledge gaps and biases, as well as the data-informed investigation of ecological and evolutionary trends and patterns.

Session: 6802499**7018596**

22/10/25 | 14:40

Room: Ballroom B2**LIGHTNING TALK • EN**

Enhancing Access to Biodiversity Knowledge through Automated Metadata Extraction

Presenter

Maria-Emilia Rodriguez-Cuicas

Authors

Rodriguez-Cuicas Maria-Emilia (St Lawrence Global Observatory • Canada)

Beauvillier Simon (St Lawrence Global Observatory • Canada)

Kutos Omnain (St-Lawrence Global Observatory • Canada)

Veyrac Benjamin (St Lawrence Global Observatory • Canada)

Couturier Mathilde (St-Lawrence Global Observatory • Canada)

Abstract

Scientific literature is an invaluable resource for biodiversity data; however, much of this information remains locked in unstructured formats, significantly limiting its use and accessibility. The St. Lawrence Global Observatory (SLGO) developed an innovative AI-driven solution specifically designed to extract structured metadata and GOOS' Essential Ocean Variables (EOVs) from grey literature documents.

Guided by carefully crafted, domain-specific prompts, Large Language Models (LLMs) generate metadata that conforms to established schemas and standards. A rigorous feedback loop continuously measures and helps refine the process, while human experts review and approve each AI suggestion to guarantee accuracy. Together, these elements transform free text into FAIR-compliant, machine-readable metadata.

In this session, we will demonstrate the full pipeline—from document ingestion and parsing to metadata extraction, validation, and packaging. The metadata obtained, conforming to international standards, reveals and promotes datasets previously hidden or difficult to access. This approach significantly accelerates metadata generation and processing. When associated data is structured (e.g., tabular format), this method additionally enables direct publication to global repositories such as OBIS and GBIF.

Ultimately, the extracted metadata makes biodiversity knowledge more findable, accessible, interoperable, and reusable, empowering researchers, policymakers, and environmental managers to make better-informed decisions and strengthen biodiversity stewardship.

Session: 6802499**7020831**

22/10/25 | 14:45

Room: Ballroom B2**ORAL • EN**

Developing an open and participatory literature data extraction workflow using Zotero and Large Language Models

Presenter

Nicky Nicolson

Authors

Nicky Nicolson (Royal Botanic Gardens, Kew • United Kingdom)**Helen Hartley** (Royal Botanic Gardens, Kew • United Kingdom)**Eve Lucas** (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

The extraction of biodiversity data from scholarly literature is essential for the population of authoritative data resources (nomenclators, classifications and distribution datasets). Nomenclators such as the International Plant Names Index (IPNI) are composed of structured data extracted from published literature. Taxonomically scoped research groups like the Taxonomic Expert Networks in the World Flora Online use literature as a resource for collaborative efforts to compile floristic accounts and monographs.

Data extraction and reformatting tasks can now be applied to literature and automated using large language model (LLM) technology. Despite the ready availability of many tools at affordable costs, some significant barriers remain – interaction through web browser interfaces requires the user to “context-switch” (move data between browser tabs or different programme interfaces); and automated (API) access to LLMs requires technical skills to develop scripts and data pipelines: these skills may not be easily available within existing research groups. There are also socio-technical challenges around how work and progress are communicated across a potentially distributed research group or project team.

This presentation will outline the use of a desktop and web accessible bibliographic manager – Zotero – in selecting articles and text to be passed to LLMs for data extraction and reformatting. We will demonstrate experiments in using this toolkit for PDF markup to select text fragments to be passed to an LLM for data extraction and formatting into a data standard, facilitating the population of a structured data resource. We will show how this pipeline enables progress to be shared among a distributed team using the group sharing features built into the system. As well as the description of the pipeline itself, we will also discuss sustainability and skills development – recognising the rapid pace of change in this area and the need for strategic investment of staff time.

Session: 6802499**7015032**

22/10/25 | 14:55

Room: Ballroom B2**ORAL • EN**

The roles of the Biodiversity Heritage Library, Wikidata, and Internet Archive in making taxonomic literature discoverable, accessible, and citable

Presenter

Roderic Page

Authors

Roderic Page (United Kingdom)

Abstract

The task of making the taxonomic literature discoverable and accessible faces several challenges. We lack a complete list of all taxonomic publications: instead we have multiple lists in various formats, sequestered in taxonomic databases, the reference lists of publications, various wikis, etc. Bringing this data together, deduplicating and merging it, and preserving the publications themselves is a challenge the taxonomic community has failed to embrace. This is ironic given the central role publications play in taxonomy.

The BHL has been retrospectively assigning CrossRef DOIs to taxonomic literature. These DOIs automatically become part of the larger citation graph, and hence cited even by publications that appeared before BHL minted these DOIs. Similar services do not exist for other kinds DOIs, reducing our ability to link taxonomic papers together. The implications of this is discussed.

The task of creating a database of taxonomic literature raises the question of whether we (a) grab every reference and put this into a “dirty bucket” of variable quality, or (b) do we carefully deduplicate and clean the references? Wikidata provides an obvious solution to (b), it is a large, community-editable database where data can be cleaned and refined. The task of building a “dirty bucket” and its relationship to Wikidata will be discussed.

Discoverability and citability are by themselves not enough – can we (or our machines) actually read the literature? Aside from the obvious restrictions imposed by publisher paywalls, many taxonomic publications on the web are ephemeral. Preservation services such as the Internet Archive and its Wayback Machine have an important role to play in enabling long-term access to these publications. Alternatives to the Internet Archive will be discussed, including the use of cryptographic hashes as persistent identifiers for publication PDFs.

Session

6803114

Symposium

22/10/25 | 14:00

Room: Tolima

Integrating (and increasing the use of) additional data types

Organizers

Silas C. Principe

Elizabeth Lawrence

Ruben Perez Perez

Description

This session will explore recent advancements in collecting, standardizing, and integrating diverse data types into global platforms to support biodiversity research. For example, traits—morphological, physiological, or phenological characteristics—are essential for understanding community structure and ecosystem functioning. Contextual information (e.g., interactions, environmental measurements and habitat descriptions) helps link species occurrences to ecosystem conditions, enhancing our ability to predict impacts of environmental changes. We will focus on how the use of extended Measurement or Fact (eMoF) extensions from OBIS and GBIF can make these data more accessible and standardized.

Session: 6803114**7020182**

22/10/25 | 14:05

Room: Tolima

ORAL • EN

Beyond Species Occurrences: Harnessing eMoF Data for Marine Biodiversity Science

Presenter

Elizabeth Lawrence

Authors

Elizabeth Lawrence (UNESCO | IOC Project Office for IODE Ocean Biodiversity Information System • Canada)**Silas C. Principe** (UNESCO | IOC Project Office for IODE Ocean Biodiversity Information System • Belgium)

Abstract

Marine researchers often record much more than just species occurrences. Environmental conditions, species counts, and sampling details form a rich data resource that should be openly shared. In the Ocean Biodiversity Information System (OBIS), these data are captured through the Extended Measurements or Facts (eMoF) extension, a flexible framework that accommodates any data related to abiotic or biotic measurements. OBIS currently hosts over 186 million individual measurements. We show the potential of this often-overlooked resource and we highlight key challenges related to accessing, downloading, and analyzing these data. One major challenge is the variety of terms used to describe measurements. While some differences reflect genuine variation, many are purely semantic. To address this, OBIS has an active working group focused on improving the use of controlled vocabularies, which will help standardize terminology and facilitate the integration of diverse datasets. This presentation will showcase examples of how eMoF can be used to address different research questions, as well as the upcoming improvements to enhance accessibility for researchers and open new opportunities for addressing critical scientific questions.

Session: 6803114**7018666**

22/10/25 | 14:17

Room: Tolima

ORAL • EN

Linking species and habitat observations: Cross-Thematic Integration in EMODnet for Context-Enriched Marine Biodiversity Data

Presenter

Ville Karvinen

Authors

Ville Karvinen (Syke (Finnish Environment Institute) • Finland)

Joana Beja (VLIZ (Flanders Marine Institute) • Belgium)

Leen Vandepitte (VLIZ (Flanders Marine Institute) • Belgium)

Ruben Perez Perez (GBIF Spain • Spain)

Bart Vanhoorne (VLIZ (Flanders Marine Institute) • Belgium)

Graeme Duncan (JNCC (Joint Nature Conservation Committee) • United Kingdom)

Helen Lillis (JNCC (Joint Nature Conservation Committee) • United Kingdom)

Dan Lear (MBA (Marine Biological Association) • United Kingdom)

Abstract

The European Marine Observation and Data Network (EMODnet) is a marine data service providing free access to harmonized and FAIR data and data products. The data holdings and products of the seven disciplinary themes – bathymetry, geology, physics, chemistry, biology, seabed habitats and human activities – are presented on the EMODnet Portal, spanning the entire marine environment from coast to open ocean and seafloor, while also supporting Blue Economy sectors and Maritime Spatial Planning, policy, research and civil society.

EMODnet Biology and EMODnet Seabed Habitats curate complementary datasets: EMODnet Biology focuses on marine species occurrences, while EMODnet Seabed Habitats collates habitat data as point records and maps. While these data might be collected together during surveys, they have traditionally been published and stored separately, limiting their use in ecosystem-level analyses.

In response, the two themes have launched a cross-cutting collaboration to integrate species and habitat point data, led by VLIZ (Flanders Marine Institute) and JNCC (Joint Nature Conservation Committee), and enabling enriched biodiversity datasets that are more ecologically informative and ready for synthesis. This initiative uses Darwin Core, the biodiversity data standard to publish linked taxa–habitat records, applying shared identifiers and protocols to maintain their association.

This effort aligns with broader initiatives to incorporate contextual data into global biodiversity platforms, such as OBIS or GBIF, via the Darwin Core extended Measurement or Fact (eMoF) extension which allows for the use of controlled vocabularies, thus improving interoperability between datasets and different types of data. It supports improved modelling, ecosystem assessments, and policy reporting (e.g., EU Marine Strategy Framework Directive and the EU Nature Restoration Law). The approach offers a replicable model for adding ecological context to biodiversity records and lowering barriers to interdisciplinary marine data integration.

Session: 6803114**7019928**

22/10/25 | 14:29

Room: Tolima

ORAL VIRTUAL • EN

Bridging biodiversity data: an ontology-driven approach

Presenter

Martina Pulieri

Authors

Martina Pulieri (University of Salento • Italy)**Parham Ramezani** (LifeWatch ERIC • Italy)**Davide Raho** (National Research Council of Italy, Research Institute on Terrestrial Ecosystems • Italy)**Cristina Di Muri** (National Research Council of Italy, Research Institute on Terrestrial Ecosystems • Italy)**Lucia Vaira** (LifeWatch ERIC • Italy)**Ilaria Rosati** (National Research Council of Italy, Research Institute on Terrestrial Ecosystems • Italy)

Abstract

The rapid growth of data in biodiversity and ecosystem domain calls for innovative approaches and technologies to support the creation of a shared and integrated knowledge base among diverse stakeholders. Semantic technologies enable the description and interpretation of data by both humans and machines, supporting automated discovery, integration, and improved interoperability of data across systems. In this context, LifeWatch Italy has developed an ontology-driven approach to unify and semantically enrich biodiversity and ecosystem data and metadata. The designed ontology builds on well-established standards such as the SOSA and PROV ontologies, and the DCAT vocabulary, extending them to incorporate taxonomic and ecological concepts. This ensures semantic consistency and supports the integration of heterogeneous datasets describing traits, occurrences, abiotic measurements, and ecological observations. A key feature of the semantic model is its ability to accommodate datasets structured using a variety of extensively adopted data models, from annotated flat-tables to the Darwin Core extension Measurements or Facts (MoF). Through formal semantic links, the proposed ontology adds to existing data models the potential for automated reasoning, data linking, and integration. This semantic layer, in addition to structured data aligned with international standards, enables advanced data discovery, complex querying, and inference across diverse datasets. Built upon this ontological framework, the LifeWatch Italy Semantic Platform provides a user-friendly web application for data navigation, integration, and download by accessing the knowledge graph through semantically enriched queries. The platform allows researchers to benefit from semantic technologies without requiring prior expertise in RDF or the Semantic Web, allowing them to seamlessly integrate diverse datasets that can be reused for multiple purposes, such as temporal analyses, ecological modeling, biodiversity assessments, and more. Hence, the platform empowers researchers to conduct faster and more impactful scientific investigations.

Session: 6803114**7020591**

22/10/25 | 14:41

Room: Tolima

ORAL • EN

Traits Thesaurus: a semantic artefact to harmonise data and metadata of aquatic organism traits

Presenter

Ilaria Rosati

Authors

Ilaria Rosati (National Research Council of Italy • Italy)

Martina Pulieri (University of Salento • Italy)

Angela Carluccio (Università degli Studi di Bari Aldo Moro • Italy)

Senem Onen Tarantini (University of Salento • Italy)

Alberto Basset (University of Salento • Italy)

Jessica Titocci (LifeWatch ERIC • Italy)

Abstract

Trait-based approaches are widely used in ecology to monitor and understand how communities and ecosystems respond to human-driven environmental impacts, such as biodiversity loss and ecosystem changes. Functional traits—organisms' measurable characteristics—are key indicators linking community structure to ecosystem processes. As a result, large volumes of trait-based data have been collected.

However, differences in scale, domain, and data management practices make it difficult to reuse this data effectively to address global ecological challenges. A major obstacle is their integration due to the lack of syntactic and semantic harmonisation, which leads to fragmented knowledge. To overcome this, the Italian Distributed Centre of LifeWatch ERIC—the e-science European infrastructure for biodiversity and ecosystem research—develops semantic artefacts to support trait-based research. Here, we present the Traits Thesaurus, designed to harmonise and formalise trait data and metadata for aquatic organisms, including phytoplankton, zooplankton, fish, macroalgae, and macrozoobenthos. This thesaurus results from the integration and revision of existing vocabularies developed within LifeWatch Italy, forming a unified and structured semantic framework. Its development combined manual and automated alignment techniques, alongside validation involving national and international experts in trait-based ecology. The Traits Thesaurus is a FAIR (Findable, Accessible, Interoperable, Reusable) controlled vocabulary that includes over 1,000 concepts, with definitions and interlinked relationships to other semantic artefacts. We believe that integrating the Traits Thesaurus into data management practices can significantly enhance data interoperability and integration. This, in turn, enables more robust large-scale analyses and ecological modeling, contributing to a deeper understanding of ecosystem functions and responses.

Session: 6803114**7020897**

22/10/25 | 14:53

Room: Tolima

ORAL • EN

Mobilizing biodiversity data hidden in centuries old written material

Presenter

Laetitia Navarro

Authors

Laetitia Navarro (Estación Biológica de Doñana (EBD-CSIC) • Spain)

Rocío Ponce Nieves (Estación Biológica de Doñana (EBD-CSIC) • Spain)

Duarte Viana (Estación Biológica de Doñana (EBD-CSIC) • Spain)

Miguel Clavero (Estación Biológica de Doñana (EBD-CSIC) • Spain)

Abstract

Historical data sources are proving instrumental in biodiversity research by providing historical baselines for species and ecosystems, and by revealing information about human-nature relationships and their sustainability (or lack thereof) over long time-scales. Among these sources, “structured written materials” such as hunting and forestry records, land surveys, and geographical dictionaries or gazetteers are particularly useful. These historical documents can be mined for information on taxa or species occurrences, ecosystem distributions, and on the societal use of land and species, including the intensity of these uses. Importantly, because the historical collection efforts of those written sources were often motivated by taxation, colonization, and more generally state record-keeping, they rely on relatively standardized sampling protocols that facilitate data comparisons across space and time. To illustrate this, we present efforts to mobilize data from geographical dictionaries produced in Spain in the 16th and 19th centuries, focusing on the species described in each settlement, as reported by their inhabitants. We also discuss the standardization and sharing of biodiversity-relevant data, along with the challenges and biases inherent to these historical sources. Lastly, we illustrate various applications of historical data from geographical dictionaries in biodiversity and conservation research, and explore opportunities for future data mobilization efforts at different temporal and spatial extents.

Session: 6803114**7016621**

22/10/25 | 15:05

Room: Tolima

ORAL • EN

Integrating plant and seed traits into Institutional collection management systems and global platforms to strengthen *ex situ* plant conservation efforts

Presenter

Udayangani Liu

Authors

Udayangani Liu (Royal Botanic Gardens, Kew • United Kingdom)

Richard Dodd (Royal Botanic Gardens, Kew • United Kingdom)

Robert Turner (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

Several factors hinder *ex situ* plant conservation practices in botanic gardens and seed banks (collecting, processing, storage, recovery), particularly for “exceptional” plants. These challenges are primarily due to the inherited biological characteristics or traits of the plants and their seeds. We primarily focus on plant and seed traits relevant to *ex situ* conservation, specifically examining plant life forms, seed characteristics (dormancy and storage behaviour). Together, these selected traits offer a comprehensive understanding of a taxon’s resilience, survival and regeneration potential under changing environmental conditions. This information is vital for conservation planning, as it identifies which taxa are more adaptable, which may require special interventions, and how *ex situ* conservation measures can effectively support their preservation. Life form is a foundational trait that influences how plants fulfil ecological roles, adapt to their environments, and respond to changes, making it indispensable in ecology and conservation. Seed dormancy, determined by morphological and physiological properties, is an innate constraint preventing seeds from germinating, even under environmental conditions that would typically promote germination in non-dormant seeds. There are eight seed dormancy classes preventing radicle emergence and germination: Physiological (PD), Morphological (MD), Morphophysiological (MPD); Physical (PY); Physiophysical (PYPD); Chemical; Mechanical; and DUST (for small seeds mostly ≤ 1.0 mm in length with undifferentiated embryos). Seed response to dehydration, known as desiccation tolerance or seed storage behaviour, is categorized into three main classes: orthodox (tolerant), recalcitrant (intolerant) and intermediate. Evaluating this trait is critical for seed conservation through seed banking, as conventional techniques involving drying and cooling are only suitable for orthodox seeds, and not all seeds respond uniformly as different taxa may exhibit varied responses. This presentation will focus on how integrating these traits into institutional collection management systems and global data platforms can enhance *ex situ* plant conservation efforts in response to the biodiversity crisis.

Session

6960773-1

Symposium

22/10/25 | 14:00

Room: Caldas

Molecular & Genetic Approaches (Contributed Oral Presentations)

Organizers

James Macklin

Mailyn Gonzalez

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-1**7020153**

22/10/25 | 14:00

Room: Caldas

ORAL • EN

The Canadian Genomic Adaptation and Resilience to Climate Change (GenARCC) project

Presenter

James Macklin

Authors

James Macklin (Agriculture and Agri-Food Canada • Canada)

Tony Kess (Fisheries and Oceans Canada • Canada)

Satpal Bilkhu (Agriculture and Agri-Food Canada • Canada)

Ian Bradbury (Fisheries and Oceans Canada • Canada)

Abstract

Genomic technologies provide the highest resolution molecular information on species biology, and can help us understand risks and potential for adaptation among species in a changing environment. The Genomic Adaptation and Resilience to Climate Change (GenARCC) project uses molecular tools to identify ecosystem composition, pathogen and pest prevalence, and adaptive capacity within species. This Government of Canada project purposefully takes a multi-department/agency approach, drawing on complementary expertise and centralized infrastructure to address the complexity of climate change spanning multiple levels of trophic and taxonomic diversity. The GenARCC project's goal is to develop capacity to use genomics to assess, predict, and adapt to climate change for the protection of Canada's biodiversity, ecosystem resilience, food security, and health. Together, the data and expertise generated in this project represent the largest single national effort and combined dataset to address climate change impacts across species and ecosystems with molecular data. GenARCC comprises research across a diversity of environments and species, including forest and tundra, arctic, marine, and agricultural ecosystems. Genomic, climate and phenomic datasets have been generated and centralized to better understand impacts to biodiversity across biological levels of organisation. To facilitate analysis of this data, we have deployed a common high performance compute environment allowing participants across multiple Canadian departments and agencies to leverage shared infrastructure, datasets and workflows. Project outputs and inputs are managed through a dedicated metadata management platform, DINA. Additionally, project participants benefit from training on scientific computing, as well as genomic methods in discussion forums for data analysis and integration best practices. Results from this project will inform evidence-based policy to support conservation of biodiversity, as well as management of natural resources and key species across ecological realms.

Session: 6960773-1

7017014

22/10/25 | 14:10

Room: Caldas

LIGHTNING TALK • EN

Traceability of Stingless Bees and their Products Using eDNA: Uncovering Biodiversity, Microbial Communities, and Bioeconomic Potential in Colombia

Presenter

Laura Salazar Jaramillo

Authors

Laura Salazar Jaramillo (Universidad de Antioquia • Colombia)

Yiehitson Correa Agudelo (Fundación Biodiversa Colombia • Colombia)

Aída Marcela Vasco Palacios (Universidad de Antioquia • Colombia)

Abstract

Environmental DNA analysis of bee-derived products offers a promising approach to studying **local biodiversity and natural history**, particularly in the **Neotropics**, where diversity of stingless bees is highest. This method allows the detection of the **bee origin** of the products, **plant species** visited by bees and the **microbial communities** present in honey—microbes that may play ecological roles and hold **probiotic potential** for health and agriculture.

Despite its promise, this line of research is still in early stages, especially in **tropical regions** where **funding is limited** and **baseline data are lacking**. Applying eDNA in these biodiversity-rich but underrepresented areas can generate valuable open data to inform **taxonomy, conservation, and bioeconomic development**.

This approach improves the **traceability and value** of **stingless bee products** by verifying their **botanical, microbial, and geographic origins**, supporting **local producers** and encouraging **biodiversity-friendly markets**. It also deepens our understanding of **plant- pollinator-microbe interactions**, offering a more complete picture of tropical ecosystems.

Our project focuses on **stingless bees in Colombia's Magdalena Medio region**, using locally attracted colonies housed in boxes. Unlike *Apis* bees, **stingless bee honeys** host **living microbial communities** involved in **natural fermentation**. We have collected honey, pollen, and bee specimens for **morphological and molecular identification**, and are isolating associated **fungi and bacteria**.

Our goal is to use eDNA to identify **bee species, diet, and microbial associates**, contributing to the understanding of bee product natural history and promoting **sustainable, high-value products** rooted in local biodiversity.

This work is part of a **pioneering regional effort** to integrate DNA technologies into biodiversity inventories for action. It calls for **greater support, collaboration, and open-access frameworks** to unlock the full potential of this approach for both **conservation and local economies**.

Session: 6960773-1**7020761**

22/10/25 | 14:15

Room: Caldas

LIGHTNING TALK • EN

From lab to landscape: Integrative approaches for next-generation pollinator monitoring with the ANTENNA project

Presenter

Peter Moran

Authors**Peter Moran** (Naturalis Biodiversity Center • Netherlands)**Leon Marshall** (Naturalis Biodiversity Center • Netherlands)**Koos Biesmeijer** (Naturalis Biodiversity Center • Netherlands)**Quentin Geissmann** (Aarhus University • Denmark)**Thomas Tscheulin** (University of the Aegean • Greece)**Javier Galeano Prieto** (Universidad Politécnica de Madrid • Spain)**Jessica Knapp** (Trinity College Dublin • Ireland)**Ignasi Bartomeus** (Doñana Biological Station • Spain)**Oliver Schweiger** (Helmholtz Center for Environmental Research - UFZ • Germany)**Abstract**

Pollinators are widely believed to be in global decline, raising concerns for food security, ecosystem functioning, and biodiversity. Yet for many species, our understanding of population trends and the drivers of decline remains limited due to gaps in taxonomic and geographic coverage, temporal resolution, and monitoring efficiency. The ANTENNA project responds to these challenges by developing scalable, integrated technologies to strengthen pollinator monitoring across Europe.

Generating robust, high-resolution data at scale requires monitoring approaches that are standardized, efficient, and cost-effective. A major bottleneck is species identification: traditional morphology-based methods are time-consuming and constrained by declining taxonomic expertise. High-throughput tools such as automated sample sorting, image recognition, and DNA barcoding offer promising alternatives to improve speed, accuracy, and scalability. However, many of these methods need further development, validation, and integration before wide deployment.

ANTENNA supports EU-wide efforts such as the European Pollinator Monitoring Scheme (EU PoMS) by testing and integrating high-throughput technologies into practical workflows. Its five core objectives are to:

1. advance image recognition, robotic sorting, and DNA barcoding into user-ready systems;
2. expand monitoring to underrepresented taxa, ecosystems, and environmental pressures;
3. evaluate the added value of novel tools, alone and with traditional methods, in terms of data quality and cost-efficiency;
4. develop frameworks for integrating diverse data and enabling near real-time early warning systems; and
5. scale from local pilots to robust, transnational monitoring pipelines.

By bridging technological innovation and practical implementation, ANTENNA will deliver tested, scalable solutions to strengthen pollinator monitoring. Its integrated approach, combining traditional and novel methods, will support evidence-based policy and adaptive management across the EU, while offering a transferable framework to benefit biodiversity monitoring efforts worldwide.

Session: 6960773-1**7018590**

22/10/25 | 14:20

Room: Caldas**ORAL • EN**

eDNA data structuration and good practices for public policies: the French use case

Presenter

Sophie Pamerlon

Authors

Sophie Pamerlon (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Aurélie Lacoeuilhe (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Louise d'Hollande (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Noëlie Maurel (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Solène Robert (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Chloé Vinet (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Thomas Bouix (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Anne-Sophie Archambeau (IRD, PatriNat (MNHN-OFB-CNRS-IRD), Global Biodiversity Information Facility (GBIF) France • France)

Yvan Le Bras (French national museum of natural history | Data-Terra PNDB research infrastructure | UAR 2047 DoHNEE | Concarneau marine statio • France)

Nicolas Buisine (UAR 2047 DoHNEE (MNHN-CNRS) • France)

Abstract

In the French research and expert communities, data providers from both public and private sectors currently use diverse and often unstructured methods to collect eDNA data. Following national-level workshops and consultations, a clear need emerged for a stable framework, recommendations on standardized fields, and good practices guides to elevate data FAIRness, and facilitate dissemination through public information systems like SINP (French natural heritage information system), PNDB (French biodiversity data hub of Data Terra research infrastructure) and GBIF.

In response, PatriNat and partners are working to structure eDNA-derived data in order to facilitate their sharing. A key part of this effort is a set of new tools (e.g. national data template, GBIF MDT), and updating data-sharing pipelines between the national and international systems. This includes adapting the mapping of the French national data standard and Darwin Core, based on the GBIF guide for publishing DNA-derived data and relevant Darwin Core extensions.

A short practical guide is already available to support eDNA data providers, and a more detailed document is in development to offer deeper insights into the recommended fields and workflows, and their integration in public databases and repositories.

More broadly, this initiative is part of the “large scale inventory of French biodiversity using molecular techniques” objective of the National strategy for biodiversity, by supporting the harmonization and structuring of biodiversity data collection, including those acquired through eDNA techniques. Through efforts like the creation of the national reference list of genetic sequences for French taxa (presented at TDWG in 2023), the French eDNA working group contributes to improving the overall quality, accessibility and interoperability of eDNA data.

In this session, we will present ongoing works and documentation available to eDNA data providers and users: data standards mapping, data templates, workflows, and technical resources to support high quality data sharing.

Session: **6960773-1****7020286**

22/10/25 | 14:30

Room: Caldas

ORAL • EN

The Swedish Reference Genome Portal: A hub for genomic data visualization, discovery, and reuse

Presenter

Angela P. Fuentes-Pardo

Authors

Angela P. Fuentes-Pardo (Science for Life Laboratory Data Centre, Uppsala University • Sweden)**Daniel P. Brink** (Science for Life Laboratory Data Centre, Uppsala University • Sweden)**Rory Crean** (Science for Life Laboratory Data Centre, Uppsala University • Sweden)**Quentin Ågren** (Swedish Museum of Natural History, Science for Life Laboratory Data Centre • Sweden)**Henrik Lantz** (National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Uppsala University • Sweden)**Hanna Kultima** (Science for Life Laboratory Data Centre, Uppsala University • Sweden)**Bengt Persson** (National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Uppsala University • Sweden)**Johan Rung** (Science for Life Laboratory Data Centre, Uppsala University • Sweden)

Abstract

The Science for Life Laboratory (SciLifeLab) is a national infrastructure for life sciences in Sweden, providing advanced technologies and expertise to researchers across disciplines like ecology, evolution, and biomedicine. In collaboration with the Wallenberg Program for Data-Driven Life Science (DDLs), SciLifeLab seeks to strengthen national capacity in computational and data science, foster collaboration, and advance data integration and reuse.

In today's increasingly collaborative and data-driven research landscape, ensuring the long-term accessibility and impact of scientific data is essential. Here we present the Swedish Reference Genome Portal (SRGP), a website developed at SciLifeLab to support the discovery, visualization, and dissemination of genomic data from non-human eukaryotic species generated by researches in Swedish institutions. The portal highlights national genomic research and enhances data findability, accessibility, and reuse in alignment with FAIR data principles through integration with public repositories. Each species in the portal has a dedicated webpage containing taxonomic, biological, and genome assembly metadata, along with links to resources such as the Swedish Biodiversity Data Infrastructure (SBDI), the European Nucleotide Archive (ENA), and Genomes on a Tree (GoaT). Genomic data are visualized through an embedded JBrowse genome browser, enabling interactive exploration of diverse data types. The portal also emphasizes the sharing of high-value genomic annotations, including methylated regions, non-coding RNAs, conserved elements and more, as well as population statistics such as Tajima's D, nucleotide diversity, and *FST*, which are often omitted from traditional publications.

The SRGP represents a step toward making genomic data accessible to everyone, including researchers, funders, and the public, regardless of their prior experience in bioinformatics. By aligning with open science and FAIR data principles, the portal aims to demonstrate how national research infrastructures can play a key role in promoting data reuse, supporting knowledge transfer, and fostering collaboration on both national and international levels.

Session: 6960773-1

7014448

22/10/25 | 14:40

Room: Caldas

LIGHTNING TALK • EN

Microbial communities associated to the cushion plant *Plantago rigida* throughout the stages of microsuccession in the Ecuadorian Andean paramo.

Presenter

Juan José Guadalupe López

Authors

Juan José Guadalupe López (Laboratorio de Biotecnología Vegetal - Universidad San Francisco de Quito • Ecuador)

Miguel Pazmiño-Vela (Laboratorio de Biotecnología Vegetal - Universidad San Francisco de Quito • Ecuador)

Emilia Loaiza (Laboratorio de Biotecnología Vegetal - Universidad San Francisco de Quito • Ecuador)

Esteban Suárez (Instituto Biósfera - Universidad San Francisco de Quito • Ecuador)

Maria de Lourdes Torres (Ecuador)

Abstract

The paramo is a unique high-altitude biome located between 2800 and 4800 meters above sea level in the Ecuadorian Andes. It covers approximately 5.94% of the national territory and consists of ecosystems characterized by cold, humid climates, intense solar radiation, and high levels of endemism. This biome provides essential ecosystem services, including freshwater storage for nearby cities and carbon sequestration. Among its characteristic vegetation, cushion-forming plants stand out for their ability to thrive under extreme conditions. In the Ecuadorian paramo, one of the predominant species is *Plantago rigida*, known for its ecological importance. *P. rigida* contributes to carbon accumulation in the soil and acts as a growth facilitator, allowing other plant species to establish under harsh environmental conditions. In this study, we propose that *P. rigida* undergoes a micro-succession process that may influence the composition and function of the associated microbial communities. We examined the microbial diversity across three different micro-succession stages to better understand how these interactions contribute to carbon cycling. Our results show that bacteria are the most diverse and abundant microbial group throughout all stages. By the third stage, *P. rigida* is replaced by grasses, which may correlate with a decline in carbon sink capacity. Additionally, we observed an increase in methanogenic archaea, potentially contributing to methane efflux and indicating shifts in microbial processes linked to carbon dynamics. This study provides an initial exploration of the micro-succession process in *P. rigida* and its broader ecological implications. These results could support the conservation of the paramo by improving our understanding of the microbial and plant interactions that take place in this unique biome. In addition, this work highlights the value of metagenomic data as a powerful tool for assessing ecosystem function and contributing to conservation strategies in times of environmental changes.

Session: 6960773-1**7015242**

22/10/25 | 14:45

Room: Caldas

ORAL • EN

A Next-Generation Approach to Monitoring Biodiversity and Ecosystem Recovery: Molecular Ecological Network Analysis (MENA) in African Protected Areas

Presenter

Jordana Meyer

Authors

Jordana Meyer (African Parks • South Africa)**Angela Gaylard** (African Parks • South Africa)**Mathias Pires** (University of Campinas • Brazil)**Gianalberto Losapio** (University of Milan • Italy)**Gloire Kibongui** (African Parks • Congo)**Gwili Gibbon** (African Parks • Congo)**Adrian Nkundimana** (African Parks • Rwanda)**Jack Buckland** (African Parks • Chad)**Joy Muchimba** (African Parks • Zambia)**Maria Costa** (African Parks • Angola)

Abstract

Species interactions form the underlying architecture of biodiversity and are central to ecosystem function. Yet most conservation monitoring focuses narrowly on species richness or abundance, often missing the critical web of relationships that sustain biodiversity. To address this gap, African Parks Network (APN) is piloting a next-generation approach: Molecular Ecological Network Analysis (MENA).

MENA integrates environmental DNA (eDNA) sampling with network analysis to track not only which species are present, but also how they interact, capturing structure, composition, and function across ecosystems. In this pilot project, we monitored five APN Parks, covering 55,218 km² (13.65 million acres) of diverse biomes including savanna, rainforest, grassland, and desert. Using non-invasive sampling of herbivore, omnivore, and carnivore faecals as well as soil and water eDNA, we reconstructed ecological networks from microbes to megafauna.

Preliminary results show that MENA can rapidly detect biodiversity, uncover rare or elusive species, and reveal trophic links essential to food web dynamics. Total effect matrices quantify both direct and indirect species interactions, allowing comparisons between managed and unmanaged areas. Analysing the dynamics of these food webs provides information on potential assessment of conservation interventions like species reintroductions and fire regimes. The method also identifies keystone species and patterns of functional redundancy critical for ecosystem resilience.

This scalable, cost-effective approach provides conservation managers with actionable indicators of ecosystem integrity, moving beyond species checklists to capture the dynamic relationships that underpin recovery. We will present the methodological framework, early findings, challenges, and future directions, including expanded implementation across Africa.

Ultimately, MENA offers a transformative, data-rich tool for monitoring and managing biodiversity at different scales. It bridges molecular ecology and applied conservation, equipping decision-makers with the insight needed to restore and protect complex ecological systems.

Session

6798633

Symposium

22/10/25 | 14:00

Room: Valle

Enhancing biodiversity monitoring and reporting at the sub-national level

Organizers

Jean-Michel Lord**David Roberts****Dominique Gravel**

Description

Biodiversity Observation Networks (BONs) play a crucial role in tracking global biodiversity change. The GEO BON framework provides a structured approach for these networks, ensuring consistency in monitoring and reporting efforts. While BONs typically operate at national or global scales, subnational programs collect valuable data that can enhance broader biodiversity assessments. However, integrating these localized efforts into a larger framework without losing their local relevance is a challenge.

BON in a Box, an open-access toolkit, can facilitate this integration by providing standardized workflows to calculate Essential Biodiversity Variables (EBVs) and biodiversity indicators. By offering transparent and reproducible analysis pipelines that are generalizable across scales, BON in a Box enables subnational monitoring programs to align with international standards while maintaining the specificity needed for local decision-making. It applies the essence of FAIR data principles to the analysis processes. This standardization ensures that independent monitoring initiatives contribute meaningfully to global biodiversity assessments, allowing them to transfer their unique expertise to other similar initiatives.

We welcome submissions from subnational institutions that have tackled similar issues and strive to harmonize monitoring programs across jurisdictions, while maintaining balance between local relevance and standardized, scalable biodiversity assessments.

Session: 6798633**7015627**

22/10/25 | 14:00

Room: Valle

ORAL • EN

Bridging Scales and Borders: biodiversity variables calculation with BON in a Box

Presenter

Jean-Michel Lord

Authors

Jean-Michel Lord (GEO BON, McGill University • Canada)

Jory Griffith (GEO BON, McGill University • Canada)

Guillaume Larocque (McGill University, Quebec Centre for Biodiversity Science • Canada)

Abstract

Assessing the status and trends of biodiversity to inform policy and halt biodiversity loss globally requires collaboration across scales. Current monitoring efforts and tools are often developed by individual actors without being shared across organizations and borders, which can lead to the duplication of effort in some places while others have less resources to allocate to biodiversity reporting. The BON in a Box platform aims to facilitate biodiversity monitoring coordination and collaboration between organisations, both within countries and across borders. The BON in a Box search portal allows people to register and share their biodiversity monitoring projects and tools. The BON in a Box modelling tool is an open-source, fully transparent platform that allows users to run and share analysis pipelines to calculate indicators, which can then be used for decision-making or to assess progress towards biodiversity targets. BON in Box can integrate diverse data and expert knowledge, from Earth observation to in-situ monitoring. We will present the analyses that are available in BON in a Box, and the potential of the platform to facilitate coordination and collaboration between subnational actors monitoring biodiversity change, and helping them contribute to the greater national effort.

Session: 6798633**7013240**

22/10/25 | 14:15

Room: Valle

ORAL • EN

Applying regionally developed SDMs to international biodiversity indicators

Presenter

Brandon Allen

Authors

Brandon Allen (Alberta Biodiversity Monitoring Institute • Canada)

David Roberts (Canada)

Abstract

The Alberta Biodiversity Monitoring Institute (ABMI) is an arm's-length, value-neutral not-for-profit organization whose mission is to track changes in wildlife and their habitats across the province of Alberta. To achieve this mission, largely in collaboration with our stakeholder partners, we have developed several biodiversity indices that report on anthropogenic disturbance, habitat conversion, landscape fragmentation, and species habitat availability. With the advancement and acceptance of Essential Biodiversity Variables (EBVs) for international reporting initiatives, including as part of the Kunming-Montreal Global Biodiversity Framework, we are seeing opportunities for aligning methodologies for calculating EBVs at local, subnational, national, and international scales. The ABMI has evaluated how regionally specific species distribution models (SDMs) can be utilized in platforms such as BON in a Box to calculate EBVs such as the Species Habitat Index and Species Protection Index. We will also highlight some of the challenges organizations will face as both the quality and parameterization of SDMs, and the underlying geospatial data products used for projecting distributions, can have substantial impacts on reported EBV scores.

Session: 6798633**7018775**

22/10/25 | 14:30

Room: Valle

ORAL • EN

Linking Biodiversity and Well-Being: A Case Study in Subnational BON Reporting for Quebec

Presenter

Vincent Beauregard

Authors

Vincent Beauregard (Université de Sherbrooke • Canada)**Claire-Cécile Juhasz** (Université de Sherbrooke • Canada)**Victor Cameron** (Université de Sherbrooke • Canada)**Benjamin Mercier** (Université de Sherbrooke • Canada)**Guillaume Larocque** (McGill University • Canada)**François Rousseau** (Université de Sherbrooke • Canada)**Sabrina Courant** (Ministère de l'Environnement, de la Lutte contre les changements climatiques, de la Faune et des Parcs (MELCCFP) • Canada)**Anouk Simard** (Ministère de l'Environnement, de la Lutte contre les changements climatiques, de la Faune et des Parcs (MELCCFP) • Canada)**Gravel Dominique** (Université de Sherbrooke • Canada)

Abstract

Biodiversité Québec (BQ) operates as a subnational Biodiversity Observation Network (BON) bringing together academic researchers, public agencies, and civil society organizations to monitor and report on the status and trends of biodiversity. In collaboration with the G15+ collective of civil organisations, we are proposing a suite of indicators designed to integrate biodiversity into their broader framework toward social, economic, and environmental well-being for Quebec. While indicators were already integrated for many environmental issues Biodiversité Québec efforts were essential to add biodiversity as a core element of this decision-making framework, ensuring that societal well-being is pursued within the ecological limits of our ecosystems.

Drawing on more than 30 million biodiversity records and harmonised environmental data, Biodiversité Québec proposes a suite of indicators to monitor biodiversity trends. These include the average decline of tracked populations of threatened and vulnerable vertebrates (–72% since 1970), the uneven state of knowledge across taxonomic groups, the progress and regional disparities in conservation coverage (17% protected overall), the steady rise in invasive species introductions, and the economic importance of nature-based activities directly tied to biodiversity such as forestry, fisheries, and agriculture, sectors.

The analysis pipelines are documented and implemented using BON in a Box, ensuring reproducibility and facilitating transfer to other jurisdictions. The indicators will also be integrated into the BQ Atlas interactive explorer, providing spatialized decision-support tools for land managers, conservation organizations, and municipal planners across Quebec.

Our presentation will (i) outline the codesign process with G15+ stakeholders, (ii) discuss the reproducible analytical pipeline, (iii) showcase indicator results and visualization, and (iv) discuss lessons learned in balancing scientific rigour with policy pragmatism. Ultimately, we demonstrate how subnational networks can deliver locally actionable and globally comparable metrics—thus supporting the implementation of the Kunming-Montreal Global Biodiversity Framework through consistent, scalable, and policy-relevant biodiversity monitoring.

Session: 6798633

7020049

22/10/25 | 14:42

Room: Valle

ORAL • EN

Harmonization of protocols across scales: Lessons learnt and advices from Biodiversa+

Presenter

Guillaume Body

Authors

Guillaume Body (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Michelle Silva del Pozo (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Mathieu Basille (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Abstract

Biodiversa+, the European partnership for biodiversity, notably aims to harmonize monitoring schemes across Europe, from Mediterranean to Arctic regions, from local to continental scales, and across diverse cultures. Through different workshops and discussions with European experts and stakeholders, we developed a governance model, paths to harmonization, and reasonable goals for harmonization. The concept of Essential biodiversity variables, a middle step between raw data and indicators, is a cornerstone of the process, providing a way to harmonize specific monitoring targets that does not require to standardize protocols. We propose guidelines and minimum requirements for monitoring schemes to improve interoperability.

Session: 6798633**7019983**

22/10/25 | 14:56

Room: Valle

LIGHTNING TALK • EN

Study and monitoring of biodiversity in France: Feedbacks on special efforts gathering Research and Policy communities

Presenter

Yvan Le Bras

Authors**Olivier Norvez** (CNRS, Data Terra • France)**Léa Riera** (PatriNat OFB-MNHN-CNRS-IRD, Biodiversa+ • France)**Anne-Sophie Archambeau** (PatriNat OFB-MNHN-CNRS-IRD, GBIF France • France)**Mathieu Basille** (PatriNat OFB-MNHN-CNRS-IRD, Biodiversa+ • France)**Guillaume Body** (PatriNat OFB-MNHN-CNRS-IRD, Biodiversa+ • France)**Thomas Bouix** (PatriNat OFB-MNHN-CNRS-IRD • France)**Jonathan Hareng** (PatriNat OFB-MNHN-CNRS-IRD • France)**Yvan Le Bras** (MNHN, PNDB-Data Terra • France)**Sandrine Pavoine** (MNHN, CESCO • France)**Abstract**

In 2024, the French biodiversity data hub – PNDB (biodiversity arm of Data Terra research infrastructure), the Policy biodiversity information system – SIB, the French GBIF node and the Biodiversa+ project team from the French biodiversity agency (OFB) organized a 3-day seminar on the theme of biodiversity monitoring at the interface of research and public policies. More than thirty participants involved in all aspects of biodiversity monitoring at different scales and using various methods and protocols were brought together as members of the French biodiversity community.

The objectives of the seminar were to facilitate scientific and technical exchanges (workshops, training and plenary sessions) between the research and public policy communities, to raise awareness of needs and expectations in terms of shared networks, to provide best practices, particularly in terms of biodiversity data management, curation and analysis, and to communicate and inform about the French BON and its future developments.

Actions have been identified for a common framework bridging the gap between Research and Public Policies, from raw data to indicators:

- Map out the skills and willingness at the national level to address the “who’s doing what” Create a mailing list for the community
- List current projects and networks from research and biodiversity survey policies and links with international related initiatives
- List current tools and services offered by the French communities (Virtual research environment, biodiversity monitoring frameworks), and make synergies with the BON in a Box tool.
- Broaden the scope and move beyond the focus on occurrence data (strengthen the AI, satellite and genetic dimensions, and integrate these communities)
- Explore the functioning of other networks such as the Knowledge-Action hub of the One Health community or the French Barcode of Life node
- Beware of the voluntary nature of the network, and avoid redundancy with currently existing initiatives.

Session: **6798633****7020604**

22/10/25 | 15:01

Room: Valle

ORAL • EN

Toward fit-for-purpose urban biodiversity indicators: a methodology for empirical testing across diverse urban contexts

Presenter

Evariste Rutebuka

Authors

Evariste Rutebuka (School of Agriculture, Food and Ecosystem Sciences, University of Melbourne • Australia)**Judy Bush** (Faculty of Architecture, Building and Planning, University of Melbourne • Australia)**Amy K Hahs** (School of Agriculture, Food and Ecosystem Sciences, University of Melbourne • Australia)

Abstract

Urban greenspaces are vital to biodiversity conservation and sustainable urban living, yet robust indicators to monitor their contributions remain scarce. Although numerous metrics exist, many lack empirical validation and context sensitivity, leading to poor adoption by policymakers, misalignment with local capacities, ecological realities, and decision-making needs.

To fill this gap, we developed a pragmatic, scalable framework for systematically guiding road-testing urban biodiversity indicators suitable for diverse urban contexts. We tested our framework on the Urban Greenspace Integrity Index (UGII)—an urban bird-trait metric—and assessed UGII performance against five criteria: methodological consistency, data sensitivity, urban ecological relevance, policy relevance, and feasibility. Ninety-eight metro areas were selected by stratified sampling across continents, population, income, and bioregion to capture global urban diversity. We leveraged 460 million Global Biodiversity Information Facility (GBIF) terrestrial bird records (2010–2020; 7,975 species) to assess UGII performance, and paired its scores with established metrics—species richness and NDVI—to validate consistency and clarify interpretation.

Our tests showed that UGII initially failed the methodological consistency checks based on continental bird distributions but passed when recalculated using global distribution records. Under data sensitivity, species richness correlated with sampling effort ($r = 0.543$, $p < 0.001$), limiting its use in data-poor metros, whereas UGII remained independent of record volume ($r = 0.054$, $p = 0.595$). In policy relevance, UGII revealed that habitat quality declines as the proportion of greenspace within the metro increases ($r = 0.55$, $p < 0.001$)—a pattern that species richness did not detect ($r = 0.01$, $p = 0.310$). Additional analyses confirmed UGII's robustness and ecological relevance across bioregions.

These results underscore the framework's effectiveness and UGII's robustness. By streamlining the road-testing of new metrics, this framework will equip urban practitioners with a robust suite of empirically validated indicators—empowering cities worldwide to self-monitor and report progress toward Target 12 of the Kunming–Montreal Global Biodiversity Framework.

Session: 6798633**7008890**

22/10/25 | 15:16

Room: Valle

ORAL • EN

Selecting indicators to track subnational progress towards the Global Biodiversity Framework: Lessons learned from Québec's 2030 Nature Plan

Presenter

Katherine Hébert

Authors

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Abstract

Selecting biodiversity indicators to report national and subnational progress towards the Kunming-Montreal Global Biodiversity Framework (GBF) is a major challenge, one made even more urgent by the fast-approaching 2030 targets. To identify appropriate indicators, the selection process must be streamlined, while remaining transparent, effective, and with the active engagement of stakeholders from the academic, public, and private sectors. We present guidelines for the selection of biodiversity indicators to track progress towards 2030 targets in the context of the GBF, with a case study of the province-level indicator recommendation process for Québec's 2030 Nature Plan. We outline six steps to develop a shortlist of indicators that are relevant to targets, fulfill minimum criteria of scientific quality given available biodiversity data, and practical to inform decisions and on-the-ground conservation actions. These steps can be used to prioritise indicators based on three key properties which are each evaluated with several criteria: relevance, scientific quality, and practicality for decision support and conservation action. We present the rationale and outcomes of this selection process, culminating in 15 biodiversity indicators that we recommended for Québec's 2030 Nature Plan. A formal process, like the one described here, ensures this selection is transparent, which is fundamental so it can be updated and reviewed in the future as we update our understanding of biodiversity indicators and their influence on decisions, actions, and policies. Going forward, we recommend continuing to build trust across sectors, developing communication guidelines to standardize indicator reporting, and testing indicator performance at national and subnational scales. Overall, this case study demonstrates that with active engagement and cooperation, we can rapidly rise to the challenge of identifying the indicators we need to track biodiversity change.

Session

6799422-2

Symposium

22/10/25 | 14:00

Room: Cauca

Indigenous Data Provenance, Local Contexts and the CARE Principles for Indigenous Data Governance (Part 2)

Organizers

Maui Hudson

Corrie Roe

Description

The provenance of Indigenous data is a key issue in the biodiversity data community particularly in the context of data governance and the establishment of a Multilateral Mechanism for sharing the benefits of DSI. Implementation activities for the CARE Principles for Indigenous Data Governance are under development providing guidance for researchers, repositories and publishers including appropriate attribution for both biocultural resources and associated traditional knowledge. Local Contexts (<https://localcontexts.org/>) is a global non-profit that provides Indigenous communities, institutions, and researchers with tools to support Indigenous data sovereignty and recognise cultural authority in collections and data - both in legacy collections as well as new and emerging biodiversity, environmental monitoring and cultural projects. In this session, the Local Contexts team and users of Local Contexts across GBIF, ODIS and TDWG will discuss and show examples of their implementation of Local Contexts and how this tool supports the operationalization of the CARE Principles of Indigenous Data Governance.

Session: 6799422-2**7020927**

22/10/25 | 14:05

Room: Cauca

ORAL • EN

Endemic or Indigenous? Data labeling tools for provenance and attribution of the origins of the world's edible biodiversity

Presenter

Katie Lee Riddle (Rongowhakaata)

Authors

Katie Lee Riddle (Rongowhakaata) (Te Kotahi Research Institute • New Zealand)**Sarah Brinkley** (The Periodic Table of Food Initiative, The Alliance of Bioversity-CIAT • Colombia)**Alex Reep** (The Periodic Table of Food Initiative • United States)**Maui Hudson** (Te Kotahi Research Institute • New Zealand)**Jane Anderson** (New York University • United States)**Selena Ahmed** (The American Heart Association • United States)

Abstract

The Periodic Table of Food Initiative (PTFI)® is advancing a global effort to map the biochemical diversity of the world's foods by providing standardized tools, training, and open data. As part of this work, the PTFI is committed to setting a high ethical bar in the stewardship of data, especially in relation to the traditional and biocultural knowledge held by Indigenous Peoples and local communities. This presentation introduces an emerging Ethical, Legal, and Social Implications (ELSI) framework that supports and enables Indigenous data sovereignty within the PTFI, informed by the FAIR (Findable, Accessible, Interoperable, Reusable) and CARE (Collective Benefit, Authority to Control, Responsibility, and Ethics) principles.

In line with decisions adopted at COP16 under the Convention on Biological Diversity, this framework reinforces the importance of respecting Indigenous rights and interests, ensuring equitable benefit-sharing, and recognizing the value of traditional knowledge in biodiversity-related data systems. It also supports mechanisms for contributing to the newly established Cali Fund for Fair and Equitable Sharing of Benefits, helping ensure that benefits derived from data use reach the rightful knowledge holders.

In this oral presentation, we will share our approach to the development of data governance and labeling tools which are informed by Indigenous-led protocols and community consultation. Beyond informing the PTFI's internal practices, this framework is designed to be adaptable for other research and policy efforts striving to uphold best practices for ethical, equitable, and culturally aware data use. This talk will highlight how living data infrastructures must evolve not only technically, but socially, to ensure just participation and recognition in global data systems.

Session: 6799422-2

7007598

22/10/25 | 14:16

Room: Cauca

ORAL • EN

Community-driven insect monitoring on Inuit Nunangat, the Canadian Arctic

Presenter

Danielle Nowosad

Authors

Danielle Nowosad (University of Calgary • Canada)

John Soghigian (University of Calgary • Canada)

Sarah Adamowicz (University of Guelph • Canada)

Thomas McIlwraith (University of Guelph • Canada)

Joey Bernhardt (University of Guelph • Canada)

Dirk Steinke (University of Guelph • Canada)

Abstract

This highly interdisciplinary monitoring program was created with the Ekaluktutiak and Kugluktuk Hunter-Trapper Organizations (HTO), located on Inuit Nunangat (Central Canadian Arctic in Nunavut), to address local concerns about biting insects. It has since expanded to an additional three Inuit communities in the Kitikmeot region. Many land-users have noticed changes in biting insect populations – for example, new insects arriving on the nuna (land) and more mosquitoes and biting flies for longer periods of time in the summer. Some species act as vectors of disease and are negatively impacting important wildlife such as tuktu (caribou), umingmak (muskoxen), and tingmiaq (birds). We are integrating expert knowledge from land-users in Kitikmeot with Western research methods and infusing Inuit Qaujimajatuqangit (Inuit societal law, values, way of life, and knowledge) into all aspects of the research process. We launched insect collections with local hires in Kugluktuk in the summer of 2024 and will begin collections in Cambridge Bay, Kugaaruk, and Gjoa Haven in summer 2025. Samples from 2024 are currently being DNA barcoded and we are co-developing semi-structured interview questions with our Inuit partners. Here, we will discuss our how and why this program was created, research/knowledge data management practices, and partnerships between the academic team and Inuit community members.

Session: 6799422-2**7013820**

22/10/25 | 14:28

Room: Cauca

ORAL • EN

Exploring how Decision Support Tools Represent Place-Based Knowledge Systems in Nova Scotia, Canada

Presenter

Jumanah Khan

Authors

Jumanah Khan (Dalhousie University • Canada)

Floris Goerlandt (Canada)

Abstract

Spatial planning is a process that is essential for the transdisciplinary management of changing coastal environments. The process aims to influence the spatial distribution of activities in a way that balances environmental, economic and social needs. As community input becomes increasingly recognized for its vital role in decision-making, there is a growing need to explore how conventional decision support tools (DSTs) account for and communicate place-based knowledge (e.g., Indigenous and Local Knowledge systems). Such knowledge systems enhance the contextual applicability of decisions that better reflect present and future uses of a place. This study explores the suitability of six Decision Support Tools (DST) used in spatial planning to collect and communicate place-based perspectives: Canada Marine Planning Atlas, participatory mapping, ArcGIS StoryMap, Marxan, the Marine Spatial Planning Board Game, and virtual reality.

Through a scoping review and semi-structured interviews with spatial planners, marine and coastal researchers, and users who reside and/or work in coastal environments in Nova Scotia, key characteristics that make DSTs suitable for communicating place-based knowledge, as well as tool design limitations, are identified. Also identified are the rightsholder and stakeholder engagement, data collection, and communication stages of the spatial planning process at which each of the selected DSTs is most effectively applied. The results are meant to inform the design and use of DSTs in a way that better accounts for and serves local coastal users throughout the stages of the spatial planning process, thereby supporting informed and sustainable decision-making in the context of coastal planning in the province.

Session: 6799422-2

7014570

22/10/25 | 14:41

Room: Cauca

ORAL • EN

From Land to Cloud: Designing a Data Repository for Indigenous Futures

Presenter

Taoho Patuawa

Authors

Taoho Patuawa (Te Roroa • New Zealand)

Mike Welling (Hemisphere Digital • Australia)

Abstract

Indigenous communities in Aotearoa New Zealand are increasingly more active in native biodiversity investigations, and adaptive management to enhance biocultural landscapes. Traditionally, functions such as data stewardship have often been the domain of collaborators from research institutes who bring this knowledge and experience into the collaboration. Formal data sharing protocols are common and expectations across all aspects of the data workflow are captured in these arrangements. However, Indigenous communities are significantly marginalised without systems to assist in the management and control of all aspects of biodiversity data with provenance to their ancestral lands and waterways.

In this presentation we showcase a prototype Indigenous-designed data and information repository to support Indigenous communities in biodiversity research and adaptive management interventions. We will display some of the features of this system, and highlight the integration of the Local Contexts Hub into the information repository system and the data analytics tool to showcase how this system supports data sovereignty and Governance for Indigenous communities.

Session: 6799422-2

7106298

22/10/25 | 14:52

Room: Cauca

ORAL • ES

Monitoreo de Derechos para la Vida: Datos Indígenas en el Marco Global de Biodiversidad

Presenter

Camilo Niño Izquierdo (CNTI • Colombia)

Authors

Camilo Niño Izquierdo (CNTI • Colombia)

Laura Parra (CNTI • Colombia)

Abstract

En febrero de 2025, durante la segunda fase de la COP16 en Roma, las Partes del Convenio sobre la Diversidad Biológica (CDB) adoptaron el marco de monitoreo y seguimiento del **Marco Mundial de Biodiversidad Kunming-Montreal (MMBKM)**, el cual establece indicadores para evaluar su implementación con enfoque de derechos. Uno de los logros más significativos fue la adopción del indicador principal de la Meta 22: *“cambio de uso de la tierra y tenencia de la tierra en los territorios tradicionales de los Pueblos Indígenas y comunidades locales”*. La Comisión Nacional de Territorios Indígenas (CNTI), a través del Observatorio de Derechos Territoriales de los Pueblos Indígenas (ODTPI), ha desarrollado sistemas de información que aportan datos clave para este indicador. El **Sistema de Información Geográfica Indígena (SIG-I)** permite visualizar y analizar información espacial de los territorios indígenas, generar mapas y detectar problemáticas de uso del suelo, traslapes y amenazas ambientales. Por su parte, el **Sistema de Información de Violencia Sociopolítica (SIVOSPI)** documenta hechos de violencia que afectan a comunidades indígenas (homicidios, desplazamientos, amenazas), generando evidencia para la exigibilidad de derechos y la formulación de medidas de protección. En este escenario, presentaremos cómo el **monitoreo de derechos**, basado en información jurídica, social y geográfica, se constituye en una herramienta fundamental para evaluar si los compromisos de conservación global se cumplen respetando la autonomía y la integridad territorial de los pueblos indígenas. Los **datos indígenas** no son un insumo secundario: son la base para medir justicia, visibilizar riesgos y garantizar que las políticas de biodiversidad se implementen con enfoque de derechos humanos. Sin ellos, las metas globales al 2030 corren un alto riesgo de incumplirse.

Session

6803194

Symposium

22/10/25 | 16:00

Room: Ballroom A

Sustainable tools and skills to work with digitised specimen data: a pathway to “specimen carpentry”

Organizers

Nicky Nicolson

Deborah Paul

Description

Our networks have digitised a huge number of specimens – a crucial information resource, made even more valuable once integrated with related data. But taxonomists and collections/data managers need skills and tools development to use and manage digital information, especially when working alongside physical specimens.

It can be difficult to identify and learn the tools best suited for taxonomic research and collection data management. Dedicated tools often face sustainability issues: developed and supported by small teams or even individuals. Generic tools can be useful but need relevant examples showing how they could be applied. With so many choices, it is difficult to decide where to invest in skills development.

Cross-domain initiatives like The Carpentries offer a compelling model for skills development: community-led resources for group-based and self-paced study. The open science and software sustainability movements also demonstrate how we could transition from single-organisation projects to open community development.

This session will explore the tools, knowledge, and resources necessary to work with digitised specimens and related data. Should we build new tools or reuse existing ones – or combine both? How can we collaborate with established initiatives like the Carpentries to deliver training and peer support, towards a “Specimen Carpentry” programme?

Session: 6803194**7016917**

22/10/25 | 16:10

Room: Ballroom A

ORAL • EN

Capturing and sharing data before your collection is fully digitised: collection descriptors in the Global Registry of Scientific Collections

Presenter

Marie Grosjean

Authors

Marie Grosjean (GBIF Secretariat • Denmark)

Marcos Lopez Gonzalez (GBIF Secretariat • Denmark)

Morten Høfft (GBIF Secretariat • Denmark)

Tim Robertson (GBIF Secretariat • Denmark)

Abstract

The best way to make collections and specimens discoverable is to digitise and share them on data aggregating platforms like GBIF.org and idigbio.org. However, what to do with the information for un-digitised or not-fully digitised collections?

In this lightning talk, we introduce the concept of collection descriptors in the context of the Global Registry of Scientific Collections (GRSciColl - <https://scientific-collections.gbif.org>) as a tool to share partial information.

GRSciColl is a community-curated registry of physical scientific collections, where institutions can share information about their collections, whether they are digitised or not. Most information in GRSciColl is captured and stored in free-text fields or via occurrence records linked from GBIF.org. Free text fields are flexible, but the information cannot easily be searched and only digitised biodiversity-related specimens can be published as occurrences.

Since 2024, institutions can now describe their collection content as tables using the Latimer Core standard terms (<https://lrc.tdwg.org/terms/>). This allows them to make their collections discoverable even with partial information. For example, an institution can list the broad taxonomic groups held in their collections as well as highlight particular collectors. Users will then be able to find the collections based on scientific names or collector names.

During the talk, we will present examples where we transformed textual information into collection descriptors and show how it improves the collection discoverability.

Session: 6803194**7020123**

22/10/25 | 16:20

Room: Ballroom A

ORAL • EN

Envisioning a resilient model for capacity building in biodiversity informatics

Presenter

Deborah Paul

Authors

Deborah Paul (University of Illinois | Species File Group • United States)

Erica Krimmel (United States)

Gary Motz (Yale University | Yale Peabody Museum • United States)

Abstract

Rich, multi-purpose data is now ubiquitous. Increasingly our effort has turned to focus on sharing and enhancement via new links and iterative curation of these data. Advances in this effort require a focus on developing a model that emphasizes the interplay between software, data, and human interactions. One way to find this balance is to federate our effort around the concept of help desks. The German National Research Data Infrastructure (NFDI) program shows us one such model to get coordinated assistance via a collaborative cluster (<https://www.nfdi4biodiversity.org/en/mou-helpdesk/>) across the earth, chemical, and life sciences. Other proven elements of this model are workshops that repeat and improve across time, cohorts and the advent of evolving tools and ideas. Both these approaches thrive when vibrant communities exist around them. All these efforts require stable funding to thrive and grow. In looking for models that embrace this thinking and that present models that might guide our efforts we find the Carpentries (<https://carpentries.org/>). These efforts, Software and Data, exemplify an approach around which we can build a resilient model and content not subject to geopolitical winds and funding cycles. We explore known software, skills, and knowledge needs and the interplay between helpdesks and workshops and highlight opportunities and shortcomings.

Session: 6803194**7020651**

22/10/25 | 16:30

Room: Ballroom A

ORAL • EN

Tools and skills for the curation of digitised herbaria

Presenter

Elspeth Haston

Authors

Elspeth Haston (Royal Botanic Garden Edinburgh • United Kingdom)

Abstract

As the digitisation of natural science collections progresses, the need for tools and skills for the staff who curate those collections becomes increasingly important and urgent. The specimens held in these collections are fundamental to research and are a critical source of data and knowledge urgently needed for the current biodiversity crisis. Without taxonomic curation, the names attached to these specimens may be synonyms, misapplied or incomplete. These issues may have a significant impact on research undertaken based on these collections.

Taxonomic curation can be carried out at different levels. At a high level, accessibility to accepted classifications at a range of taxonomic ranks and the ability to compare with alternatives, including those currently being used within a collection, is a key requirement. Having a digitised collection can provide curation staff with a detailed understanding of the changes needed to follow an updated classification if the tools are available. At specimen level, tools to access specimen citations, identifications of duplicates as well as managing online determinations are becoming more important for curation staff and volunteers. These processes require digital skills for curators. Training in the use of tools, where they are available, also requires accessible documentation.

In this presentation we review the taxonomic curation of digitised natural science collections and the digital tools and skills required.

Session: 6803194**7020659**

22/10/25 | 16:40

Room: Ballroom A

ORAL • EN

Developing a standard, open and replicable course curriculum to enable mobilization and use of biodiversity data

Presenter

Laura Anne Russell

Authors

Laura Anne Russell (GBIF • Denmark)

Sharon Grant (Field Museum of Natural History • United States)

Sophie Pamerlon (GBIF France • France)

David Bloom (VertNet • United States)

Laban Musinguzi (GBIF Africa Regional Support Team • Uganda)

Tsiky Rabetrano (GBIF Africa Regional Support Team • Madagascar)

Dag Endresen (GBIF Norway • Norway)

Veronika Johansson (GBIF Sweden • Sweden)

Abstract

The Global Biodiversity Information Facility (GBIF) empowers its global network through capacity-building activities that promote and enable the efficient mobilization and use of information about biodiversity. These activities work across capacity development levels, targeting individuals, institutions, nations, and global regions. Training plays a key role in expanding the communities of practice engaged with the collection and curation of biodiversity.

GBIF's training efforts build partnerships that institutionalize new capacity within a growing network of data publishing institutions. Development and delivery of training materials is supported through GBIF Participant nodes, regional support teams, and the GBIF community of practice.

This presentation will highlight the work GBIF has undertaken over the last 10 years to develop a standardized, open, and replicable training curriculum with examples from the Biodiversity Information for Development (BID) programme and the Capacity Enhancement Support Programme (CESP) where materials have been reused and adapted. The presentation will also outline newly developed materials and encourage their further translation, adaptation and reuse. And finally, we will discuss how the community can engage with the development and delivery of the materials.

Session

6803179

Symposium

22/10/25 | 16:00

Room: Ballroom B1

Sustaining and Building Knowledge Through Long-Term Biological Monitoring

Organizers

Chandra Earl

Edward Gilbert

Kelsey Yule

Description

Long-term biological monitoring is essential for understanding changes in ecosystems, species populations, and environmental conditions over time. By sustaining consistent data collection efforts, researchers and practitioners can uncover trends that inform scientific discovery, resource management, and conservation efforts. These datasets provide unique opportunities to investigate ecological dynamics, detect emerging patterns, and generate predictive models that improve our understanding of biological systems. They are also critical for assessing climate change impacts, evaluating biodiversity loss, guiding habitat restoration, and improving ecological forecasting.

This session invites contributions from those involved in long-term biological monitoring, highlighting the successes, challenges, and innovations that sustain these efforts. How are monitoring programs adapting to new tools, standards and analytical approaches? What strategies ensure data continuity and accessibility across decades? What key scientific findings have emerged from long-term datasets, and how have they been applied to conservation, land management, and ecological research? Case studies, research findings, and discussions on best practices for designing, implementing, and maintaining long-term biological monitoring programs are encouraged.

Session: 6803179**7016505**

22/10/25 | 16:00

Room: Ballroom B1

ORAL VIRTUAL • ES

Observatorio de Cambio Global de Sierra Nevada: seguimiento ecológico a largo plazo y gestión de datos siguiendo los principios FAIR

Presenter

Andrea Ros Candeira

Authors

Andrea Ros Candeira (University of Granada • Spain)

Regino Zamora (University of Granada • Spain)

Ricardo Moreno Llorca (University of Granada • Spain)

Manuel Merino Ceballos (University of Granada • Spain)

Abstract

La comunidad científica internacional considera que, tanto la región mediterránea como las áreas de montaña, se encuentran entre las zonas más amenazadas por el cambio climático. La región montañosa de Sierra Nevada (SE España) está considerada como uno de los puntos calientes de biodiversidad más importantes de la Cuenca Mediterránea, albergando en ella el área protegida “Espacio Natural de Sierra Nevada”, considerada Reserva de la Biosfera (1986), Parque Natural (1989) y Parque Nacional (1999).

Con el objetivo de recopilar información ambiental útil y relevante para estudiar los efectos del cambio global en Sierra Nevada y apoyar la toma de decisiones, en 2008 nace el “Observatorio de Cambio Global de Sierra Nevada” (<https://obsnev.es/>), un proyecto institucional de colaboración entre la Consejería de Sostenibilidad y Medio Ambiente (Junta de Andalucía) y la Universidad de Granada (UGR) para desarrollar un programa de seguimiento a largo plazo y de gestión de la información.

Desde entonces, el Observatorio genera largas series temporales de datos realizando seguimientos de los ecosistemas y las especies de Sierra Nevada bajo la coordinación científica de la UGR, y también recopilando datos de otros proveedores. Sin embargo, la toma de datos es sólo el inicio de un proceso a lo largo del cuál es importante aplicar buenas prácticas de documentación (metadatos) y gestión de datos, para poder asegurar cuestiones como su preservación, accesibilidad y reutilización.

Por esta razón, el Observatorio sigue una estrategia de gestión de datos en base a los principios FAIR que consiste en 1) desarrollar servicios de datos propios destinados a mejorar la gestión de los datos (como el Sistema de Información Linaria y el portal de datos ClimaNevada), pero también 2) dedicar esfuerzos a estar presente y compartir datos en infraestructuras y redes internacionales de seguimiento ecológico y de la biodiversidad como GBIF y LTER.

Session: 6803179**7020336**

22/10/25 | 16:12

Room: Ballroom B1

ORAL • EN

The ecocomDP app: lessons learned from a convergence effort to develop tools for cross-network biodiversity synthesis

Presenter

Eric Sokol

Authors

Eric Sokol (National Ecological Observatory Network (NEON), Battelle • United States)

Abstract

Answering broad-scale questions in biodiversity will require tools that facilitate the discovery and exploration of analysis ready data. Here we describe a convergence collaboration among the US National Ecological Observatory Network (NEON), Environmental Data Initiative (EDI), US Long Term Ecological Research (LTER) network, a working group from the 2024 ESIL Innovation Summit, and interns from the St. Edwards University's i4 internship program to develop an R Shiny user interface to leverage the ecocomDP data model and R library to access and explore long-term ecological community survey data published by NEON and EDI. This convergence approach provided real-world scientific coding experience for computer science undergraduates while generating insights into user community needs for continental-scale biodiversity questions. Through user testing and feedback, the team identified implementation possibilities, technical challenges, and community desires, some of which may be addressable with the implementation of cloud-native tools, such as Apache Arrow. This collaboration demonstrates three key outcomes: (1) a window into data user needs for analysis-ready biodiversity data for synthesis questions at broad scales, (2) a roadmap for scaling these tools to integrate with GBIF and other global datasets, and (3) a training model fostering convergence between computer scientists, data scientists, developers, and ecologists. The initiative exemplifies how sustained interdisciplinary partnerships can advance both scientific discovery and workforce development in data-intensive ecological research.

Session: 6803179

7020755

22/10/25 | 16:23

Room: Ballroom B1

ORAL • EN

Biodiversity Monitoring in Protected Areas in Brazil: Building a Path to Turn Data into Evidence-Based Environmental Management Decisions

Presenter

RODRIGO JORGE

Authors

RODRIGO JORGE (Instituto Chico Mendes de Conservação da Biodiversidade • Brazil)

Abstract

Brazil's Biodiversity Monitoring Program—known as the Monitora Program—is currently operating or being implemented in 129 federal protected areas managed by ICMBio. Covering all Brazilian biomes, the program monitors biodiversity targets that reflect the conservation status of various taxonomic groups using low-cost, easy-to-implement protocols that do not require specialists.

In 2024, Monitora marked ten years since the start of data collection for its forest component. To celebrate this milestone, a report was published with results from 2014 to 2022, based on data from 57 protected areas—45 of them in the Amazon. The analysis covered four targets: mammals, birds, fruit-feeding butterflies, and plants. The results were shared in two formats:

- A digital report summarizing trends across all protected areas;
- An interactive dashboard enabling users to explore trends by target and by area.

The dashboard uses a color-coded system to simplify interpretation:

Green indicates stability or increase;

Yellow indicates slight decline, suggesting the need for further investigation;

Red indicates significant decline, highlighting the urgency of management action.

Raw data are publicly available, promoting transparency and supporting the generation of new knowledge.

Recent progress in data management and accessibility has strengthened the program's impact. However, faster data analysis and integration into decision-making are still needed. Future developments aim to improve the dashboard to suggest possible causes for detected changes and recommend management actions directly. Similar tools are also planned for other environments covered by the Monitora Program, including marine-coastal and freshwater-inland ecosystems.

Session: 6803179**7015170**

22/10/25 | 16:36

Room: Ballroom B1

ORAL • EN

Integrating of global and regional information on direct and indirect drivers of Neotropical biodiversity

Presenter

Martha Paola Barajas Barbosa

Authors

Martha Paola Barajas Barbosa (German Centre for Integrative Biodiversity Research (iDiv) • Germany)**Jorge Andrey Beltrán Barbosa** (University of Bremen Faculty Biology and Chemistry • Germany)**Alban Sagouis** (German Centre for Integrative Biodiversity Research (iDiv) • Germany)

Abstract

Human activities are rapidly altering the complex interactions between biotic and abiotic components of the environment at a global scale. These changes have accelerated in recent decades, particularly in megadiverse regions such as the Neotropics. However, the influence and magnitude of biodiversity drivers in these regions—commonly shaped by distinct socio-economic contexts—remain poorly characterized, which can be partly attributed to limited collaboration with local researchers and lack of integrative research initiatives. To address this, we are synthesizing global and regional datasets to assess both direct and indirect drivers of biodiversity change across ecoregions in the Neotropics. Using time-series data from the past two decades, we examine trends in agricultural expansion, forest cover change (using annual fractional tree cover, and Land Use Land cover from MapBiomas and HILDA+), and economic growth (using nighttime lights as proxies for urban growth and electrification). Our preliminary results show that temporal dynamics across Neotropical ecoregions is quite diverse. Regions such as the Brazilian Atlantic Forest, Mato Grosso and the Caatinga show a decrease in forest cover, potentially linked to agricultural expansion. In contrast, Neotropical dry forests such as the Ecuadorian dry forests and Magdalena Valley dry forests in Colombia have experienced an increase in forest or vegetation cover over the past two decades. Our preliminary findings evidence the complexity of temporal changes of biodiversity drivers, and the need for further integration with indirect drivers, such as economic development, to further understand potential causes of the changes. By integrating global and regional datasets, our approach attempts to provide a comprehensive understanding of biodiversity drivers and its interactions over time, highlighting the critical need for region-specific research to better understand dynamics and patterns of biodiversity drivers on megadiverse regions such as the Neotropics.

Session

6803206

Symposium

22/10/25 | 16:00

Room: Ballroom B2

Developing capacity through regional cooperation: how regional hubs enhance local scientific voices

Organizers

Laurent Chmiel

Ana Carolina Peralta

Ruben Pérez

Description

Local scientific communities might lack the mobilizable expertise and adapted resources needed to participate in international biodiversity data initiatives fully, depriving global systems of precious local insights. Regional hubs can address these challenges by encouraging capacity development, cooperation, and knowledge transfer between scientific communities. The Hubs would break away from a North/South approach to create a multidirectional dynamic in which all participants would contribute.

This session explores strategies to boost regional cooperation and create sustainable, long-term regional collaboration initiatives. It will examine successful case studies and strategies supporting regional capacity development, from content to funding. We will also explore how regional hubs can increase engagement by bridging gaps between local researchers and global data-sharing networks, ensuring that research outcomes are accessible and actionable while highlighting how contributing to data repositories can enhance researchers' ability to monitor and study their own environments more effectively.

Session: 6803206**7014783**

22/10/25 | 16:05

Room: Ballroom B2**LIGHTNING TALK VIRTUAL • EN**

Strengthening collaboration with data-poor areas of the Mediterranean through regional training programs: The case of the Autumn Data School

Presenter

Dimitra Mavraki

Authors

Dimitra Mavraki (Hellenic Centre for Marine Research • Greece)

Ioannis Rallis (Hellenic Centre for Marine Research • Greece)

Melina Loulakaki (Hellenic Centre for Marine Research • Greece)

Abstract

MedOBIS, the Regional OBIS node for the Mediterranean Sea, aims to support the scientific community by facilitating open access to marine biodiversity data across the region. Despite efforts since 2013, the number of biological occurrence records for the Mediterranean remains significantly lower than in other marine areas, such as the Atlantic Ocean. This data gap stems from various socioeconomic and geopolitical factors, including limited awareness of open science practices in several non-EU Mediterranean countries.

To address this issue, a targeted data workshop – organized under the EMODnet Biology initiative – was held in Lecce, Italy, in November 2023. Led by MedOBIS, the “Autumn Data School” united researchers from non-EU Mediterranean nations with the goal of improving biogeographic data availability and promoting sustainable data-sharing practices. Key objectives included fostering cross-border collaboration, sharing best practices for data standardization and publication, and encouraging the contribution of local marine biodiversity datasets.

Participants engaged in practical sessions on FAIR and open data principles, Darwin Core standards, metadata documentation, and dataset preparation for publication. This initiative resulted in the successful collection, standardization, and publication of seven new datasets via the OBIS and GBIF platforms. Feedback from attendees, particularly from North African countries, emphasized the urgent need for continued training and knowledge exchange in data management.

The outcomes of the workshop underline the importance of targeted capacity-building efforts in closing the Mediterranean data gap. Both EMODnet Biology and medOBIS are committed to furthering these initiatives by organizing additional workshops and reinforcing open data practices throughout the region. These ongoing efforts aim to enhance data availability and support marine biodiversity research and conservation across the Mediterranean.

Session: 6803206**7019903**

22/10/25 | 16:10

Room: Ballroom B2**LIGHTNING TALK • EN**

Bridging Conservation Technology Gaps Through the WILDLABS Community

Presenter

Vanesa Reyes

Authors**Talia Speaker** (WILDLABS at World Wildlife Fund • United States)**Vanesa Reyes** (WILDLABS at Wildlife Conservation Society • Argentina)**Alexandra Roods** (WILDLABS at World Wildlife Fund • United States)**Abstract**

As technology becomes increasingly vital to conservation, practitioners, especially those in underrepresented regions, need access to the right tools, knowledge, and networks to maximize impact. WILDLABS is the global hub for conservation technology, providing a free, open platform that connects 11,000+ innovators, researchers, and conservationists across more than 120 countries to resources that advance their work and strengthen regional capacity.

In this talk, we will introduce WILDLABS' key services, including community resources that bridge knowledge gaps, research projects that map global and regional trends and needs, programs that deliver consensus on data and tool integration, and capacity-building initiatives that support technology adoption and scaling. These services are implemented both globally and regionally through community-led hubs such as the Latin America and East Africa groups, which foster knowledge exchange and cooperation tailored to local priorities. Programs like Women in Conservation Technology also exemplify WILDLABS' commitment to supporting specific communities and addressing equity in access to tools and opportunities. We will share how these services work together to bridge the gap between policy, data, technology, and funding. Finally, we will highlight how collaboration across sectors and regions breaks down adoption barriers, mobilizes innovative funding, and ensures that solutions are accessible, effective, and scalable.

This contribution to the session will offer practical insights into how global platforms like WILDLABS can support regional cooperation, amplify local voices, and contribute to sustainable biodiversity data initiatives.

Session: 6803206**7020026**

22/10/25 | 16:15

Room: Ballroom B2**LIGHTNING TALK • EN**

Amplifying African Biodiversity Voices through Regional Support: Lessons from GBIF's Africa Support Team

Presenter

Tsiky Rabetrano

Authors

Tsiky Rabetrano (GBIF • Madagascar)

Laban Musinguzi (National Fisheries Resources Research Institute (NaFIRRI) • Uganda)

Mélianie Raymond (Global Biodiversity Information Facility • Denmark)

Maheva Bagard Laursen (Global Biodiversity Information Facility • Denmark)

Abstract

The GBIF Africa Regional Support Team offers a compelling example of how regionally embedded cooperation can empower local scientific communities and expand participation in global biodiversity data initiatives. Acting in strong coordination with the GBIF Secretariat, the Africa support team plays a critical role in bridging gaps between institutions, national nodes, and global infrastructure through tailored multilingual support.

This presentation highlights the team's work supporting more than 20 countries across the continent through distributed helpdesk services, targeted virtual training, mentorship, and peer-learning initiatives. Over the past year, the Africa team has led the delivery of thematic webinars, co-facilitated multi-country training courses, and supported institutions with practical guidance for data cleaning, metadata preparation, and dataset publishing.

A key strength of this regional approach lies in its responsiveness to local needs. For example, the team's bilingual support (English and French) ensures wider accessibility, while one-on-one sessions help institutions navigate challenges like georeferencing, IPT use, and licensing. The team also facilitates regional exchanges through interactive events.

By embedding support close to the users in biodiversity informatics, the Africa Regional Support Team model enhances both technical capacity and long-term engagement, helping to respond more directly to the needs of the region. It demonstrates how locally anchored teams can increase biodiversity data publication and use while making sure African institutions not only contribute to but also benefit from global data infrastructure. This presentation will share lessons learned, showcase successes, and suggest ways this model could inspire similar regional cooperation elsewhere.

Session: 6803206

7020052

22/10/25 | 16:20

Room: Ballroom B2

LIGHTNING TALK VIRTUAL • EN

Governance of biodiversity monitoring across scales, a European perspective

Presenter

Guillaume Body

Authors

Guillaume Body (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Aino Lipsanen (Finnish Environment Institute • Finland)

Petteri Vihervaaara (Finnish Environment Institute • Finland)

Mathieu Basille (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Michelle Silva del Pozo (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Léa Riera (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Abstract

Europe aims at addressing the governance of biodiversity monitoring to improve production and comparability of information about the state of nature amongst member states. Three biodiversity partnerships, Biodiversa+, EuropaBON and MARCO-BOLO are thinking about joined forces to develop and share ideas on governance at the continental scale, including national and subnational levels and responsibilities. In particular, Biodiversa+ advocates for a governance based on the subsidiarity principle, and adequate split of responsibilities and scientific expertise. We detail the implementation through a European Biodiversity Observation Coordination Center, a network of National Biodiversity Monitoring Coordination Centers, and European Thematic Hubs to manage the hundreds of currently existing national monitoring schemes.

Session: 6803206**7020435**

22/10/25 | 16:25

Room: Ballroom B2**LIGHTNING TALK VIRTUAL • EN**

Building Capacity for Marine Biodiversity Data Sharing: Reflections from the Marine Biological Data Mobilization Workshops

Presenter**Ana Carolina Peralta****Authors****Ana Carolina Peralta** (University of South Florida | Caribbean OBIS • United States)**Jonathan Pye** (Ocean Tracking Network • Canada)**Tim van der Stap** (Hakai Institute • Canada)**Elizabeth Lawrence** (UNESCO | IOC Project Office for IODE Ocean Biodiversity Information System • Canada)**Laura Brenskelle** (Integrated Systems Solutions • United States)**Tylar Murray** (University of South Florida • United States)**Mathew Biddle** (NOAA Integrated Ocean Observing System • United States)**Stephen Formel** (Formel Data Services • United States)**Abstract**

The Marine Biological Data Mobilization Workshops—co-organized by participants in the Standardizing Marine Biological Data (SMBD) Working Group, a global network of OBIS data managers who meet regularly and collaborate year-round to build training content and coordinate activities. This dedicated team comes together annually to organize the workshop supporting researchers, data managers, and marine biologists in learning how to publish marine biodiversity data using global standards and infrastructures. Since 2022, three virtual workshops have brought together participants from dozens of countries for hands-on training in FAIR data principles, Darwin Core standards, taxonomic tools, data cleaning techniques, and publication pathways through OBIS and GBIF.

The workshops address a persistent barrier to data sharing: finding time and advisors for standardizing and publishing data. The workshops are designed not only to transfer technical skills, but also to foster international collaboration and confidence in navigating complex data workflows. The curriculum continues to evolve, incorporating lessons learned and responding to participant feedback to remain relevant to current community needs.

Although long-term impacts are still emerging, the workshops have already demonstrated value in building cross-cultural networks, increasing familiarity with biodiversity data infrastructures, and providing a dedicated space for data providers to focus on preparing and documenting datasets for publication. Some participants have published multiple datasets to OBIS and GBIF, and supported similar efforts in their home institutions.

This presentation will highlight the design, implementation, and evolution of the workshops, along with key takeaways from participant experiences. It will reflect on how structured training initiatives can contribute to more inclusive participation in global biodiversity data networks, and how virtual collaboration can galvanize capacity development toward achieving the goals of the UN Decade of Ocean Science and the Kunming-Montreal Global Biodiversity Framework.

Session

6803090

Panel

22/10/25 | 16:00

Room: Tolima

Taxonomy and DNA Technologies: Shaping the Future of Biodiversity Inventories for Action

Organizers

Adriana Radulovici

Saara Suominen

Description

The exploration, conservation, and management of biodiversity have long relied on species being classified, named, and described through a rigorous, yet often time-consuming, taxonomic process. Over the past two decades, advancements in DNA technologies have significantly accelerated biodiversity assessments, leading to the generation of tens of millions of DNA sequences assigned to numerous Molecular Operational Taxonomic Units (MOTUs). These MOTUs are often well-georeferenced, imaged, and databased, but many still lack formal species names. While efforts are underway to integrate DNA data with classical taxonomy, the rapid generation of molecular data — particularly with the advent of environmental DNA (eDNA) metabarcoding — coupled with a global taxonomic impediment, raises important questions about the future of using DNA-based data for biodiversity research, conservation, and policy-making.

This panel aims to bring together representatives from biodiversity databases hosting DNA data, scientists, and decision-makers to discuss the future of inventorying and monitoring biodiversity in a world facing unprecedented biodiversity loss alongside a significant shortage of taxonomic expertise.

Session

6960773-4

Symposium

22/10/25 | 16:00

Room: Caldas

Data Governance (Contributed Oral Presentations)

Organizers

Andre Zerger

Brittany Carter

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-4**7015428**

22/10/25 | 16:00

Room: Caldas

LIGHTNING TALK • EN

Beyond Interoperability: Exploring Governance Barriers to Effective Biodiversity Data Use at the Local Level

Presenter

David Stella

Authors

David Stella (CzechGlobe, Czech Academy of Science • Czechia)

Tomáš Badůra (Czechia)

Eliška Tichopádová (Czechia)

Simona Zvěřinová (Czechia)

Julia Leventon (Czechia)

Abstract

Efforts to standardize and open biodiversity data have made significant technical progress in recent years. Yet in practice, the transformative impact of such data on biodiversity policy remains limited—especially at the local level where decisions are made and conservation actions are implemented. ENABLElocal, a European research project working across case studies in the Czechia, Germany, and Sweden, explores these limitations from a governance and social science perspective.

Rather than focusing solely on data availability or interoperability in a technical sense, ENABLElocal investigates how different actors across governance levels perceive, access, and use biodiversity information. Using a combination of living lab methodology, stakeholder workshops, and surveys, the project identifies critical gaps between data supply and actual decision-making needs-demand. Findings suggest that even in data-rich contexts, fragmentation persists—not only due to technical barriers, but also institutional silos, misaligned incentives, and epistemic mismatches between data producers and users.

This presentation argues that improving biodiversity data usability requires more than harmonizing datasets; it requires rethinking the socio-institutional infrastructures in which data circulates. We emphasize the importance of early-stage stakeholder engagement, iterative knowledge co-production, and attention to contextual governance arrangements. ENABLElocal thus contributes to ongoing efforts to integrate local data practices into broader reporting and decision frameworks, while cautioning against purely top-down or techno-centric approaches.

By drawing on cross-country insights, this case supports the broader claim that governance readiness—especially at local levels—must be addressed alongside data openness. Without this, even the best-designed platforms and standards risk falling short of enabling real-world conservation outcomes.

Session: 6960773-4**7020781**

22/10/25 | 16:05

Room: Caldas

LIGHTNING TALK • EN

Harmonising FAIR and CARE; Navigating Synergies and Trade-Offs in Data Governance

Presenter

AIDIN NIAMIR

Authors

AIDIN NIAMIR (SENCKENBERG SOCIETY FOR NATURE RESEARCH • Germany)

Renske M. Gudde (Germany)

Rainer M. Krug (Switzerland)

Yanina V. Sica (Germany)

Abstract

The FAIR principles are widely regarded as essential for enabling open and reusable data in scientific research. However, their emphasis on openness can inadvertently overlook the rights and interests of Indigenous peoples. To address this, the CARE Principles for Indigenous Data Governance were introduced, focusing on collective benefit, control, responsibility and ethics. Drawing on our practical experience in data management, this paper explores the interplay between the FAIR and CARE principles. We categorise the relationship between them into three types: (a) aligned sub-principles, where implementing one supports the other; (b) independent sub-principles, which coexist without interacting; and (c) contradictory sub-principles, where implementing one may impede the other. Understanding these dynamics enables the development of strategies that reconcile openness with data sovereignty. By identifying the synergies and tensions, this work supports a more equitable and responsible approach to data stewardship in science-policy contexts.

Session: 6960773-4**7020103**

22/10/25 | 16:10

Room: Caldas

ORAL • EN

Mobile Applications to Conservation Applications: Incentivizing FAIR principles through flexible mobile data collection tools

Presenter

Catherine Jardine

Authors

Catherine Jardine (Birds Canada • Canada)**Denis Lepage** (Birds Canada • Canada)**Kyle Horner** (Birds Canada • Canada)

Abstract

Accessible, open data is critical for the conservation of biodiversity, but data collected by small-scale research and monitoring programs, or those with limited resources, are often not integrated into FAIR platforms and remain unavailable to the conservation community. Birds Canada seeks to resolve this issue using the NatureCounts mobile app.

The app's extremely flexible and customizable data architecture allows users to define protocols tailored to nearly any effort-based monitoring project. Once defined, the app dynamically renders user-friendly and intuitive data entry forms specific to each protocol. In this way, it can provide mobile data entry support to almost any standardized avian survey with just a few hours of setup. The app also includes a first-of-its-kind point count feature, using satellite imagery to improve and digitize one of the most important methodologies for biodiversity monitoring.

By removing the step of data transcription, the app offers immense time and cost savings and reduces errors. These benefits incentivise users to adopt the platform. In doing so, their data are integrated into a FAIR repository at the outset, eliminating the need for re-formatting or upload; steps which are often overlooked or unfunded.

Data collected through the app flow into the NatureCounts database which, at 250 million records, is the largest biodiversity database in Canada and supports thousands of data requests annually. Data from NatureCounts have been used for species assessments, land use planning, impact assessment, climate change mitigation, and over 4200 scientific publications to date. Flexible data access permissions support the security of sensitive records and Indigenous data sovereignty.

By providing software tools across the data pipeline, from collection through application, the NatureCounts platform seeks to support projects to meet FAIR principles and contribute to the targets of the The Kunming-Montreal Global Biodiversity Framework.

Session: **6960773-4****7018697**

22/10/25 | 16:20

Room: Caldas

ORAL • EN

From Principle to Practice: A Systematic FAIR Assessment of Plant Genetic Resources Data in EURISCO

Presenter

Stephan Weise

Authors

Catherine Hazel M. Aguilar (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) • Germany)**Markus Oppermann** (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) • Germany)**Stephan Weise** (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) • Germany)

Abstract

The FAIR principles (Findable, Accessible, Interoperable, Reusable) were developed to make research results more transparent and efficient and to increase their sustainability (Wilkinson et al. 2016). FAIR-compliant datasets are also becoming increasingly important in the field of plant genetic resources. However, the practical implementation of the FAIR principles sometimes proves to be very complex. In addition to significant effort, e.g. in terms of data curation and standardisation, this also includes activities that go beyond the level of datasets and concern, for example, data aggregators and other repositories (Koers et al. 2020). This complexity is clearly visible in the conservation and use of plant genetic resources. Here, there is a close link between digital data and physical biological materials described by the former, different legal frameworks in different countries, and infrastructures for the cross-border exchange of materials and data. In addition, the roots of many collections of plant genetic resources go back decades (Weise et al. 2025), which does not necessarily simplify the application of the FAIR principles.

The European Search Catalogue for Plant Genetic Resources (EURISCO) brings together information on more than two million samples (both *ex situ* accessions and *in situ* crop wild relative populations) from more than 430 collections in 43 countries (Kotni et al. 2023). On the one hand, the advantages of consolidating and integrating such extensive amounts of data become clear, but on the other hand, the pitfalls associated with a general implementation of the FAIR principles in a heterogeneous and globally important area also become apparent.

Using the example of EURISCO, the talk will provide an overview of a comprehensive assessment of data in the field of plant genetic resources with regard to their compliance with the FAIR principles (Aguilar et al. 2025). Potential weaknesses will be evaluated, areas of tension identified and possible solutions proposed.

Session: 6960773-4**7012269**

22/10/25 | 16:30

Room: Caldas

ORAL • EN

The NFDI4Earth Label as a tool to harmonize Earth System Science data repositories

Presenter

Jonas Grieb

Authors

Robert Brylka (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**Jonas Grieb** (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**Ronny Gey** (Helmholtz Centre for Environmental Research – UFZ • Germany)**Claus Weiland** (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**Claudia Müller** (Alfred Wegener Institute for Polar and Marine Research • Germany)**Stephan Frickenhaus** (Alfred Wegener Institute for Polar and Marine Research • Germany)

Abstract

Data repositories play a key role in enabling sustainable research data management. In the Earth System Science domain (ESS), numerous data repositories exist, but varying support for community standards is a challenge for cross-repository data integration. Additionally, researchers looking for sustainable repositories for data deposition need trustworthy indicators to guide their decision. In NFDI4Earth, the German national research data infrastructure for the ESS, the NFDI4Earth Label is being developed to tackle these challenges.

The NFDI4Earth Label provides a framework to assess the FAIRness of data infrastructures, including particularly interoperability and trustworthiness. Thus, it will support the harmonization of these infrastructures by (1) providing specific metrics to assess the interoperability of repositories within a growing landscape of interconnected digital services, and (2) recommending actions to close the identified gaps.

Existing certifications, like the Core Trust Seal, are also considered during the assessment. However, they are often too difficult to achieve due to intensive organizational and financial requirements, especially for smaller repositories. Therefore, the NFDI4Earth Label is designed as a lightweight, complementary framework that enables a semi-automatic assessment of repository capabilities.

Key concepts include:

- The pre-requirement of registering the repository in re3data, thus fostering the collaboration with an established registry within the community.
- A set of metrics on data standards and interfaces against which the information of a repository in re3data is assessed. A minimal threshold must be exceeded to obtain the Label.
- A self-assessment on additional aspects focusing on the sustainability and trustworthiness of the repository. An optional evaluation of the repository's datasets based on the F-UJI assessment tool.
- Facilitate the embedding of NFDI4Earth's distributed architecture in cross-domain dataspace such as EOSC.

We will present the assessment workflow of the NFDI4Earth Label and how this process interacts with community repositories during the transformation into the permanent operation of NFDI4Earth.

Session: 6960773-4**7020749**

22/10/25 | 16:40

Room: Caldas

ORAL • ES

Building Capacity for Open Biodiversity Knowledge: Plazi's Approach to Training and Community Engagement

Presenter

Donat Agosti

Authors

Julia Giora (Plazi • Brazil)

Felipe Lorenz Simoes (Plazi • Brazil)

Valdenar Gonçalves (Plazi • Brazil)

Donat Agosti (Plazi • Germany)

Abstract

Liberating biodiversity data from traditional scientific literature and transforming it into FAIR (Findable, Accessible, Interoperable, and Reusable) digital resources is a foundational step toward a more inclusive and open biodiversity knowledge system. Since 2008, Plazi, a Swiss-based non-profit organization, has been leading this effort by developing tools, workflows, and training initiatives that support the conversion of taxonomic literature into accessible digital data. Plazi's output is deposited in major repositories such as TreatmentBank (TB), the Biodiversity Literature Repository (BLR) and the Global Biodiversity Information Facility (GBIF), by means of taxonomic treatments, figures and tables. However, ensuring the quality and scalability of this process depends on a broad, trained community. Plazi addresses this need by offering both in-person and online training, including certification programs that equip researchers, students, and curators to contribute to data extraction, validation, and reuse. These participants not only help scale up the production of FAIR data, but can also gain tools to evaluate the scientific impact of researchers, institutions, journals, or taxa using the resulting statistics which can also be transformed into dynamic dashboards. As the demand for high-quality biodiversity data continues to grow, so does the need for community-led engagement in the curation and reuse of this information. By empowering individuals to become active contributors, Plazi fosters a more equitable and sustainable ecosystem for biodiversity data sharing.

Session: 6960773-4**7012664**

22/10/25 | 16:30

Room: Caldas

ORAL • EN

The impact of the proportion of the national land area protected on biodiversity loss

Presenter

Oscar Andrés Martínez

Authors

Oscar Andrés Martínez (Pontificia Universidad Católica de Chile • Colombia)**Oscar Melo** (Pontificia Universidad Católica de Chile • Chile)

Abstract

International agreements for biodiversity conservation have promoted an increase in protected areas (PAs) worldwide by setting percentage area targets. Previous studies have attempted to measure the impact of PAs on deforestation, poverty rates, and individual species using impact evaluation methods with discrete treatments. However, few studies have assessed their effects on biodiversity indices using continuous treatment. This novel research assesses how progress toward the global goal of increasing the percentage of national territory designated as PAs affects various biodiversity indicators. The difference-in-differences method with continuous treatment was employed to assess the effectiveness of PAs on biodiversity loss, using the Red List Index (RLI), Biodiversity Intactness Index (BII), and Species Habitat index (SHI) at the country level for a panel of 142 countries from 2001 to 2014. We found statistically significant dynamic effects of strictly PA (IUCN categories I-II) on the RLI, the dynamic effect is in the ninth period, suggesting that a one percent rise in strictly protected areas increases the RLI by 0.92 percentage points after nine years, decreasing species extinction risk. Using these three indices, we conclude that annual changes in these biodiversity indices do not allow us to identify the robust significant effects of national protected areas on reducing biodiversity loss. This research contributes evidence about the impact of percentage area targets on biodiversity in international agreements to improve policy decisions at the national, regional and global levels to develop new protected areas and conserve biodiversity.

Session

6960773-9

Symposium

22/10/25 | 16:00

Room: Valle

Citizen Science & Community Engagement (Contributed Oral Presentations)

Organizers

Maria Cornthwaite**Henrique M. Pereira**

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-9**7011636**

22/10/25 | 16:00

Room: Valle

ORAL • EN

Recognition and completeness metrics from iNaturalist and GBIF can inform future citizen science: a case study on Namibian arthropods

Presenter

Martha Alfeus

Authors

Martha Alfeus (Brandenburg University of Technology Cottbus–Senftenberg • Germany)**Klaus Birkhofer** (Department of Ecology, Brandenburg University of Technology Cottbus–Senftenberg • Germany)**John Irish** (Namibia Biodiversity Database • Namibia)

Abstract

Arthropods are the most diverse animal phylum and play crucial roles in ecosystem functioning through their contributions to ecosystem processes. Accurate knowledge about their distribution and diversity is essential for effective ecosystem management and biodiversity conservation. Public biodiversity databases and citizen science records could contribute to our understanding of arthropod diversity, particularly in data-deficient regions. To test this assumption, we evaluated the efficacy of citizen science platforms and global biodiversity databases in documenting arthropod diversity in Namibia by comparing records from iNaturalist (iNat) and the Global Biodiversity Information Facility (GBIF) with regional Namibian Biodiversity Database (NBD). We assessed two metrics: (i) recognition – the proportion of observations identified to species level within each arthropod order, and (ii) completeness – the extent to which species recorded in iNat and GBIF reflect the known species richness documented in NBD. Only 54.4% of iNat and 63.1% of GBIF arthropod observations in Namibia are recorded at species level. While certain orders like Scorpiones (scorpions) and Odonata (dragonflies and damselflies) showed high recognition and completeness rates (>60%), most arthropod orders exhibited rates below 50% in both databases. The high recognition and completeness for certain orders could be attributed to species traits that make them recognizable such as distinct morphological features (e.g. large body size, colouration), a low species richness and the taxonomic familiarity of the public. Recognition and completeness rates were further compromised by nomenclatural inconsistencies, typographical errors, and misidentifications. While global biodiversity databases provide valuable broad-scale insights, regional and national biodiversity databases remain essential for comprehensive biodiversity understanding. The large citizen science biodiversity networks would benefit from collaboration between delegated regional taxonomic expertise and the public to achieve excellent taxonomic nomenclature accuracy.

Key words: Arthropod diversity; biodiversity databases; citizen science; taxonomic recognition

Session: 6960773-9**7020400**

22/10/25 | 16:10

Room: Valle

ORAL • ES

Educando para reconocer y valorar la biodiversidad local: desde la Universidad a la comunidad con ayuda de iNaturalist.

Presenter**Juan M. Cancino****Authors****Juan M. Cancino** (Departamento de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción • Chile)**Paola González-Kother** (Departamento de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción • Chile)**Jaime Villafaña** (Departamento de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción • Chile)**Natalia Rebolledo** (Departamento de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción • Chile)**Leonardo Mondaca** (Departamento de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción • Chile)**Abstract**

iNaturalist es una plataforma digital de ciencia ciudadana que permite identificar y geolocalizar la presencia de biodiversidad. En Chile, adoptada por el Ministerio de Medio Ambiente (<https://inaturalist.mma.gob.cl/>), y que es ampliamente utilizada por académicos, estudiantes y público general. Esta plataforma se ha convertido en una valiosa herramienta educativa en la Universidad Católica de la Santísima Concepción (UCSC), permitiendo que el estudiante experimente la vivencia de ser protagonista en la generación de conocimiento, disponible instantáneamente a una comunidad de millones de naturalistas alrededor del mundo. En el proceso, las/os estudiantes aprenden a reconocer las diversas especies que existen en el sitio de estudio, paso fundamental para valorar y promover la conservación de la biodiversidad. El objetivo del presente trabajo es compartir los avances obtenidos con 13 proyectos creados desde 2021 hasta el presente, reunidos en el proyecto paraguas “Naturalistas en Acción”, y su aplicación concreta al registro de la biodiversidad en el principal Campus Universitario y la progresión hacia proyectos de interés ciudadano. En estos proyectos han participado 164 estudiantes de diversas carreras de pregrado y de diplomados de la UCSC, con más 5900 observaciones, 1151 especies registradas e identificadas con colaboración en línea de más de 790 especialistas y naturalistas en general. Un 70% de los/las estudiantes que conocieron la aplicación en actividades curriculares de la UCSC se han mantenido activos en iNaturalist mostrando el interés que genera el conocimiento de la biodiversidad local. Las acciones más recientes involucran la creación de proyectos de colección para áreas delimitadas mediante un archivo .kml, como el creado para el Campus San Andrés (UCSC). Además, estudiantes y académicos han colaborado con organizaciones ciudadanas que desean promover la conservación de la naturaleza, en sitios de interés, en virtud de la biodiversidad que albergan y por el valor cultural que representan.

Session: 6960773-9

7013584

22/10/25 | 16:20

Room: Valle

ORAL • EN

Comparative Data Analysis of Data Set Collected from Four Biodiversity Survey Projects in Nigeria on the iNaturalist Platform

Presenter

Babajide Agboola

Authors

Babajide Agboola (Agbo-Veterinary and Environmental Consult Limited • Nigeria)

Taiye Adeyanju (University of Ibadan • Nigeria)

Abubakar Ringim (Federal University Dutse • Nigeria)

Olly Owen (Ekiti State Government • Nigeria)

Akinyemi Akinyugha (Ekiti State Government • Nigeria)

Venmak Agboola (Federal University of Technology, Akure • Nigeria)

Abstract

Biodiversity maintains healthy ecosystems, and policies to protect habitats and populations are based on assessments of species occurrence and distribution. Unfortunately, quantitative data on species occurrence in Nigeria remains limited. iNaturalist is dependent on citizen science to populate information on occurrence of biodiversity using spatial and temporal scales. This study presents four ongoing biodiversity survey projects across Ékiti, Lagos, Bauchi, and Plateau States in Nigeria, hosted on the iNaturalist platform. The projects were initiated to improve awareness of biodiversity and of the platform and bridge data collection and curation gaps in the area. Across the four projects, a total of 1,234 species of 6,373 total observations. Specifically, there were 1,583 observations for the Ekiti project, 1,901 for the Bauchi project, 1,318 for the Lagos project, and 1,571 for the Jos Plateau project. Forest-chestnut winged starling range extension was detected via the iNaturalist platform for Jos Plateau, Ibadan malimbe an endemic but endangered species was detected on the Ekiti project, Rufous-tailed Scrub-Robin was also identified as a range extension for the Jos Plateau. In Jos, approximately 89% of observations came from two Local Governments-LGA's (Jos East - 69.70%). The dominant taxonomic groups observed were Aves (39.21%), Insecta (37.05%), Plantae (16.42%) and Mammalia (3.44%). In Bauchi, 90% of observations were reported from two LGA's (Alkaleri 68.39%). Dominant groups were Aves (43.22%), Plantae (24.30%), Insecta (20.37%) and Mammalia (8.03%). In Ekiti, 80% of observations were reported from four LGA's out of fourteen (Ikere 34.30%). Dominant groups were Plantae (53.19%), Insecta (19.77%), Aves (13.83%), and Reptilia (5.11%). In Lagos, around 81% of observations came from six LGA's (Eti-Osa 32.47%). The predominant groups were Aves (46.73%), Insecta (18.43%), Plantae (14.72%), Reptilia (10.85%), and Mammalia (4.62%). This paper emphasizes the importance of citizen science as a valuable tool for gathering biodiversity data for monitoring and conservation.

Session: 6960773-9**7014414**

22/10/25 | 16:30

Room: Valle

ORAL • EN

Ground-Truthing Nature: Community Science for Environmental Monitoring in Data-Poor Regions

Presenter

Lauren Oakes

Authors

Lauren Oakes (Adventure Scientists • United States)

Abstract

A major challenge in scaling nature-based solutions is the lack of high-integrity field data from some of the world's most ecologically important but data-scarce regions. While satellites, AI, and remote sensing technologies offer powerful insights, they often require on-the-ground validation to build trust and improve accuracy—especially in biodiverse and remote areas. Citizen and community science offer a promising and underutilized pathway to close these validation gaps.

This session presents a global initiative that positions citizen science as a core component for improving and validating emerging technologies in environmental monitoring. The effort begins with an assessment—conducted in collaboration with companies across the biodiversity and carbon monitoring space—to identify key geographic and thematic data gaps. These insights guide the design of pilot projects that test scalable models for high-integrity, field-based data collection.

The first pilot engages trained volunteers and community members to collect field data for aboveground biomass estimates in data-poor regions, contributing to validation of existing models. The second pilot explores how emerging technologies—such as acoustic sensors and environmental DNA—can be paired with community-based fieldwork to improve biodiversity monitoring. These hybrid approaches open new possibilities for generating open, high-quality datasets in collaboration with tech providers and local stakeholders.

Field protocols are designed to support open standards and are published in alignment with FAIR and CARE principles. We emphasize inclusive participation, data transparency, and adaptable methods that can be scaled across diverse geographies.

Together, these pilots demonstrate how citizen and community science can enhance data equity, reduce risk in biodiversity and carbon markets, and support trusted, scalable monitoring systems. We invite collaboration on new projects and on building a global consortium dedicated to advancing open, credible, and participatory data systems for nature.

Session: 6960773-9**7021368**

22/10/25 | 16:40

Room: Valle

ORAL • EN

Constructing effective science communication: narrative templates

Presenter

Dean Pentcheff

Authors

Dean Pentcheff (Natural History Museum of Los Angeles County • United States)

Abstract

The practice and products of science are humanity's crowning achievement — science lets us understand the world and apply that understanding to benefit humanity. If we succeed in sharing biodiversity science with everyone else, we will substantially improve human life. But scientists have historically failed to effectively share the value and joy of science — a failing that is glaringly apparent in the current public rejection of science. For our communication to succeed, we must be willing to look beyond academia to find the best tools. It turns out that effective communicators in all fields converge on core narrative templates. Ignoring narrative expertise has put us where we are today. Using effective narrative tools, we can transform the communication of science into a force more powerful than the negative messaging opposing us.

Session: 6960773-9**7021001**

22/10/25 | 16:30

Room: Valle

ORAL • ES

PROGRAMA DE MONITOREO, SEGUIMIENTO Y EVALUACIÓN DE LA BIODIVERSIDAD URBANA MEDIANTE ESTRATEGIAS DE INVESTIGACIÓN Y CIENCIA CIUDADANA EN BOGOTÁ, COLOMBIA

Presenter

Juliana Rodríguez Ortiz

Authors

Iván Darío Melo Cuéllar (Secretaría Distrital de Ambiente • Colombia)

Juliana Rodríguez Ortiz (Secretaría Distrital de Ambiente • Colombia)

Sara Lucía Colmenares-Trejos (Secretaría Distrital de Ambiente • Colombia)

Abstract

A partir de la identificación, reconocimiento y análisis de la biodiversidad urbana se encontró que en Bogotá D. C. habita un gran número grupos biológicos y diversidad de especies que interactúan entre sí en un esquema de complejas interacciones con los socio-ecosistemas, las organizaciones ambientalistas, las organizaciones estatales y demás interesados con incidencia en la administración, gobernanza y sostenibilidad de las áreas protegidas declaradas por los instrumentos normativos habilitantes que garantizan la conservación de los hábitats para la supervivencia de formas de vida que cohabitan y comparten los ambiente urbanos.

Con el fin de evaluar la biodiversidad y contar con un instrumento de soporte técnico para la toma de decisiones, aplicada a los instrumentos de conservación y manejo de las áreas protegidas urbanas, entre el año 2020 y hasta la fecha el grupo de monitoreo de la biodiversidad de la Secretaría Distrital de Ambiente (SDA) fórmula e inicia la implementación del programa de monitoreo, seguimiento y evaluación de la biodiversidad de las áreas protegidas y otras de interés ambiental en el Distrito Capital.

Como parte del programa se han elaborado protocolos estandarizados para el monitoreo de los diferentes grupos biológicos como flora, avifauna, herpetofauna, mastofauna y artropofauna, los cuales con su aplicación han permitido la toma sistemática de datos, soportando las acciones de manejo y conservación, así como la actualización de los Planes de Manejo Ambiental (PMA) de las áreas protegidas, basados en datos cuidadosamente curados; adicionalmente, se han implementado diferentes estrategias de investigación y ciencia ciudadana que han contribuido a la estructuración de datos relevantes.

Actualmente, con la implementación del programa de monitoreo se cuenta con el levantamiento de la línea base de la biodiversidad en veinte (20) áreas protegidas locales, administradas por la SDA; también, se cuenta con caracterizaciones en otras áreas de interés ambiental para la ciudad.

Session

6803097

Symposium

22/10/25 | 16:00

Room: Cauca

Unlocking and sharing fragmented biodiversity data to advance nature conservation and management

Organizers

Ximena Velez-Zuazo

Marconi Campos-Cerqueira

Reynaldo Linares

Description

Megadiverse countries harbor an extraordinary share of the world's biodiversity, serving as living vaults of evolutionary history. However, conservationists, policymakers, and development decision-makers often struggle to access integrated, high-quality biodiversity data. As climate change, habitat loss, and resource extraction intensify, data-driven strategies become essential for balancing economic development with nature conservation.

This session explores how governments, scientists, the private sector, and Indigenous communities can combine their collective knowledge and collaborate to unlock biodiversity data for informed decision-making. What are the pathways for unifying disparate data sources into a sustainable national biodiversity monitoring system? How can national biodiversity monitoring systems, corporate sustainability metrics, and scientific databases cooperate to drive conservation impact? What are the barriers to integrating biodiversity data into financial investments, infrastructure planning, and policy frameworks, and how can emerging technologies, including AI, help to overcome them?

We invite researchers, conservation practitioners, Indigenous people, and industry leaders to share their insights and visions on baselines, long-term monitoring, innovative AI-powered data-sharing platforms, and case studies where biodiversity insights have influenced real-world decisions. The session will highlight ongoing efforts, identify gaps and challenges, and propose alternative approaches to unlocking and applying biodiversity data.

Session: 6803097**7020768**

22/10/25 | 16:10

Room: Cauca

LIGHTNING TALK VIRTUAL • ES

Ascenso y caída del Centro de Datos para la Conservación de Perú

Presenter

Antonio Tovar

Authors

Antonio Tovar (Universidad Nacional Agraria La Molina • Perú)

Abstract

En los años 80 se crearon varios Centros de Datos para la Conservación en Latinoamérica (Perú, Panamá, Bolivia, etc.), siguiendo el modelo de los Programas de Patrimonio Natural de Estados Unidos, como oficinas especializadas en acopio, sistematización y análisis de datos sobre especies y ecosistemas amenazados.

En mayo 1983 se creó el Centro de Datos para la Conservación en la Universidad Nacional Agraria La Molina (CDC-Perú), el mismo que generó bases de datos sobre registro de especies, reportes de estado de conservación, áreas protegidas, otros.

Inicialmente, The Nature Conservancy apoyó técnica y financieramente las operaciones de este y otros Centros de Datos, pero luego cada organización tuvo que buscar los recursos necesarios ejecutando proyectos específicos por encargo de terceros: evaluaciones biológicas, planes ecorregionales de conservación, bases de datos de manejo de especies, otros.

En ese sentido, el CDC-Perú buscaba proporcionar información de calidad, en forma permanente, sobre la diversidad biológica del Perú y servir de nexo entre sectores que producen información (investigadores, científicos) y los que deben utilizarla (administradores, planificadores, autoridades, otros), especialmente para tomar decisiones que afectan el estado de los recursos naturales del país.

A lo largo de 35 años produjo decenas de informes técnicos, mapas de ecosistemas y cerca de 40,000 récords de ocurrencia de especies amenazadas (parte de los datos fueron subidos a la plataforma GBIF pero una porción significativa aún necesita ser publicada).

Lamentablemente, tuvo que cerrar sus operaciones, al no poder cubrir sus presupuestos, en especial debido a la crisis económica, la competencia con otras organizaciones y las prioridades de las potenciales fuentes de financiamiento, más sensibles a los temas sociales que a los ambientales.

Actualmente se está buscando actualizar y publicar en línea las bases de datos para disponibilidad de todos.

Session: 6803097**7020932**

22/10/25 | 16:15

Room: Cauca

LIGHTNING TALK • EN

Bridging Conservation and Development: PERU LNG's Role in a National Biodiversity Monitoring Framework

Presenter

Bruno Vildoso

Authors

Bruno Vildoso (PERU LNG|HUNT LNG • Perú)

Abstract

PERU LNG's long-term partnership with Smithsonian Conservation Biology Institute (SCBI) in the Biodiversity Monitoring and Assessment Program (BMAP) exemplifies how the private sector can catalyze robust, long-term, and science-based biodiversity data systems in megadiverse regions. Since 2011, the BMAP has evolved into an integrated marine and terrestrial monitoring initiative, employing traditional and innovative tools—including eDNA, acoustic telemetry, and ecosystem modeling—to inform environmental management and policy from the Andes to the Pacific Ocean. Along 15 Ecological Landscape Units, PERU LNG has supported sustained data collection across ecological dimensions (taxonomic, functional, and phylogenetic), enabling compliance and proactive conservation.

This session highlights our collaborative model, where industry, academic institutions, and local communities converge to co-generate high-quality biodiversity data. We will share lessons on integrating such data into impact assessments, infrastructure planning, and national conservation strategies. Our approach to data harmonization and sharing, including open-access platforms, has improved the detection of trends and the identification of best practices while reinforcing trust among stakeholders.

By aligning corporate environmental responsibility with national and global biodiversity frameworks, PERU LNG and the BMAP contribute to developing scalable, transparent, and policy-relevant monitoring systems. Yet, challenges remain, including regulatory fragmentation, limited interoperability of datasets, and gaps in support for long-term data curation. We call for greater cross-sectoral alignment to unlock biodiversity data's full potential in development decision-making. Through this session, we aim to foster dialogue on sustaining these partnerships and advancing innovations that turn biodiversity information into actionable insights.

Session: 6803097**7021010**

22/10/25 | 16:20

Room: Cauca

LIGHTNING TALK VIRTUAL • EN

Building a biodiversity data aggregator to improve accessibility for decision-making

Presenter

Trisha Moriarty

Authors

Trisha Moriarty (Dept. Biodiversity, Conservation and Attraction • Australia)

Cassia Piper (Australia)

Abstract

The Biodiversity Information Office (BIO) developed the Dandjoo Biodiversity Data Repository to mobilize Western Australia's biodiversity data from various sources, including industry, government, and research sectors. The goal is to make the data more discoverable and accessible from a single platform, which can then be integrated into federal and state/territory repositories across Australia.

Early analyses identified private sector data from planning approval processes as valuable for Dandjoo. Biodiversity survey data for environmental assessments is submitted digitally to the Department of Water and Environmental Regulation (DWER) through the Index of Biodiversity Survey Assessments (IBSA) portal. Depending on licensing, this data is available via the BioCollect tool from the Commonwealth Atlas of Living Australia. Ingesting this data into Dandjoo applies quality assurance measures, enhancing data quality and interoperability by mapping it to the Darwin Core standard. Dandjoo's model allows multiple surveys to be grouped under proposals or projects, linking to additional contextual information like reports or GIS data files.

Challenges arose with the metadata around surveys due to varying interpretations of data and templates. Collaboration with DWER improved this process, resulting in agreed mappings. Ensuring correct data ownership attribution was another hurdle. Licensing arrangements upon submission to DWER and the IBSA portal limited the data available to BIO and how it could be attributed. Ensuring that corporations and organizations retained their rights to the data while informing other users of these rights was crucial.

The aggregation and provisioning of biodiversity survey data from regulatory processes by a single platform is expected to benefit all users of biodiversity data. This initial step in building Western Australia's Biodiversity Data Repository simplifies complex environmental data supply chains for government decision-making and makes the data more accessible to the community.

Session: 6803097**7023560**

22/10/25 | 16:25

Room: Cauca

ORAL • EN

Quantifying the Impact of Forestry Practices on Biodiversity Using Causal Inference Methods

Presenter

Vun Wen Jie

Authors

Vun Wen Jie (Uppsala University, Department of Information Technology, Division of Systems and Control, Department of Organismal Biology, Sys • Sweden)

Jakob Nyström (Uppsala University, Department of Organismal Biology, Systematic Biology • Sweden)

Torbjörn Wigren (Uppsala University, Department of Information Technology, Systems Engineering • Sweden)

Thomas Schön (Uppsala University, Department of Information Technology, Systems Engineering • Sweden)

Tobias Andermann (Uppsala University, Department of Organismal Biology, Systematic Biology • Sweden)

Dave Zachariah (Uppsala University, Department of Information Technology, Division of Systems and Control • Sweden)

Abstract

There is cumulative evidence that human impact and land-modifications negatively affect global biodiversity. However, understanding in more detail to what extent specific human interventions—particularly forestry practices—affect biodiversity on a local basis is a complex and currently underexplored challenge. Investigating the causal links between these practices and biodiversity changes is essential for evidence-based conservation and restoration strategies. This study applies causal modeling to quantify the impact of different forestry management strategies on biodiversity across thousands of observational plots sampled over several decades across the entirety of Sweden. These long-term and large-scale observational studies, conducted as part of the Swedish National Forest Inventory (Riksskogstaxeringen), provide a rich dataset that contains information on several types of human impacts in the forest, lists of detected species, as well as other biotic and abiotic features. In our modeling approach, we specifically distinguish association from causation, providing robust insights into how different forestry interventions affect biodiversity. The findings address critical gaps in forest ecology by providing a novel analytic approach that moves beyond descriptive assessments toward causal understanding. The results will also aim to better inform policymakers and forest managers seeking to implement sustainable forest management practices that balance economic demands with conservation goals.



Day 3 - Thursday, October 23
Día 3 - Jueves 23 de octubre

Symposia & Panel Sessions

*Sesiones de
Simposios y Paneles*

Session

6798502-2

Symposium

23/10/25 | 10:45

Room: Ballroom A

Scaling AI For and Across Biodiversity: Data Collection and Curation in AI-Driven Biodiversity Research (Part 2)

Organizers

Sanson Poon

Arianna Salili-James

Ben Scott

Rukaya Johaadien

Michal Torma

Nicky Nicolson

Kit Lewers

Wouter Koch

David R. Williamson

Description

Artificial Intelligence (AI) is revolutionising the way biodiversity data are managed, studied, and preserved, offering groundbreaking possibilities for research, curation, conservation, policy-making and public engagement. Digital representations of organisms are central in biodiversity data collection, curation and use. It is these representations, rather than the physical organisms themselves, that are increasingly the basis for research. Digital representations allow the use of machine learning, AI, and computer vision to measure the physical properties of organisms and to classify them taxonomically and phenologically, on an unprecedented scale.

While AI-driven innovations are emerging across institutions and disciplines, a critical question remains: how can these advancements be successfully embedded and scaled to maximise impact? This session explores cutting-edge AI applications, from large-scale digitisation and automated species identification to advanced data management and predictive analytics. We will examine strategies for integrating AI across institutional frameworks, addressing challenges in adoption, collaboration, and sustainability. We welcome talks investigating the complexities of maintaining these services in the long term, addressing the financial burdens of API access and the rapid evolution of AI models and services that can quickly render solutions obsolete. By tracing the AI journey within our organisations, we aim to define best practices that unlock its full potential, as well as to understand what others are working on, and what we can learn from other domains. Finally, we are also interested in topics including:

- Novel data collection and analysis techniques or novel uses of established ones
- Data collection, digitization, standardization and curation for future applications
- Practical implications of AI use on data quality, interpretability, and legal aspects

Session: 6798502-2**7019829**

23/10/25 | 10:45

Room: Ballroom A

ORAL • EN

Mining Botanical Literature with Machine Learning

Presenter

Ben Scott

Authors**Ben Scott** (Natural History Museum • United Kingdom)**Ana Claudia Araujo** (United Kingdom)**Arianna Salili-James** (United Kingdom)**Qianqian Gu** (London • United Kingdom)**Michela Leonardi** (Natural History Museum • United Kingdom)**Neil Brummitt** (Natural History Museum • United Kingdom)**Abstract**

The functional traits of species underpin their ecological roles, yet for the vast majority of plant species, these traits remain understudied in the field. However, every named species must have a published taxonomic description—an underused but information-rich source of morphological and ecological insight.

We present a machine learning workflow designed to extract structured trait data from botanical literature. The project focuses on the Biodiversity Heritage Library (BHL), leveraging a transformer-based text classifier to identify taxonomic descriptions within its 63 million scanned pages. This addresses a key limitation in previous approaches: the lack of machine-readable, relevant text at scale.

In Phase 1, we apply a rule-based Named Entity Recognition (NER) pipeline, guided by an expert-curated vocabulary of botanical traits. This system is tailored to the semi-structured syntax of taxonomic descriptions and focuses on extracting functionally informative morphological traits. The pipeline has been applied across the entire BHL corpus for all known angiosperm species, resulting in a large dataset of structured plant trait data.

In Phase 2, we shift from rule-based extraction to using Large Language Models (LLMs) to automatically extract traits mapped to the Flora Phenotype Ontology (FLOPO), enabling semantic integration with other biodiversity knowledge sources.

In this presentation, we report results from both phases, including pipeline performance, data quality, and computational cost. We also outline the implications of this approach for large-scale trait data mobilisation and its potential to support ecological and conservation research.

Session: 6798502-2**7020014**

23/10/25 | 10:55

Room: Ballroom A

ORAL • EN

LLM-based transcription of botanical catalogues for digital access to special collections

Presenter

Ishaipiriyar Karunakularatnam

Authors

Ishaipiriyar Karunakularatnam (Royal Botanic Gardens, Kew • United Kingdom)

Nicky Nicolson (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

The Royal Botanic Gardens, Kew is home to a world-renowned herbarium collection. Much like other natural history institutions, it encompasses several specialist sub-collections alongside the main herbarium which are organised and curated differently. Rapid digitisation processes can be designed for application to the main herbarium but expensive custom processing for special collections is required. Without digitisation, the significant historical and scientific data held in these special collections remain inaccessible, accessed only via physical catalogues.

Manual transcription of printed catalogue information to create digitisation “stub” records is labor intensive, time-consuming and can be prone to errors. To automate this process we have implemented a process using Tesseract OCR [1] for page cropping and text extraction of images of catalogue pages, generating text outputs which are then cleaned and organised into a structured format with help of Large Language Models (LLMs) such as QWEN2.5 [2] and Mistral [3] models. The user is able to adapt the organisation process for each unique catalogue through prompt engineering.

This project will allow for rapid digitisation of physical and PDF catalogues without the need for manual transcription; thus, reducing the time and labor needed significantly.

The resulting outputs will be integrated into biodiversity databases and linked to herbarium specimen records, making them more accessible to researchers. In this presentation, we will walk through the development of the tool, demonstrate its performance on different catalogues and explore its use in digitisation of botanical data.

References:

- R. Smith, “An Overview of the Tesseract OCR Engine,” in Proceedings of the Ninth International Conference on Document Analysis and Recognition (ICDAR 2007), vol. 2, pp. 629–633, 2007, doi: 10.1109/ICDAR.2007.4376991.
- A. Yang et al., “Qwen2.5 Technical Report,” arXiv preprint arXiv:2512.15115, 2024. [Online]. Available: <https://arxiv.org/abs/2412.15115>
- A. Q. Jiang et al., “Mistral 7B,” arXiv preprint arXiv:2310.06825, 2023. [Online]. Available: <https://arxiv.org/abs/2310.06825>

Session: 6798502-2**7020094**

23/10/25 | 11:05

Room: Ballroom A

ORAL VIRTUAL • EN

Multimodal AI Algorithm for Year-Over-Year Forest Change Detection at SJER Using NEON LiDAR, Hyperspectral, RGB, and GBIF Mediated Data

Presenter

Kristen “Kit” Lewers

Authors

Kristen “Kit” Lewers (NASA Goddard Space Flight Center and University of Colorado Boulder • United States)

Abstract

Forest ecosystems are dynamic, yet capturing their fine-grained, individual-scale year-over-year changes remains a challenge especially across spatial scales and data modalities. This talk presents a pipeline under development that integrates airborne LiDAR, hyperspectral imagery, high-resolution RGB data, and NEON field-collected ground truth to track ecological change over time. Focused on the San Joaquin Experimental Range (SJER) in California, the pipeline combines individual tree crown delineation, spectral species classification, RGB (red, green, blue) classification, and structural metrics to map shifts in canopy cover, species turnover, and vegetation health annually with geo-location being a huge hurdle.

The algorithm aims to link repeated NEON Airborne Observation Platform (AOP) flights with woody vegetation data and applies time-aware spatial matching to monitor changes in both structure and identity at the tree level. Deep learning models such as DeepForest are used for tree crown detection, while spectral features derived from AVIRIS-NG hyperspectral data inform species classification and vegetation condition [1, 2]. LiDAR point clouds are used to quantify vertical growth and mortality.

This approach contributes to the broader goal of dematerializing physical observations into scalable, machine-readable biodiversity records. The resulting outputs are designed to be compatible with biodiversity data infrastructures like GBIF and the up and coming Darwin Core DP, supporting long-term ecological forecasting and informing conservation decisions.

References

- Weinstein, Ben G., et al. “Individual tree-crown detection in RGB imagery using semi-supervised deep learning neural networks.” *Remote Sensing* 11.11 (2019): 1309.
- Weinstein BG, Marconi S, Aubry-Kientz M, Vincent G, Senyondo H, White EP. DeepForest: A Python package for RGB deep learning tree crown delineation. *Methods Ecol Evol.* 2020; 11: 1743–1751.

Session: 6798502-2**7020272**

23/10/25 | 11:15

Room: Ballroom A

ORAL • EN

AI-Assisted Quality Checks for Herbarium Sheet Digitisation

Presenter

Arianna Salili-James

Authors

Naifeng Zhang (Natural History Museum • United Kingdom)**Arianna Salili-James** (Natural History Museum • United Kingdom)**Sanson Poon** (Natural History Museum • United Kingdom)**Ben Scott** (Natural History Museum • United Kingdom)**Robyn Drinkwater** (Royal Botanic Garden Edinburgh • United Kingdom)**Milo Phillips** (Royal Botanic Garden Edinburgh • United Kingdom)**Elsbeth Haston** (Royal Botanic Garden Edinburgh • United Kingdom)

Abstract

It is estimated that there are almost 400 million herbarium specimens, across approximately 3500 herbaria around the world. In the last decade, many institutions have embarked on mass digitisation schemes in order to efficiently digitise their herbarium sheet collections. While processes can often be fast, with some workflows processing 600-1,000 herbarium sheets daily, post-digitisation checks are often performed by hand. Challenges during imaging, such as misalignment, blurring, or incorrect metadata capture, can compromise data quality and lead to costly reprocessing. To tackle this, the Natural History Museum UK (NHMUK) teamed up with Royal Botanic Gardens Edinburgh (RBGE) to develop an Artificial Intelligence (AI)-based herbarium sheet digitisation Quality Assurance (QA) workflow. This was supported by the UK government's Department for Culture, Media and Sport (DCMS) through the DCMS - NHM AI Pilot Programme.

The QA framework was trained on collections at RBGE, and enabled quality checks of digitised herbarium sheets. These checks included detecting missing objects (such as colour reference cards or barcodes), identifying cropping errors, and highlighting focus issues. The pipeline comprised various techniques, including object detection, decision trees, classical statistics, and deep learning tools. Finally, whilst the tool can be used to test samples post-digitisation, a simple interface was also developed to enable in-situ checks during the imaging stages.

The proposed workflow underwent evaluation with RBGE herbarium digitisers, which will refine the model and pipeline. Now, our next step is to expand on this pilot project and one day provide an AI-based quality check service that can be integrated into workflows not just at RBGE but institutions across the globe.

Session: 6798502-2**7019820**

23/10/25 | 11:25

Room: Ballroom A

ORAL VIRTUAL • EN

AI-Driven Solutions for Optimising Drawer Expansion and Storage Management of Entomology Collections

Presenter

QIANQIAN GU

Authors

QIANQIAN GU (Natural History Museum, London • United Kingdom)**Ben Scott** (Natural History Museum, London • United Kingdom)**Geoff Martin** (Natural History Museum, London • United Kingdom)**Arianna Salili-James** (Natural History Museum, London • United Kingdom)**Laurence Livermore** (Natural History Museum, London • United Kingdom)**Peter Wing** (Natural History Museum, London • United Kingdom)**Vincent S. Smith** (Natural History Museum, London • United Kingdom)

Abstract

The digitisation of natural history collections at scale raises logistical and curatorial challenges. One concern is the physical expansion of storage infrastructure. As part of the DiSSCo UK programme (Smith et al, 2022), the Natural History Museum, London (NHM) will rehouse a significant proportion of its 36 million pinned entomological specimens, around 130,000 collection drawers. Digitisation involves imaging every specimen and attaching a unique physical identifier readable by both humans and machines, typically a small card with a Data Matrix barcode. As these must be readable from above, their addition increases the physical footprint within drawers during digitisation. Manual estimation of this expansion is impractical at scale.

To address this, NHM has developed an AI-driven approach to estimate specimen drawer expansion and support resource planning. The deep learning pipeline auto-detects key drawer objects, including specimens, labels, barcodes, notes, unit trays, and drawers, from high-resolution images. Our dataset includes 11,090 digitised pinned Coleoptera (beetle) drawers, part of the Index Lot collection (Natural History Museum, 2014), broadly representative of typical entomological collections. The AI-pipeline supports pre- and post-digitisation analysis by calculating bounding areas, handling overlaps, and estimating the net footprint change.

Our object detection models performed well under real-world conditions, with a mean average precision (mAP) of 85.45% across all objects. Barcode detection reached 86.63% mAP, and unit tray detection/classification achieved 99.5% accuracy.

In addition to estimating expansion and supporting budget planning, the modular components can be used independently at various stages of digitisation and curation—for example, to flag missing labels or barcodes, assist with tracking specimen relocation, and support re-curation decisions. All code will be openly available, promoting reuse and scalability across the community.

Our findings demonstrate that automated spatial analysis improves accuracy and efficiency in collection management, supporting predictive modelling for large-scale digitisation.

Session: 6798502-2**7020716**

23/10/25 | 11:35

Room: Ballroom A

ORAL VIRTUAL • EN

Multimodal Question Answering for Botanical Archives: Adapting PaLI-GEMMA 2 to Enhance Exploration of Herbarium Collections

Presenter

Ahmed Zine Eddine Marhoum

Authors

Ahmed Zine Eddine Marhoum (Ecole Supérieure en Sciences et Technologies de l'Informatique et du Numérique • Algeria)**Anis Oukid** (Ecole Supérieure en Sciences et Technologies de l'Informatique et du Numérique • Algeria)**Youcef Sklab** (Institut de Recherche pour le Développement (IRD) • France)**Hanane Ariouat** (Institut de Recherche pour le Développement (IRD) • France)**Eric Chenin** (Institut de Recherche pour le Développement (IRD) • France)**Nicolas Turenne** (Institut de Recherche pour le Développement (IRD) • France)**Jean-Daniel Zucker** (Institut de Recherche pour le Développement (IRD) • France)**Edi Prifti** (Institut de Recherche pour le Développement (IRD) • France)

Abstract

Herbarium collections represent an invaluable resource for research in systematics, functional ecology, and biogeography. However, the exploration of these massive collections remains a major challenge owing to the frequent absence of structured metadata.

In this context, deep learning offers unprecedented opportunities for automatic annotation of these collections, thereby facilitating navigation within digital archives. Nonetheless, a persistent challenge lies in the scarcity of expert-annotated datasets and the inherent richness and variability of potentially observable functional traits.

In parallel, floristic texts—such as species descriptions—constitute a rich and underexploited source of botanical information.

Leveraging this information requires methods capable of linking textual content with visual features. Recent advances in multimodal learning, particularly with vision-language models such as PaLI-GEMMA 2, open new avenues for the joint exploitation of visual and textual modalities. These models demonstrate remarkable capabilities for performing complex semantic interpretation and multimodal reasoning tasks.

In this context, we present an adaptation of Google's PaLI-GEMMA 2 multimodal model for Visual Question Answering (VQA) tasks applied to botanical data.

We curated a specialized dataset comprising high-resolution botanical images paired with detailed textual annotations and domain-specific questions. The model was fine-tuned to align its reasoning capabilities with the specific requirements of herbarium data. Evaluation, conducted using BLEU, ROUGE, and METEOR metrics for generation quality, as well as SBERT and BERTScore for semantic relevance, demonstrates that our model significantly outperforms unimodal approaches and general-purpose VQA models.

Beyond simple question answering, our system enables interactive exploration of botanical archives, with potential applications in intelligent search engines, identification support systems, and educational platforms.

This work highlights the value of domain-adapted multimodal models for the large-scale valorization of herbarium collections, thereby enhancing access to botanical knowledge for research, conservation, and scientific outreach.

Session: 6798502-2**7020729**

23/10/25 | 11:45

Room: Ballroom A

ORAL • EN

Learning from Digital Collections: Digitisation and Machine Learning for Large Scale Museum Studies

Presenter

David Williamson

Authors

David Williamson (Norwegian University of Science and Technology • Norway)

Abstract

Museums around the world collectively hold and preserve billions of natural history specimens: identified by experts, carefully curated, verified, and organised. These specimens represent a source of unique and irreplaceable historical data that can help to answer some of our most pressing questions relating to climate change, changes in phenology, habitat and species range, and biodiversity loss. Large-scale studies incorporating museum collections are vital to our understanding of these topics, but unlocking the information in such collections typically requires physical access to the specimens and careful examination by experts. For the kind of studies needed to truly understand global changes, involving millions of specimens across many nations, this is impractically expensive and time consuming.

For this reason, digitisation is becoming increasingly important to museums, providing digital representations of specimens that can be accessed by researchers anywhere on the planet through searchable online databases such as GBIF. Collections of digital specimens open the door to modern computational analysis such as computer vision and machine learning, allowing studies to be conducted at a geographic and temporal scales that would previously have been impossible.

We present a case study demonstrating the value of such an approach, in which we investigated global flowering phenology using millions of digital specimens from hundreds of museums and herbaria, applying machine learning to rapidly extract phenological information from images and reveal long-term, worldwide trends. Using this study and other, ongoing work we consider the advantages and limitations of digitisation and working with digital specimens, and the necessity of close collaboration with domain experts when applying computational methods. We aim to stimulate conversation on best practices around digitisation, data collection and dissemination, as well as the use, integration and sharing of software tools for large-scale analysis of museum specimens.

Session: 6798502-2**7020746**

23/10/25 | 11:55

Room: Ballroom A

ORAL • EN

A Centralized Service for Automated Biodiversity Data Integration: The MfN DataHub

Presenter

MAJID VAFADAR

Authors

MAJID VAFADAR (Museum for Natural History Berlin • Germany)

Abstract

MfN DataHub (Museum fuer Naturkunde Data Hub) is a central service designed to execute multiple automated data integration and migration workflows in continuous and parallel scenarios. Developed for the Natural History Museum in Berlin, the service supports the institution's scientific data management systems.

Functioning as an open-source web service and workflow engine, the DataHub manages complex digitization pipelines by iterating through datasets and files for migration to designated target systems. Operations are controlled and monitored via a dashboard and can be executed automatically, with an AI-agent operational support.

The DataHub accesses storage and databases within digitization pipelines to validate, enrich, transform and integrate data. This centralized approach ensures data integration quality, with a dedicated validator, assessing each object's quality against predefined requirements.

Consequently, datasets are transformed into the compliant structure and format of the target systems. A persistent data integration pipeline facilitates the import of datasets into the museum's collection management system and portal.

Furthermore, packages are prepared for external partners – including the Global Biodiversity Information Facility (GBIF) – adhering to international standards like Darwin Core, as well as specific requirements from the collection, digitization, and target systems. All operational steps encompassing data and service interactions are logged for comprehensive reporting and real-time monitoring.

An API endpoint enables the DataHub to interface with a workflow scheduler and an AI-agent, which automates workflows and maximizes efficiency by optimizing the balance between data volume, prioritization, and target system performance. The DataHub thus offers a flexible, general-purpose engine that can be tailored to the specific needs of any collection and digitization operation at the museum, ensuring a more robust and efficient data integration landscape.

Session: 6798502-2**7020803**

23/10/25 | 12:05

Room: Ballroom A

ORAL • EN

Integrating Digitization and AI for a Multi-Specimen Imaging Workflow and Downstream Research

Presenter

Chandra Earl

Authors

Chandra Earl (NEON (National Ecological Observatory Network) • United States)**Isabelle Betancourt** (NEON (National Ecological Observatory Network) • United States)**Alyson East** (University of Maine • United States)**Elizabeth Campolongo** (Imageomics Institute • United States)**Michael Belitz** (Michigan State University • United States)**Sydne Record** (University of Maine • United States)

Abstract

Digitized specimen images are opening new frontiers in biodiversity science, enabling large-scale morphological analyses that were previously impractical. While many digitization efforts have focused on accessibility and phenotypic documentation, fewer workflows are optimized for downstream computational analysis. As artificial intelligence becomes increasingly important in biology, bridging the gap between traditional imaging practices and machine learning-ready data is essential.

To address this gap within our own data infrastructure, the National Ecological Observatory Network (NEON) collaborated with the Imageomics Institute and affiliated researchers to develop a scalable imaging and segmentation pipeline centered on pinned beetle specimens from the NEON Biorepository. Using standardized photography of full unit trays—with embedded color and scale references and protocols tailored for machine learning applications—we generated over 3,000 high-resolution images, covering approximately 70% of the NEON carabid collection. An image segmentation pipeline was used to extract individual beetles from the tray images, dramatically reducing imaging time compared to individual specimen photography. Segmented images were linked to specimen records, including taxonomy, collection site, and date, placing them in a rich ecological context and enabling their future use in biologically-driven computer vision research. The pipeline has been integrated into NEON's data systems to support ongoing and future multi-specimen imaging workflows.

This pipeline supported the creation of a dataset for a NeurIPS 2025 AI competition, Beetles as Sentinel Taxa: Predicting Drought Conditions from NEON Specimen Imagery, which investigates whether morphological variation in beetle traits can be used to detect ecological responses to drought. The challenge launched on July 1 and runs through October 31, with final results and comparative analyses to be presented at the NeurIPS 2025 conference in December. By integrating digitization, automated processing, and ecological metadata, this workflow demonstrates how biodiversity collections can directly support high-impact machine learning research while preserving scientific context and traceability.

Session: 6798502-2

7021037

23/10/25 | 12:15

Room: Ballroom A

ORAL • EN

Antenna: A Platform for Automated Insect Monitoring

Presenter

David Rolnick

Authors

Michael Bunsen (United States)

Anna Viklund (Sweden)

Yuyan Chen (Canada)

Aditya Jain (Canada)

Andre Poremski (United States)

Kent McFarland (United States)

Maxim Larrivée (Canada)

David Rolnick (McGill University • Canada)

Abstract

With the growth of camera traps for nocturnal insects, AI has been proposed as an effective way to parse large volumes of data. However, there remain challenges for non-AI experts in deploying computer vision algorithms and processing data at scale. Antenna is an open- source platform for insect monitoring that aims to bridge these gaps, allowing users to deploy AI models for insect detection and species identification and to manage their data to derive ecological insights. Antenna’s user-centric approach minimizes technological barriers through an intuitive interface crafted for a wide-range of expertise and can efficiently handle large volumes of data from diverse sources and hardware to allow for insect monitoring across large spatial and temporal scales.

Session

6798479-2

Symposium

23/10/25 | 10:45

Room: Ballroom B1

Community Engagement and Capacity Building for Increased Biodiversity Data Accessibility (Part 2)

Organizers

Maheva Bagard Laursen

Katherine Tattersall

Elizabeth Lawrence

Mélianie Raymond

Description

The critical importance of capacity building and globally accessible biodiversity knowledge in addressing the global biodiversity crisis is highlighted in the Kunming-Montreal Global Biodiversity Framework (GBF), particularly Targets 20 and 21. How are we taking action to address these priorities? What are the benefits of capacity development and organized biodiversity data on different scales from local communities to global networks?

For this session, we invite speakers to present approaches to community engagement, skills development, and knowledge-sharing for increased biodiversity data and information aggregation, sharing and use. We aim to inspire new ideas and partnerships that further support the knowledge needs of the global community.

Through compelling examples and success stories, we aim to showcase how empowering communities can result in enhanced data accessibility. We can also explore how we can nurture and strengthen collaborations to align efforts and share expertise for maximum impact.

Session: 6798479-2**7020558**

23/10/25 | 10:45

Room: Ballroom B1

ORAL • EN

Enhancing Institutional Capacity for Biodiversity Data Mobilization in the Hindu Kush Himalayan Region

Presenter

Lily Shrestha

Authors

Lily Shrestha (Global Biodiversity Information Facility Asia Support Team • Nepal)

Bandana Shakya (International Centre for Integrated Mountain Development • Nepal)

Ramesh Kathariya (International Centre for Integrated Mountain Development • Nepal)

Abstract

The biodiversity in Hindu Kush Himalaya (HKH) region face significant threats from land-use change, habitat degradation, climate change, pollution, and invasive species. However, efforts to address these challenges are hindered by gaps in awareness, capacity, and access to biodiversity data despite advancements in biodiversity research across HKH countries.

International Centre for Integrated Mountain Development (ICIMOD), a regional intergovernmental organization is making an effort to build awareness and capacity of the biodiversity-mandated institutions in this region with regards to open-access biodiversity data. ICIMOD became an associate participant to the Global Biodiversity Information Facility (GBIF) in 2009 and has been encouraging the institutions to share their biodiversity data.

In 2025, ICIMOD led a Capacity Enhancement Support Programme (CESP) project funded by GBIF with an objective of enhancing capacity of institutions within HKH towards biodiversity data mobilization, in collaboration with National Biodiversity Centre-Bhutan, Chinese Academy of Sciences, Zoological Survey of India and Forest Action Nepal. As a part of this project, ICIMOD hosted a regional training in Kathmandu, bringing together participants from the HKH countries. The training was based on the GBIF Biodiversity Data Mobilization Course, guiding participants on the process of data standardization, cleaning, validation and publishing through GBIF. During the training, participants also published their own datasets. Further, to extend the outreach of the project to a wider network of data holding institutions within the region, participants organized post training in-country webinars sharing knowledge and skills acquired during the workshop to key biodiversity institutions from their countries.

This presentation will cover the outcomes of the regional training and post-training webinars towards building awareness and capacity in open-access biodiversity data in the HKH region. It will encourage others to build on and reuse the training approach and materials presented here to further strengthen biodiversity data sharing in Asia and globally.

Session: 6798479-2**7020695**

23/10/25 | 11:00

Room: Ballroom B1

LIGHTNING TALK • EN

What data products from the OBIS platform effectively engage local governments?

Presenter

Takashi Hosono

Authors

Takashi Hosono (Japan Agency for Marine-Earth Science and Technology • Japan)

Abstract

In coastal regions of Japan, some local governments have been conducting long-term biological monitoring. With the growing acceptance of open data and open science principles, there is an increasing awareness among local governments about the importance of standardizing and publishing their monitoring data. However, few local governments have reached the level where they integrate their rich datasets with other sources for comprehensive analyses. While standardization and publication of monitoring data can be valuable goals in themselves, the added value of post-publication data integration and enhanced analytical capabilities has yet to be fully recognized. To increase the motivation for local governments to actively utilize their own data and global data, it is necessary to lower the technical barriers to analysis. These barriers may include basic data visualization techniques, simple data processing methods, and knowledge on interpreting results. Considering recent advancements in AI, these technical barriers have been significantly reduced. Environments now exist where analytical procedures can be executed simply by providing instructions in natural language, swiftly generating relevant scripts. Thus, instead of merely offering detailed technical procedures for data analysis, demonstrating compelling and practical applications that can be achieved through the OBIS platform is the key to transforming local governments from passive data providers into proactive data users. This presentation aims to discuss the types of content that would inspire local governments to actively utilize their own data and pursue capacity development.

Session: 6798479-2**7005752**

23/10/25 | 11:05

Room: Ballroom B1

LIGHTNING TALK • EN

Serving a sustainable coding community: the INBO Coding Club story

Presenter

Damiano Oldoni

Authors**Damiano Oldoni** (Research Institute for Nature and Forest (INBO) • Belgium)**Raïsa Carmen** (Research Institute for Nature and Forest (INBO) • Belgium)**Emma Cartuyvels** (Research Institute for Nature and Forest (INBO) • Belgium)**Oberon Geunens** (Research Institute for Nature and Forest (INBO) • Belgium)**Dirk Maes** (Research Institute for Nature and Forest (INBO) • Belgium)**Rhea Masele** (Research Institute for Nature and Forest (INBO) • Belgium)**Amber Mertens** (Research Institute for Nature and Forest (INBO) • Belgium)**Hans Van Calster** (Research Institute for Nature and Forest (INBO) • Belgium)**Abstract**

In January 2018, inspired by similar initiatives, a group of enthusiastic researchers at the Research Institute for Nature and Forest (INBO) launched a coding club. The INBO Coding Club (<https://coding-club.inbo.be/>) was, is, and will continue to be a welcoming space for anyone interested in learning more about programming and data analysis, with a particular focus on biodiversity, conservation and ecological topics. Our goal has always been to foster an environment of collaborative experimentation, where participants share code, learn from one another, and grow together—regardless of their level of experience. Everyone is encouraged to contribute, express their ideas freely, and engage as equals. We firmly believe that learning is a mutual process, independent of expertise levels, and that doing it together is not only more effective but also more enjoyable.

More than seven years—and a pandemic—later, the INBO Coding Club remains vibrant and thriving. We are excited to share the strategies that have helped sustain this initiative, transforming initial enthusiasm into a widely recognized and enduring effort both within and beyond INBO.

Key lessons learned include:

- **Learn together:** Create a supportive space where every question is valued, and mistakes are celebrated as opportunities for growth.
- **As live as possible, as remote as necessary:** Live coding in the same room is far more engaging and effective than remote sessions.
- **Community-driven evolution:** The club should always prioritize the needs of its community, with feedback playing a central role in shaping its activities.
- **Dedication:** A committed core team is essential for the consistent and sustainable organization of club activities.
- **Full openness:** All session materials—including data, slides, code, and recordings—are freely available to everyone.

Session: 6798479-2**7019779**

23/10/25 | 11:20

Room: Ballroom B1

ORAL • EN

Datathons: Regional Collaboration to Reuse Microbial Biodiversity Data

Presenter

Clara Arboleda-Baena

Authors

Clara Arboleda-Baena (German Centre for Integrative Biodiversity Research, iDiv • Germany)**Santiago Castillo** (German Centre for Integrative Biodiversity Research, iDiv • Germany)**Silvia Garaycochea** (Instituto Nacional de Investigación Agropecuaria de Uruguay • Uruguay)**Eva Figuerola** (Consejo Nacional de Investigaciones Científicas y Técnicas • Argentina)**Stephanie Jurburg** (Helmholtz Centre for Environmental Research, UFZ • Germany)

Abstract

The global biodiversity crisis demands urgent action to collect, organize, and share species inventory data that enable broad analyses and predictions. In this context, the Datathons are initiatives aimed at promoting data reuse among microbial ecologists by facilitating the archiving and analysis of existing metabarcoding data. This approach expands global reach without requiring additional resources, generates new knowledge, and helps bridge the gap between data producers and users, especially in the Global South. Datathons are conducted virtually over three days. The first day, “Inspire,” includes a hybrid symposium on the importance of open data and the current landscape of biodiversity synthesis research. The second day, “Enable,” provides practical guidelines for depositing microbial sequences in the NCBI. The final day, “Collaborate,” focuses on leveraging deposited or reused data to build collaborative networks among researchers and develop synthesis projects. Subsequently, metadata and microbial species abundance data are centralized in the Microbial Community Database (MiCoDa), which enhances their visibility, interoperability, and accessibility. During the Latin America 2023 and Africa 2024 Datathons, a total of 5,708 and 1,000 bacterial and fungal metabarcoding samples were compiled. These events also led to the formation of several working groups that foster collaborative research among Global South researchers, enriching our understanding of biodiversity across ecosystems at Latin American, African, and global scales. MiCoDa will continue to promote new Datathons to bridge data gaps between the Global North and South, strengthening collaboration among researchers. Upcoming events include the Datathon China in 2025, the Polar Datathon in 2026, and the Datathon Eastern Europe & Balkans in 2027. We invite new participants to join working groups that address global research questions and deepen the study of microbiomes across diverse environments.

Session: 6798479-2**7020901**

23/10/25 | 11:35

Room: Ballroom B1**LIGHTNING TALK • EN**

2Involve -- Data and stakeholder diversity for biodiversity

Presenter

Thore Engel

Authors**Aletta Bonn** (German Centre for integrative Biodiversity Research (iDiv) • Germany)**Thore Engel** (German Centre for integrative Biodiversity Research (iDiv) • Germany)**Diana Bowler** (Centre of Ecology and Hydrology • United Kingdom)**Martin Friedrichs-Manthey** (German Centre for integrative Biodiversity Research (iDiv) • Germany)**Abstract**

Biodiversity data are collected and distributed across stakeholders. Within the national research data infrastructure for biodiversity (NFDI4Biodiversity) and the sMon network, we collaborate with stakeholders from academia, natural history societies, museums, conservation agencies and citizen science.

We integrate biodiversity data from different sources and develop data pipelines to foster FAIR data and added value for biodiversity research and conservation, e.g. for data driven red list assessments. For occupancy data we have now 8 years of experience of community work in mobilizing and integrating data from different sources and have developed species trend analyses for different taxa, including dragonflies, carabids, fish as well as plants. In this talk, we present our learnings from bringing communities together to develop data and stakeholder integration and joint analyses at the national level, and we discuss the opportunities and challenges in fostering these partnerships. We are interested to link up with initiatives in other countries and at the international level.

Session: 6798479-2

7010137

23/10/25 | 11:40

Room: Ballroom B1

LIGHTNING TALK • EN

Digitising Botanical Archives: Collaborative Workflows for Enhancing Accessibility, Integration, and Research Across National and International Collection Networks

Presenter
Robert Cubey

Authors
Robert Cubey (Royal Botanic Garden Edinburgh • United Kingdom)

Abstract
To enhance accessibility and integration of the collections at the Royal Botanic Garden Edinburgh, we have undertaken a project to digitise and transcribe historic collection books, accession cards, and donation files. This initiative employs a collaborative approach involving core staff, volunteers, community scientists, online transcription platforms and AI tools. This paper outlines the end-to-end workflow—from the identification and prioritisation of archival materials, via the creation of contemporary collections management systems records, to working with people, institution & item identifiers – and discusses how this digitised content is aggregated with national and international collections to support broader accessibility and research.

Session: 6798479-2

7020576

23/10/25 | 11:55

Room: Ballroom B1

ORAL • EN

Counting on Citizens: Unveiling Butterfly Diversity Through 30 minute counts

Presenter
Vijay Barve

Authors
Rohit George (Ashoka Trust for Research in Ecology and the Environment • India)
Nandita Barman (Nature Mate-Nature Club • India)
Shantanu Dey (Sppondrift OPC Pvt. Ltd • India)
Sohail Madan (Sppondrift OPC Pvt. Ltd • India)
Arjan Basu Roy (Nature Mate-Nature Club • India)
Vijay Barve (Natural History Museum of Los Angeles County • United States)

Abstract
The “Big Butterfly Month” (BBM) is an annual citizen science initiative launched in September 2020, dedicated to monitoring butterfly populations across diverse landscapes. This program leverages the power of community participation to gather crucial ecological data, contributing significantly to our understanding of local biodiversity and conservation needs. Two primary data collection methodologies are employed: spot occurrences, which record the presence of specific butterfly species are posted on iNaturalist or the India Biodiversity Portal, and standardized 30-minute counts. The latter, a highly replicable method, proves invaluable for assessing species diversity, population dynamics, and relative abundances over time and across different habitats.

A core objective of the BBM initiative is the mobilization of this invaluable citizen-generated data to open-access platforms, most notably the Global Biodiversity Information Facility (GBIF). This ensures that the collected information is not only accessible to researchers and conservationists worldwide but also contributes to broader global biodiversity datasets, facilitating large-scale ecological analyses and informed policy decisions. This abstract shares our experience in engaging and training a diverse network of citizen scientists, detailing the development and refinement of a robust workflow designed to streamline data collection, validation, and publication. We highlight the challenges encountered and the innovative solutions implemented to foster high-quality data submission and ensure the seamless integration of citizen science efforts into the broader scientific community.

This initiative also ensures a broader habitat understanding, gives options to compare data from urbanised areas and its adjoining forest areas.

Session: 6798479-2**7012049**

23/10/25 | 12:10

Room: Ballroom B1

LIGHTNING TALK • EN

Building capacity in open and reproducible science for the next generation of ecologists through the International Plant Functional Traits Courses

Presenter

Aud Halbritter

Authors**Aud Halbritter** (University of Bergen • Norway)**Brian Enquist** (University of Arizona • United States)**Brian Maitner** (University of South Florida • United States)**Sean Michaletz** (University of British Columbia • Canada)**Richard J. Telford** (University of Bergen • Norway)**Vigdis Vandvik** (University of Bergen • Norway)**Abstract**

The global climate and biodiversity crises pose imminent threats to biodiversity, ecosystems, and human lives and livelihoods. Ecological science and scientists have played key roles in providing knowledge and raising awareness of the severity and urgency of these global crises. Ecological understanding is also crucial in developing sustainable, nature-based solutions that safeguard both people and nature. As ‘big data’ approaches are gaining traction in ecology, progress is increasingly limited by barriers to data availability, and by the ability of researchers to effectively handle big data. A key missing piece in ecological science practice are reproducible workflows, which underlie the ability to integrate data and to rapidly assemble and compare data. Reproducible workflows are also critical to ensure a reliable and trustworthy foundation for evidence-base for policy and decision-making. This requires that scientists have access to appropriate training and resources in open and reproducible science practices, adapted to the needs of their specific fields.

Over the past decade, we have developed a unique series of international Plant Functional Traits Courses, where PhD and MSc students, in an active learning setting, build skills and competencies by collecting, managing, analysing and sharing, and publishing real research data in global change and trait-based ecology. Over the years, we have had 180 participants from 30 countries and five continents. Much of our work focuses on mountains because they harbour 25 % of the world’s biodiversity, provide important ecosystem functions and services, are vulnerable to global change, and are generally understudied. Each course is conducted along an elevation gradient in a new mountain region, and we collaborate with local scientists to ensure comprehensive system knowledge and background data. Through this capacity building effort, we have fostered a research community for the next generation of ecologists who share a common interest in transparent and data-driven ecological research.

Session: 6798479-2**7018417**

23/10/25 | 12:15

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

Teaching community scientists how to analyze iNaturalist data using R

Presenter

Wai-Yin Kwan

Authors

Wai-Yin Kwan (Natural History Museum of Los Angeles County • United States)

Abstract

iNaturalist is a program that encourages people to document the biodiversity around them using a smart phone. With 230 million observations, iNaturalist is one of the biggest sources of biodiversity data in the world. In February 2025 the Natural History Museum of Los Angeles County held a workshop to teach community scientists and community organizers how to analyze iNaturalist data using R. Many iNaturalist projects encourage community scientists to collect data, but leave data analysis to “real” scientists. Our goal was to teach community scientists some basic skills so that they could look for answers to their own questions. We believe it is important to teach community scientists that their voice and questions matter. During the first class, we covered how to download iNaturalist CSV data, create maps, and create charts using R. During the second class, each attendee presented their analysis. This presentation will cover what we learned from teaching the workshop.

Session

6799056-2

Symposium

23/10/25 | 10:45

Room: Ballroom B2

Overcoming challenges in biodiversity modelling (Part 2)

Organizers

Natalie Briscoe

Santiago Velazco

Mark Urban

Greta Bocedi

Damaris Zurell

Description

The availability of biodiversity and environmental data is rapidly increasing. Yet to address global challenges, support informed decision-making, and plan effective mitigation, we also need models that can integrate these data to identify the drivers underpinning species and ecosystem responses to environmental changes and reliably forecast future impacts. This is no small task: biodiversity data are often patchy and geographically and taxonomically biased; including biological mechanisms can improve accuracy, but these mechanisms are often complex and poorly understood; and models need to be applied to varying spatial extents, time periods, divergent climate and management scenarios, and millions of species. While many promising modelling frameworks exist to support management and policy, the wider use of models to assess and project environmental change impacts on biodiversity is hampered by data and methodological challenges and limited coordination of modelling efforts. We aim to explore recent advances to overcome these challenges including (i) emerging approaches and data integration methods to incorporate mechanisms into models for many species; (ii) methods to scale results across different spatial extents and time periods; and (iii) how to coordinate efforts and compare modelling frameworks to advance knowledge and protect nature.

Session: 6799056-2**7015491****23/10/25** | 10:45**Room:** Ballroom B2**ORAL • EN**

Biases Overpower Biodiversity-Scale Relationships: Insights from ~10 000 plant species

Presenter

Abbie Gail Jones

Authors

Abbie Gail Jones (McGill University • Canada)**Pollock Laura** (McGill University • Canada)

Abstract

Land protection is looked towards as a feasible solution to the looming global biodiversity crisis, with growing commitments to protect 30% of the world by 2030. To this end, reliable knowledge of the distribution of diversity across landscapes is vital to select lands to be protected. However, very few species have complete sampling records within single databases to adequately interpret their distributions at relevant scales. Here, we show how various methods of bias-corrective SDMs for biodiversity estimating purposes may inadvertently cloud resulting biodiversity patterns, biodiversity-scale relationships, and conservation efforts. Using the biased European data landscape, with a strong data lineation between the East and West, we integrate two types of spatial data for ~10 000 species to assess the impacts of sampling biases on biodiversity estimates at various spatial scales - ranging from 1x1km to biogeoregion-wide. We highlight the importance of data selection and offer a strong comparison of algorithm, pseudoabsence, and covariate selection methods. Finally, we assess how these differing input data, scales, and bias-control methodologies impact conservation scenarios in which land is prioritized for 30x30. We show that even after addressing sampling biases using traditional methods, strong spatial biases remain throughout all modelled scales - with sampling biases overpowering expected regional biodiversity-scale relationships as well as classic endemism and turnover patterns in key hotspot areas (e.g., the Mediterranean). In highly biased landscapes such as Europe, the integration of systematic surveys remains essential to limit biases, even if limited in taxonomic scope. Assessing the limitations of our current methodologies is vital to answer our applied and fundamental ecological questions pertaining to the relationships between biodiversity and its landscape. As 30x30 initiatives continue growing, overcoming sampling biases and establishing SDM best practices will be key to pinpoint priority areas for conservation.

Session: 6799056-2**7019831****23/10/25** | 11:00**Room:** Ballroom B2**ORAL • EN**

Can we predict biodiversity across large geographic and taxonomic scales?

Presenter

Jakob Nyström

Authors

Jakob Nyström (Uppsala University • Sweden)**Lisa Mandle** (Natural Capital Project, Stanford University • United States)**Jeffrey Smith** (Princeton University • United States)**Tobias Andermann** (Uppsala University • Sweden)

Abstract

Accurate and reliable monitoring is crucial for halting the global biodiversity crisis. Model-based biodiversity intactness indicators can be used to assess current state, explain past trends, and make projections. However, they often rely on biodiversity meta-databases – collating data from numerous source studies – which subject to well-known geographic and taxonomic gaps and biases. Here we systematically evaluate the out-of-sample predictive performance of such large-scale intactness models, an important gap in previous literature. We leverage data from 681 studies and 26,754 locations in the PREDICTS database, covering a broad set of taxonomic groups. Our findings suggest that linear mixed models (LMMs) with study-level random effects perform poorly out-of-sample, both in terms of generalization within sampled populations (interpolation) and transferability under cross-study validation (extrapolation). LMMs are common in biodiversity meta-synthesis, and underpin established biodiversity intactness indicators, but suffer from low attribution of variance to observable effects. To mitigate these limitations, we develop a Bayesian hierarchical model that only uses hierarchical features available at prediction time.

This model generalizes better (interpolation) but transferability (extrapolation) is still low. The low transferability is explained by large distribution shifts between train and test data, when the model is trained on some studies and used to predict on others, i.e. predicting out- of-distribution. These shifts reflect both underlying heterogeneity in sampled populations and methodological inconsistencies. Our analysis highlights important limitations in our ability to build large-scale predictive biodiversity models based on existing biodiversity data, compiled from heterogeneous sources. This has implications for how biodiversity indicators are used and interpreted by scientists, policymakers and the private sector. We argue that significantly larger amounts of geographically and taxonomically representative, standardized biodiversity data are required to overcome these limitations. More work is also needed on refining predictive methods for heterogeneous biodiversity data, with particular emphasis on systematic evaluation protocols.

Session: 6799056-2**7020989**

23/10/25 | 11:15

Room: Ballroom B2**ORAL VIRTUAL • EN**

A model-based global indicator of the capacity of ecosystems to retain biodiversity under climate change: the Bioclimatic Ecosystem Resilience Index

Presenter

Simon Ferrier

Authors

Simon Ferrier (Australia)

Abstract

The Bioclimatic Ecosystem Resilience Index (BERI) combines advances in remote sensing, high-performance computing and macroecological modelling with data for over 400,000 plant, vertebrate and invertebrate species to assess the capacity of landscapes to retain species diversity in the face of climate change, as a function of the area, integrity, and connectivity of natural ecosystems. Results for the BERI are generated at 30-arcsecond grid resolution across the entire terrestrial surface of the planet, with potential to be applied nationally and sub-nationally at finer spatial resolutions as required. The Monitoring Framework for the KM-GBF recognizes the BERI as a component indicator for the climate-focused Target 8. However, due to its highly integrative nature, the BERI also offers considerable potential to play a broader role in KM-GBF implementation, by addressing several key interlinkages with other targets and goals. It effectively integrates the impact that change in three of the ecosystem-level components specified in Goal A – i.e. ecosystem area, integrity and connectivity – are expected to have on reducing the extinction risk of all species in the face of climate change, and therefore on achieving the fourth ecosystem-level component specified in that goal – i.e. ecosystem resilience. The BERI can also serve as a leading indicator for assessing the contribution that protective or restorative actions proposed or implemented under area-based Targets 1, 2 and 3 are expected to make to enhancing the present capacity of landscapes to retain species diversity. This can allow actions under these targets to be better linked both to the achievement of Target 8, and to achieving outcomes under Goal A, thereby providing a stronger foundation for strategic prioritisation of such actions.

Session: 6799056-2**7019914****23/10/25** | 11:30**Room:** Ballroom B2**ORAL • EN**

Testing a terrestrial biodiversity model in the ocean: hierarchical Bayesian beta diversity modelling with simulated plankton communities

Presenter

Harold Horsley

Authors

Harold Horsley (NTNU • Norway)

Morten Omholt Alver (NTNU • Norway)

Ingrid Helene Ellingsen (SINTEF Ocean • Norway)

Abstract

Modelling plankton diversity in marine ecosystems presents distinct challenges: data are often sparse, patchy, and taxonomically incomplete, and ocean dynamics strongly shape community composition across space and time. Many biodiversity modelling frameworks, including Generalised Dissimilarity Modelling (GDM) and its hierarchical Bayesian extension (spGDMM), were developed primarily for terrestrial systems and remain underexplored in marine settings.

To explore the specific challenges of marine environments, we applied spGDMM to model pelagic planktonic beta diversity in coastal Norway. We assessed how different gridded environmental predictors influenced model performance, tested the contribution of spatial random effects, and evaluated the model's ability to generalise across time. We used simulated community data from SINMOD, a high-resolution, coupled physical-biological ocean model designed to represent ocean dynamics. Physical predictors (temperature, salinity, vorticity, spatial and temporal distances) were extracted and transformed into pairwise differences. Biological state variables representing plankton community composition were used to compute Bray-Curtis dissimilarities, which served as the response variable. spGDMM was trained and evaluated across multiple predictor combinations and configurations. Model performance was assessed using CRPS, RMSE, and MAE across cross-validation folds.

The model framework appears well-suited to representing spatial structure but faces limitations in capturing temporal variability. Differences in model behaviour across predictor combinations highlight the importance of careful feature selection. Spatially structured uncertainty highlights the potential for using model outputs to optimise future sampling.

Spatial Generalised Dissimilarity Mixed Modelling (spGDMM) is a promising framework for marine biodiversity modelling, offering flexibility and uncertainty quantification. Applied to simulated data, it successfully captured spatial patterns but revealed limitations in representing temporal dynamics. These findings support the framework's applicability and motivate future use with real-world eDNA data, alongside efforts to refine the model formulation to better account for temporal variation.

Session: 6799056-2**7020618**

23/10/25 | 11:45

Room: Ballroom B2**ORAL • EN**

Improved forecasts of biodiversity exposure to climate variability and change using decadal climate predictions

Presenter

Andreas Schwarz Meyer

Authors

Andreas Schwarz Meyer (University of Cape Town • South Africa)**Carlos Delgado-Torres** (Barcelona Supercomputing Center • Spain)**Ben Carslon** (University of Connecticut • United States)**Josep Serra-Diaz** (Botanical Institute of Barcelona • Spain)**Cory Merow** (University of Connecticut • United States)**Alex Pigot** (University College London • United Kingdom)**Markus Donat** (Barcelona Supercomputing Center • Spain)**Christopher Trisos** (University of Cape Town • South Africa)

Abstract

Ecological forecasts are essential for assessing climate change risks to biodiversity. While current forecasts often rely on mid- and end- century projections, the accelerating pace of climate change increasingly requires conservation efforts to prepare for near-term climate risks. This creates a critical gap between the temporal scales of existing ecological forecasts and the immediate needs of conservation planning in the face of rapid environmental change. Decadal climate predictions (DCPP) offer a valuable opportunity to bridge this gap by enabling ecological forecasts at more actionable timescales. DCPP aims to capture both long-term climate trends and natural internal variability over 1- to 10-year timescales, and shows promising skill in forecasting temperature globally. Here, we assessed DCPP's performance in retrospectively predicting (2001–2014) species exposure to temperatures beyond their observed thermal niches. By combining data on over 30,000 terrestrial vertebrate species with monthly temperature predictions, we estimated when and where exposure occurred. We then compared these DCPP-based exposure estimates with those derived from CMIP6 historical simulations (HIST) and validated both against ERA5 reanalysis data, representing observed conditions. Our results show that DCPP demonstrated greater ability to predict true exposure events while exhibiting lower rates of false positives compared to HIST. These findings suggest that DCPP can improve ecological forecasts, providing a higher-quality assessment of which species will be most at risk, when adaptation interventions are needed, and where to target locations for monitoring before impacts occur. We argue that the yearly release of updated DCPP provides a unique opportunity for ecologists to evaluate their predictions, update their models, and consequently improve biodiversity risk forecasts.

We call for a coordinated effort from the scientific community to bridge the gap between DCPP and biodiversity impact forecasts to meet the urgent need for near-term, climate-informed action on biodiversity.

Session: 6799056-2**7020081**

23/10/25 | 12:00

Room: Ballroom B2**LIGHTNING TALK • EN**

Empowering abundance-based species distribution models with the new R adm package

Presenter

Santiago Velazco

Authors**Santiago Velazco** (San Diego State University • United States)**Admir Cesar de Oliveira Junior** (Universidade Federal da Integração Latino-Americana • Brazil)**Abstract**

Abundance-based species distribution models (ADM) are similar to species distribution models; however, ADM correlate species abundance with environmental data to model and project species abundance throughout space or time. Despite ADM has gained significant attention in recent years, they remain less developed than SDMs. Here, we introduce the *adm* R package, a novel modeling tool developed to support the construction of ADM, including data preparation, model fitting, prediction, and model exploration. This package offers several modeling approaches with an emphasis on Artificial Intelligence algorithms ranging from Support Vector Machine, Random Forest, Extreme Boosted Regression Trees to Deep Neural Networks and Convolutional Neural Networks. All algorithms can be customized flexibly, and their hyperparameters can be fine-tuned. Models can be predicted in geographic space and explored regarding performance and response curves. To date, *adm* provides 35 functions in three categories, i) modeling: to tune, fit, and validate models with nine different algorithms, with a suite of possible model-specific hyperparameters; ii) post-modeling: to predict abundance across space and construct partial dependence plots to explore the relationships between abundance and environmental predictors; and iii) miscellaneous tools: to support the workflow in all steps, including data handling, transformations, and hyperparameter selection. Our goal with *adm* is to provide a flexible, user-friendly, and compact toolkit to help users in developing and leveraging the potential of the ADM field.

Session: 6799056-2**7014457****23/10/25** | 12:05**Room:** Ballroom B2**LIGHTNING TALK • EN**

drmr: A Bayesian approach to Dynamic Range Models in R

Presenter

Lucas da Cunha Godoy

Authors

Lucas da Cunha Godoy (University of California Santa Cruz • United States)

Alexa Fredston (University of California Santa Cruz • United States)

RMWJ Bandara (Rutgers University • United States)

Mark Morales (University of California Santa Cruz • United States)

Malin Pinsky (University of California Santa Cruz • United States)

Abstract

Predicting species' responses to environmental change is a critical challenge in ecology. Traditional species distribution models (SDMs) often rely on correlative relationships with strong equilibrium assumptions and limited skill at forecasting distributions under novel conditions. Dynamic range models (DRMs) offer a more mechanistic approach by explicitly incorporating the demographic processes (recruitment, death, movement) that drive range dynamics. However, the complexity of DRMs has hindered their widespread adoption. We introduce drmr, an open-source R package that substantially lowers the barrier to entry for DRM applications. drmr provides a user-friendly framework for building, fitting, visualizing, evaluating, and projecting age-structured DRMs, leveraging the power of Stan for efficient Bayesian inference. Users can readily relate environmental drivers to demographic processes based on observations for a species across space and time. Models can be tailored to specific ecological systems, and competing hypotheses can be tested for range shift mechanisms. By explicitly modeling demographic processes and their environmental drivers, drmr provides a powerful and accessible tool for ecologists to understand and predict changes in species distributions, thereby contributing to improved conservation planning and management in the face of global change.

Session: 6799056-2**7014646****23/10/25** | 12:10**Room:** Ballroom B2**LIGHTNING TALK • EN**

Getting a handle on model complexity and extrapolation when making future forecasts with biodiversity models

Presenter

Jamie M. Kass

Authors**Jamie M. Kass** (Tohoku University • Japan)**Gonzalo E. Pinilla-Buitrago** (City University of New York • United States)**Robert P. Anderson** (City University of New York • United States)**Abstract**

Global change in climate and land-use is resulting in a rearrangement of species' ranges under a relatively short time span, and this is expected to intensify and accelerate the transformation of the biodiversity patterns we know. This can lead to unprecedented biological invasions, extinctions, and novel interactions that perturb or even disrupt vital ecosystem services that people depend on. We are thus very interested in forecasting how species' ranges will shift in response to changing environments. However, without data from the future to evaluate our models, the best we can do is ensure they will make reasonable predictions when trained on current data. Particularly, we need to be mindful of the way our models are extrapolating to conditions outside the training data (i.e., "non-analog" conditions).

Furthermore, with so many variables and machine-learning algorithms at our disposal, models can become overly complex and extrapolate in unexpected ways. In this talk, I will explain methods to tune complexity for biodiversity models and optimize their ability to make predictions for non-analog conditions, as well as a new framework to guide decisions on and control model extrapolation behavior. I will also discuss how we can leverage the diversity of tools for ecological modeling in R and community-driven platforms like Wallace EcoMod and BON in a Box to make these methods more accessible and educate researchers about how they can improve biodiversity forecasts.

Session: 6799056-2**7020713**

23/10/25 | 12:15

Room: Ballroom B2**LIGHTNING TALK • EN**

BATIS: A Benchmark and Framework for Uncertainty-Aware Species Distribution Modeling

Presenter

Catherine Villeneuve

Authors**Catherine Villeneuve** (McGill University | Mila (Quebec AI Institute) • Canada)**Benjamin Akera** (Mila (Quebec AI Institute) • Canada)**Mélisande Teng** (Université de Montréal | Mila (Quebec AI Institute) • Canada)**David Rolnick** (McGill University | Mila (Quebec AI Institute) • Canada)**Abstract**

Citizen science initiatives such as eBird are playing a critical role in enabling species distribution modeling at vast geographical and temporal scales. Machine learning is increasingly being used to develop species distribution models (SDMs), and has been shown in some cases to outperform traditional approaches when applied to these large-scale datasets. However, leveraging millions of volunteer-based observations to derive robust ecological knowledge still presents numerous analytical challenges due to the strong biases in citizen science data. Spatial bias is notably a major limiting factor, and can compromise the accuracy of SDMs outside of intensively sampled areas.

Moreover, this problem can be further exacerbated when SDMs are not updated in real time with occasional observations collected in data-scarce locations.

In this study, we introduce a Bayesian approach to species distribution modeling that aims at iteratively refining prior model predictions as new data becomes available. By explicitly modeling uncertainty, both from inherent noise in the data and from gaps in the model's knowledge, our framework effectively combines finer local insights with broader ecological patterns learned by an SDM. We show that our approach can greatly improve SDM performance, even when using fewer than 10 additional field samples. Our results suggest that our approach can improve the reliability of SDMs in low-data regimes, but also highlights that room for improvement remains in estimating model uncertainty under these challenging conditions.

To evaluate progress in that area, we additionally introduce BATIS, an open-source dataset including observations from the eBird platform. We benchmark a variety of state-of-the-art uncertainty estimation methods, representing one of the most complex settings in which such approaches have been evaluated. We believe that our work lays the groundwork for improved, uncertainty-aware machine learning methods for species distribution modeling, thereby advancing our understanding and protection of biodiversity.

Session: 6799056-2**7020385**

23/10/25 | 12:20

Room: Ballroom B2**LIGHTNING TALK • EN**

Scaling sustainable land use planning from global to national levels for biodiversity, energy, and agriculture under climate change

Presenter

Amy Frazier

Authors

Amy Frazier (University of California, Santa Barbara • United States)

Nicholas McManus (United States)

Patrick Roehrdanz (United States)

Susana Rodriguez Buritica (Colombia)

Elkin Noguera Urbano (Colombia)

Lei Song (United States)

Wenxin Yang (United States)

Dan Willett (United States)

Joana Krieger (Brazil)

Abstract

The world is at a critical juncture for climate change research where we must shift from the problem of forecasting the implications of climate change to focusing on how to use these forecasts to facilitate the transformative changes necessary to avoid biological and human catastrophe. Global models attempting to balance future sustainable land use needs for biodiversity conservation, energy, and agriculture suggest that if the world attempts to meet future demand and targets, like the Global Biodiversity Framework's 30x30, there is not enough land globally to meet both conservation and development targets. Therefore, more concerted planning efforts are needed at national and regional scales. This work advances basic scientific models of land use planning under future climate scenarios by integrating diverse, multi-scale and living data into dynamic forecasting models to inform actionable and sustainable land use plans to prevent the loss of biodiversity and ecosystem services. Using a minimum set optimization mode, we prioritize future land use for conservation, energy, and agriculture in mega-biodiverse Colombia out to 2100 to achieve '30x30' goals and meet the future energy and food demands of a growing population. We identify areas where there are likely to be conflicts between competing land use needs and which areas should be prioritized for species conservation under climate change. Lastly, we discuss efforts to better support sustainable land use decisions-making with these projections on the ground.

Session: 6799056-2**7016145**

23/10/25 | 12:25

Room: Ballroom B2**ORAL VIRTUAL • EN**

Theory and ecological trait data standards can improve the utility of functional trait databases

Presenter

Michael Kearney

Authors

Michael Kearney (The University of Melbourne • Australia)**Natalie Briscoe** (The University of Melbourne • Australia)**Starrlight Augustine** (Institute of Ecotechnics • United States)**Kristoffer Wild** (The University of Melbourne • Australia)**Elizabeth Wenk** (University of New South Wales • Australia)**Nina Marn** (Rudjer Boskovic Institute • Croatia)**Konstadia Lika** (University of Crete • Greece)**Marko Jusup** (Tokyo Institute of Technology • Japan)**Sebastiaan Kooijman** (Netherlands)

Abstract

Trait databases have an important role to play in facilitating the broad application of mechanistic niche models to many species. Yet there are challenges in how to structure them, how to prioritise content, and how to limit bias towards traits based on ease of measure or taxonomic peculiarities. Theory can guide which traits (and metadata) to measure, but it is less prescriptive about how to best structure and store data. Ecological trait data standards aim to address the storage and structure problem and to facilitate efficient re-use of trait data.

Here we explore how both theory and trait data standards can be used to inform the design of a functional trait database of life history and metabolic observations required to quantify the processes of energy and mass exchange and allocation during individual ontogeny. We specifically use Dynamic Energy Budget (DEB) theory and its associated parameter database, which has >6000 species across the tree of animal life, and the traits.build framework for trait database construction. We present a database of nearly 50,000 ‘zerovariate’ life history trait measurements that have passed through the ‘theoretical filter’ of the DEB parameter estimation process. We illustrate patterns in these raw data and compare them to those in other databases without a ‘theoretical filter’. Finally, we introduce the concept of metabolic and life history ‘trait reanalysis data’, an analogous concept to ‘weather reanalysis’, whereby the theoretical model can impute raw trait data gaps to produce a complete dataset of all traits used in parameter estimation and additional implied traits that emerge from the theoretical model. We discuss how the integration of theoretically-derived trait databases with a generic trait database framework can help overcome the patchy and biased nature of available data, and thereby broaden the application of mechanistic models of species responses to environmental change.

Session

6798638-2

Symposium

23/10/25 | 10:45

Room: Tolima

Beyond 2030: Building the Data Foundations for Biodiversity Action to support the KMGBF (Part 2)

Organizers

Andrew Rodrigues

Lina Estupinan Suarez

Description

With the Kunming-Montreal Global Biodiversity Framework setting ambitious targets to halt biodiversity loss by 2030, the pressure is on to ensure that effective monitoring systems are in place—not just for 2030, but for the long-term future of biodiversity governance.

Are we ready? Do we have the capacity, technology, and data infrastructure to track progress, measure policy effectiveness, and support biodiversity action beyond 2030? This session explores how different regions, sectors, and organizations are addressing these challenges—developing new data products, tools, and systems to meet growing policy demands.

We invite researchers, practitioners, and decision-makers to share innovative approaches to biodiversity monitoring, data synthesis, and reporting. By fostering discussion and bringing together global expertise, we aim to identify best practices and pathways for building a stronger, more connected biodiversity data ecosystem for the decades ahead. Join us as we explore how to transform biodiversity commitments into long-term, measurable success.

Session: 6798638-2**7000276****23/10/25** | 10:50**Room:** Tolima**ORAL • EN**

Vital Design Principles for 2050: Towards Less Tech-Driven and More Ecosystem-Driven Data Systems

Presenter

Michelle Westerlaken

Authors

Michelle Westerlaken (MIT Climate and Sustainability Consortium | Massachusetts Institute of Technology • United States)

Abstract

The long-term goal of the *Kunming-Montreal Global Biodiversity Framework* (KMGBF) is to “fulfill a shared vision of living in harmony with nature by 2050”. This statement helps to raise important questions on how current biodiversity data technologies can better connect to this long-term vision. Rather than developing harmonious ways of living with nature, emerging data technologies currently predominantly focus on showcasing new technological features, increasing the quantity of different types of data, or further fragmenting ecosystems into separate data streams. Although ambitious in their goals and contributing to increased knowledge on ecosystems, it can be argued that these types of innovation continue to follow anthropocentric design patterns that do not align with the KMGBF, because their outputs firstly aim to benefit humans in their quest for increasing ecosystem data. As these systems mature over the next decade, future innovations will benefit from approaches that can redirect developments from adhering to human-centric goals towards more planet-centric objectives.

This talk reports outcomes from four years of design research into emerging digital biodiversity systems with the goal to identify challenges and produce design principles that can encourage more planet-centric types of innovation. The qualitative research methods that were used in this study include desk research into current innovation landscapes, 40+ interviews with global technology developers and project managers, 10+ interviews and workshops with biodiversity assessment specialists at keystone corporations, and 6+ months of fieldwork and workshops with local biodiversity restoration communities in the Netherlands. From this data, various stakeholder perspectives, user needs, innovation gaps, and technological challenges were identified and translated into a series of Design Principles for 2050. These guidelines propose future innovation that is more directly aligned with the long-term KMGBF vision and encourage developers to build more socio-ecologically engaged biodiversity systems.

Session: 6798638-2**7020245**

23/10/25 | 11:00

Room: Tolima

ORAL • EN

The Biodiversity Progress Index: A Scalable AI-Powered Tool for Tracking Biodiversity Targets Using Participatory Science and Remote Sensing Data

Presenter

Courtney Davis

Authors

Courtney Davis (Cornell University • United States)

Abstract

Recent commitments to reverse global biodiversity loss, such as those outlined in the Kunming-Montreal Global Biodiversity Framework (KMGBF), face persistent challenges—chief among them, establishing robust biodiversity baselines and tracking the effectiveness of conservation interventions at relevant spatial and temporal scales. Despite growing urgency, progress toward developing scalable biodiversity metrics remains limited, largely due to data gaps. Participatory science programs have recently emerged as a powerful and cost-effective complement to national biodiversity monitoring efforts by harnessing the collective knowledge, and observations of local communities. Yet, the non-systematic nature of data collection in these programs presents methodological challenges that must be addressed to ensure the accuracy of derived biodiversity indicators. To meet this need, we introduce the Biodiversity Progress Index (BPI)—a scalable, policy-relevant tool that integrates participatory science and remote sensing data with emerging AI technologies. The BPI delivers standardized, interpretable metrics that support local decision-making and biodiversity reporting at multiple levels. It enables users to establish biodiversity baselines and evaluate the impacts of conservation interventions across space and time. We demonstrate the utility of the BPI using data from eBird – the world’s largest biodiversity database, with over 1.9 billion bird observations contributed by more than 1 million participants globally. Through real-world applications, we highlight how the BPI has been used to guide the prioritization and implementation of nature-based and regenerative agricultural solutions for the private sector. We also discuss its broader potential to support governments, NGOs, and researchers in more cost-effectively estimating the status of biodiversity and tracking progress toward national and international targets, including those defined under the KMGBF. By translating vast, underutilized data streams into accessible, actionable insights, the BPI represents a practical and scalable solution for strengthening biodiversity monitoring systems and building the databases and technology needed to support global biodiversity governance beyond 2030.

Session: 6798638-2**7019841**

23/10/25 | 11:10

Room: Tolima

ORAL • EN

Leveraging global data to inform biodiversity policy: Implementing Species occurrence cubes for scalable analysis and FAIR reporting

Presenter

Lina Estupinan-Suarez

Authors

Lina Estupinan-Suarez (iDiv - German Centre for Integrative Biodiversity Research • Germany)

Andrew Rodrigues (GBIF Secretariat • Denmark)

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Matthew Blissett (GBIF Secretariat • Denmark)

Tim Robertson (GBIF Secretariat • Denmark)

Hanno Seebens (Justus-Liebig-Universität Gießen • Germany)

Heliana Teixeira (University of Aveiro • Portugal)

Abstract

Effective biodiversity policy depends on the timely and robust analysis of increasingly large and diverse datasets. The Biodiversity Building Blocks for Policy (B-Cubed) project addresses this challenge by developing tools and workflows that streamline the management and analysis of species occurrence data using data cubes. These species occurrence cubes are generated through SQL-based workflows that aggregate data, sourced primarily from the Global Biodiversity Information Facility (GBIF), though not exclusively, into structured, interoperable formats. These data cubes can be used to monitor and report on the status and trends in biodiversity.

Current applications include assessments of the status and trends of biological invasions, improved species distribution modelling, and the development of indicators that can directly inform environmental policy at both European and global levels. B-Cubed outputs are designed to meet European legislative requirements and contribute to international biodiversity commitments. This approach is closely aligned with the Essential Biodiversity Variables (EBVs) framework and leverages the EBVCube geospatial data standard developed by GEO BON, ensuring compatibility and interoperability with global biodiversity monitoring initiatives. Lastly, by adhering to FAIR principles (Findable, Accessible, Interoperable, and Reusable), B-Cubed ensures that all workflows and resulting datasets are openly available through public data repositories. This commitment to transparency and standardization not only enhances data integration across domains but also fosters reproducibility and collaboration within broader biodiversity domains and the policy community.

Session: 6798638-2**7019774**

23/10/25 | 11:30

Room: Tolima

ORAL VIRTUAL • EN

The Biodiversity State Indicator -- how can we capture biodiversity with an ecosystem-based approach

Presenter

Verena Schrameyer

Authors

Verena Schrameyer (DHI A S • Denmark)

Lars O. Mortensen (DHI A S • Denmark)

Ole Bjørn Brodnicke (DHI A S • Denmark)

Abstract

The anthropogenic effect on the world's biodiversity is now widely recognized and several marine operators, developers, stakeholders, and legislators are now pledging to reverse the current trend of massive global biodiversity loss. In order to harness the biodiversity footprint of human society it is essential to be able to quantify biodiversity. However, there are no current comprehensive, quantitative guidelines on how to assess biodiversity. Commonly applied single biodiversity indices such as Simpson index considering number of species and abundance of each species does not cover the broad complexity of biodiversity how we understand it in present time. With the green transition and industry sectors urged to disclose biodiversity impacts, it is crucial to align on how we capture the state of biodiversity. The Biodiversity State Indicator is a tool to capture and resolve the intricate interactions within a marine ecosystem, based on species' ecological traits, and thereby the driving forces that realize specific ecosystem services and overall 'functioning' of an ecosystem. The BSI gives compelling information that is necessary for biodiversity impact disclosure but most importantly to pinpoint where extra conservation efforts are needed.

Session: 6798638-2**7020672**

23/10/25 | 11:40

Room: Tolima

ORAL • EN

Unlocking fossil biodiversity: Moving from project-centered data management to integrating international biodiversity data infrastructures from Latin America

Presenter

Ana Valenzuela-Toro

Authors

Ana Valenzuela-Toro (CIAHN Atacama • Chile)

Nicholas Pyenson (Smithsonian Institution • United States)

Martín Chávez Hoffmeister (CIAHN Atacama • Chile)

Abstract

Latin America has produced significant fossil discoveries that have transformed our understanding of past biodiversity in the marine and terrestrial realms. However, paleontological science infrastructure in this region faces considerable challenges in data management.

Traditional project-centric data practices have resulted in fragmented information, limiting both integrative analyses and broader accessibility. While global databases like the Paleobiology Database have significantly contributed to aggregating fossil data across regions, the under-resourcing and fragmented capacity of Latin American paleontology data institutions limit their relevance to measuring biodiversity loss and the climate crisis. Specifically, data integration, interoperability, and equitable access all arise from the intersectional difficulties related to regional and country-specific cultural, economic, and political landscapes. In Chile, paleontological data management is gradually shifting from project-specific practices to integration with international biodiversity data infrastructures, including the establishment of specialized institutions, which are especially relevant in the Latin American context. We will specifically discuss the benefits of paleontological data mobilization and integration, identify technical and cultural barriers, and propose a roadmap for fostering more effective collaboration among Latin American paleontological data holders and users, collection managers, and international biodiversity initiatives. These practices would give a pathway to contribute to the global biodiversity data landscape, helping to reduce geographical and temporal gaps in data that are critical for global issues like climate change, and ensuring a more comprehensive and regionally relevant understanding of life's past, present, and future.

Session: 6798638-2**7019994**

23/10/25 | 11:50

Room: Tolima

ORAL • EN

French BON EBV operationalization pilot: A flexible approach based on existing international initiatives to help scale up biodiversity monitoring

Presenter

Yvan Le Bras

Authors

Coline Royaux (MNHN Data Terra PNDB Biodiversity Data Hub UAR 2047 DoHNÉE • France)

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Marie Jossé (CNRS IFREMER Data Terra • France)

Marc Eléaume (MNHN UMR ISYEB • France)

Dominique Pelletier (IFREMER • France)

Björn Grüning (Freiburg university • Germany)

Jean-Baptiste Mihoub (Sorbonne Université • France)

Yvan Le Bras (France)

Abstract

Thanks to the Data Terra (French digital research infrastructure for Earth system and environment), at the PNDB (French Biodiversity data hub), we started in 2018 the use of existing informatics solutions to propose operational ways to manage, share and analyze biodiversity and auxiliary data and metadata using existing standards, communities and related tools.

We propose here to showcase interest of the combination of the “atomization-generalization framework” designed for Galaxy Ecology initiative <https://doi.org/10.1093/gigascience/giae122> and the use of a mature and rich metadata standard to mobilize existing capacities, technologies and infrastructures to help biodiversity indicators production at all scales, from local to global. Particularly, we will focus on illustrating how this approach can be a relevant way to help building rapidly a first version of global biodiversity observing system, relying mainly on highly structured metadata without needing to harmonize directly all datafiles, protocols and source codes.

Session: 6798638-2**7020144**

23/10/25 | 12:00

Room: Tolima

ORAL • EN

The National Biodiversity Information System: a cloud-based tool to support conservation planning, monitoring, and reporting

Presenter

Alexander Killion

Authors

Claire Hoffmann (Yale Center for Biodiversity and Global Change • United States)

Alexander Killion (Yale Center for Biodiversity and Global Change • United States)

Abstract

The increase in the prevalence and breadth of big data in conservation has opened doors to deeper innovation, more informed decision making, and more robust impact evaluations. However, it has also introduced additional challenges around ensuring species data is applicable to conservation objectives, but also accessible to the many institutions working to achieve those objectives. We have developed The National Biodiversity Information System (NBIS) to address this problem. NBIS is a cloud-based solution co-designed with government ministries to support local to national scale biodiversity monitoring, decision-making, and reporting. The system provides spatially detailed measurement and decision-support addressing national and regional monitoring and planning needs and international reporting. NBIS also provides annually updated standardized information on species conservation status, threats, habitat and connectivity changes, and data coverage, alongside conservation prioritization products and indicators adopted in the GBF. NBIS includes a range of planning tools that can be readily extended and customised, and is fully integrated in an Esri system that can link to existing government GIS platforms. The system is designed to be accessible to non-technical audiences to streamline uptake and application by everyone from high-level decision-makers reporting on progress towards GBF goals and targets, to on-the-ground managers making decisions about ranger priorities. NBIS is powered by the people, data, and products of the Yale Center for Biodiversity and Global Change, Map of Life, Esri, and the E.O. Wilson Biodiversity Foundation.

Session: 6798638-2**7016181**

23/10/25 | 12:10

Room: Tolima

ORAL • EN

Using NatureCounts to support the Kunming-Montreal Global Biodiversity Framework in Canada

Presenter

Catherine Jardine

Authors

Catherine Jardine (Birds Canada • Canada)

Denis Lepage (Birds Canada • Canada)

Kyle Horner (Birds Canada • Canada)

Abstract

Targets 20 and 21 of the Kunming-Montreal Global Biodiversity Framework establish that access to good data and innovative data products are crucial to halting and reversing biodiversity loss. Birds Canada's NatureCounts platform seeks to meet these needs by supporting easy and accurate data collection, interpreting data to produce meaningful knowledge and data products, and sharing data to support conservation action and policy.

FAIR-abiding data starts with collection. The NatureCounts mobile app and web interface are customizable data collection solutions that integrate standardized data from the field directly into a sharing-ready repository. The flexible architecture, user-friendly interface, unique tools, and instantaneous upload incentivize adoption, encouraging open data participation by projects of all types and sizes.

Data collected using these tools are uploaded to the NatureCounts database. Hosting over 250 million records, this repository holds extensive potential for conservation application. Flexible data access permissions support the security of sensitive records and Indigenous data sovereignty.

Various data products support research, conservation, and the targets of the Global Biodiversity Framework. For example, a dedicated workflow uses the data to identify Canada's Key Biodiversity Areas (Target 3). Another uses the data to set and evaluate federal population goals for Canada's birds (Target 14). A third feeds data directly into the Canadian process for identifying endangered species (Target 4), seamlessly connecting data collection to policy.

NatureCounts also facilitates sharing of raw data, processing over 9000 data requests yearly. To date the data have supported over 4200 scientific publications and an immeasurable amount of unpublished work. Data from NatureCounts are used for species assessments, land use planning, impact assessment, academic research, climate change mitigation, and much more. Through NatureCounts, Birds Canada aims to help fulfil the goals of the Global Biodiversity Framework, and make measurable progress for biodiversity in Canada.

Session: 6798638-2**7019966**

23/10/25 | 12:20

Room: Tolima**ORAL • EN**

Biodiversity consultancies have a role to play in achieving KMGBF objectives

Presenter

Cédric Elleboode

Authors

Cédric Elleboode (Biotope • France)

Abstract

With the aim of making the best available biodiversity data accessible to achieve target 21 of the Kunming–Montreal Global Biodiversity Framework, it is essential not to overlook the data produced by biodiversity consultancies.

On the one hand, these consultancies produce large volumes of primary data on biodiversity, often in under-surveyed areas and for taxonomic groups for which data are less abundant. On the other hand, many of them employ professional field naturalists with specialized expertise in species identification and monitoring within specific taxonomic groups and geographic regions.

The data they collect are frequently gathered using standardized survey protocols, making them particularly useful for assessing local species populations and monitoring trends over time.

In this session, we will showcase the resources, methodologies, and innovative tools employed by consultancies such as Biotope to collect, manage, and publish high-quality primary biodiversity data.

Session: 6798638-2**7018591**

23/10/25 | 12:30

Room: Tolima

ORAL • EN

Mycelium of Diplomacy: Cultivating Gulf Biodiversity Data Sharing in Low-Trust Ecosystems

Presenter

Reem AlMealla

Authors

Reem AlMealla (Nuwat • Bahrain)

Nicholas Pyenson (Smithsonian Institution • United States)

Abstract

In the Persian-Arabian Gulf, biodiversity conservation is uniquely complicated by transboundary ecosystems, migratory species, and region-wide climate and anthropogenic pressures that combine to make it the world's hottest and increasingly crowded sea. The Gulf is additionally challenged by inadequate science infrastructure with gaps both in funding and data interoperability that limit discovery and the ability to shape evidence-based environmental policy. Cross-border collaboration is therefore vital in the region but hindered by political and historical tensions, creating a low-trust environment that limits data sharing among Gulf Cooperative Council (GCC) countries, Iran, and Iraq. We propose a model for biodiversity data diplomacy inspired by the decentralized, adaptive networks of mycelium. We argue that biodiversity institutions in the Gulf must cultivate flexible, peer-to-peer partnerships that prioritize transparency, reciprocity, and decentralized collaboration. By fostering informal networks of trust, promoting interoperable data practices, and embracing inclusive governance, the Gulf region can unlock the potential of biodiversity data to strengthen ecological resilience, support climate adaptation, and establish scientific leadership. While some existing institutions (e.g., Regional Organization for the Protection of the Marine Environment [ROPME]) can enable data diplomacy for Gulf states, we identify additional steps including: establishing regional data-sharing frameworks; strengthening national capacities for data management; and prioritizing initiatives that build educational and scientific capacity. Specific bodies such as the GCC could take leadership roles in these efforts, especially through platforms that encourage cooperation and reduce data politicization risks. Like other examples of science diplomacy in low-trust geopolitical regions, we see renewed opportunities in the Gulf for politically neutral, peer-driven spaces for data sharing. These spaces would build capacity through regional training and mobility programs, and promote equitable value exchanges to mutual benefit. Most importantly, Gulf states and non-state actors can seize the opportunity to establish shared scientific priorities as foundations for broader diplomatic engagement.

Session

6788879-2

Symposium

23/10/25 | 10:45

Room: Caldas

Long Live Biodiversity Data: Knowledge Transfer and Continuity across Research Projects (Part 2)

Organizers

Christos Arvanitidis

Niels Raes

Lyubomir Penev

Peter Bozakov

Nikol Yovcheva

Description

Research projects transcend disciplines and national borders to pursue tomorrow's scientific insights. However, their duration is limited and the question arises: How can the data they generate remain impactful for future endeavours? In the context of open science and its principles, securing the legacy of research results is essential for fostering lasting collaboration and innovation.

This session will showcase how a continuous knowledge transfer over time can be ensured by open data and effective science communication across research projects. Representatives of several such international initiatives will reveal how the longevity of their work is guaranteed with success stories of tools, information hubs and workflows enabling exchanges that truly consolidate the global biodiversity data space.

The presentation of this multi-level approach to information sharing and continuity will also demonstrate the potential impact of sustainable research on decision-making. In that context, the session will explore how targeted communication can help transform science results into actionable knowledge by raising awareness among agenda-setters. Thereby, methods bridging the gap between science and policy in relation to an increasingly ambitious global environmental agenda will be discussed.

Session: 6788879-2**7015659**

23/10/25 | 10:50

Room: Caldas

ORAL • ES

Transforming Knowledge into Practice: Science, Technology and Innovation in Support of the UN SDGs

Presenter

Christos Arvanitidis

Authors

Christos Arvanitidis (LifeWatch ERIC • Spain)**Boris Barov** (Bulgaria)**Alberto Basset** (Italy)**Klaas Deneudt** (Belgium)**Montserrat González Ferreira** (United Kingdom)**Federico Drago** (Italy)**Cristina Isabel Huertas Olivares** (LifeWatch ERIC • Spain)**Declan Kirrane** (Belgium)**Dimitrios Koureas** (Netherlands)**Natalia Manola** (Greece)**Daniel Mietchen** (FIZ Karlsruhe - Leibniz Institute for Information Infrastructure • Germany)

Abstract

This white paper presents the unified perspectives of a diverse network of European legal entities—including Research Infrastructures, e- Infrastructures, global aggregators, and publishers—from the fields of biodiversity, ecology, and computer engineering. Together, they are committed to advancing Science, Technology, and Innovation (STI) in support of the United Nations Sustainable Development Goals (SDGs) and the emerging post-SDG agenda.

Coordinated by LifeWatch ERIC and its partners, the initiative underscores the pivotal role of research infrastructures, overarching digital platforms such as the European Open Science Cloud (EOSC), and advanced tools like Digital Twins in tackling the biodiversity crisis and climate-related challenges. The paper aligns its strategic vision with the Kunming-Montreal Global Biodiversity Framework (K-M GBF), recognizing it as a key instrument for achieving biodiversity targets and guiding international cooperation beyond 2030, particularly within the context of the upcoming UN Pact for the Future.

Through integrated, data-driven approaches and participatory governance, the paper outlines contributions to all seven strategic considerations of the K-M GBF. The white paper also emphasizes the importance of strengthening science-policy interfaces, advancing open science, enhancing biodiversity monitoring, and fostering cross-domain innovation at scale.

Particular attention is given to synergies between biodiversity and human health (One Health), as well as to promoting equitable access to knowledge infrastructures globally.

The paper advocates embedding biodiversity knowledge at the heart of sustainable development and proposes actionable pathways such as science-informed governance, fair and equitable benefit-sharing, and investment in biodiversity-centric STI innovation. As the world approaches key milestones—such as the 2030 SDG deadline and the 2026 UN Summit of the Future—the paper calls for a transition from fragmented efforts to integrated, globally coordinated scientific systems.

It concludes with a call to build a global alliance that positions biodiversity as a fundamental pillar of resilience, equity, and planetary well-being.

Session: 6788879-2**7014920**

23/10/25 | 11:01

Room: Caldas

ORAL • EN

Making biodiversity science available for policy: the Knowledge Expert Network on European biodiversity monitoring.

Presenter

Maria Blasi

Authors

Maria Blasi (Spain)

Ute Jacob (Helmholtz Institute for Functional Marine Biodiversity at the University of Oldenburg (HIFMB) • Germany)

Sandra Luque (INRAE • France)

Marie Vanderwalle (Helmholtz Centre for Environmental Research – UFZ • Germany)

Dani Villero (Spain)

Lluís Brotons (CREAF • Spain)

Abstract

How to organise data and information on Biodiversity so that it is easily accessible for policymakers? How to bring experts and projects together to discuss and produce impact from their research? The EU project BioAgora is working on creating the upcoming Science Service for Biodiversity for the European Commission. The mandate of this Horizon project is to work with other EU-funded projects to answer the questions above. For example, BioAgora is creating Knowledge Expert Networks (KENs) to inform policy decisions related to the EU Biodiversity Strategy 2030.

The Monitoring Knowledge Expert Network (KEN) activates the existing network of key institutions, EU projects, and experts in Biodiversity monitoring. The Monitoring KEN works closely with the established networks of EuropaBON and Biodiversa+ and has policy-relevant links outside the EU with IPBES. We will show how we enable pathways to increase the impact of research by bringing together projects and initiatives to address key policy needs identified by the European Commission, by providing concrete examples. The main objective of the network is to mobilise information from existing or expected project outputs, but also to explore synergies and trade-offs across projects to support the Science Service of Biodiversity.

From the collaboration with EuropaBON, we will present the web-based biodiversity monitoring network database developed in EuropaBON and the analysis that allowed us to identify the bottlenecks that prevent producing EBVs to inform policy.

Session: 6788879-2**7014044**

23/10/25 | 11:14

Room: Caldas

ORAL VIRTUAL • EN

From Projects to Platforms: Building a Modular Biodiversity Data Space for Continuity and Integration

Presenter

Sharif Islam

Authors

Sharif Islam (Naturalis Biodiversity Center • Netherlands)

Abstract

How can data and knowledge generated from different biodiversity projects remain discoverable, and actionable across domains, technologies, and policy cycles? Rather than building yet another platform, the Biodiversity Meets Data (BMD) project is designing an extensible, modular, and composable infrastructure that integrates new monitoring tools, harmonises legacy and high-throughput sources, and supports reproducible analysis pipelines across research infrastructures.

At the heart of BMD is a Single Access Point (SAP) for high-throughput biodiversity monitoring, data, and analyses to support conservation action across Europe. The architecture applies open lakehouse principles, FAIR (Findable, Accessible, Interoperable, and Reusable) workflows, and the design logic of Common European Data Spaces to deliver long-term, interoperable infrastructure. It uses open table formats (e.g., Delta Table) and cloud-native geospatial formats (e.g., Parquet, GeoParquet, Zarr), alongside metadata-driven orchestration (RO-Crate, GeoNetwork, STAC, INSPIRE). This ensures seamless data alignment and reuse without format and vendor lock-in.

The BMD data space also reuses existing APIs and services, such as data cubes developed in the B-Cubed project, allowing flexible integration of different types of datasets and metadata. It is designed to support Virtual Research Environments (VREs), map and visualisation tools in a plug-and-play model, enabling scientific workflows to evolve while preserving metadata provenance and computational reproducibility. BMD goes beyond technical design. It recognises that sustainable knowledge transfer requires community-driven governance, infrastructure reusability, and long-term alignment. By federating national and EU-level data resources, and aligning with EOSC and the Green Deal Data Space, BMD offers a robust framework for continuity. This presentation will showcase how a FAIR, open-source, and modular data space enables biodiversity monitoring to outlive projects, adapt to emerging tools, and support both science and policy agendas.

Session: 6788879-2**7019804**

23/10/25 | 11:26

Room: Caldas

ORAL VIRTUAL • EN

Dinosaurs, Data, and Decisions: Writing a Data Policy for the Museum für Naturkunde Berlin

Presenter

Caitlin Thorn

Authors

Caitlin Thorn (Museum für Naturkunde Berlin • Germany)

Mareike Petersen (Museum für Naturkunde Berlin • Germany)

Abstract

At the Museum für Naturkunde Berlin (MfN) we see responsible research data management as one of the keys to the scientific mission of natural history museums. Since our collections span centuries, and disciplines, institutions like ours face challenges in how we standardise data practices across diverse research domains.

To address these challenges, we developed a formal data policy: it's a comprehensive and adaptable framework designed to support the responsible handling, publication, and preservation of research data across the museum. We ensured the policy includes a practical catalogue of measures, from file naming and storage guidance to repository workflows and data management templates. It is structured to reflect the full data life cycle and rooted in FAIR principles.

To ensure everyone understood and could work with the policy it was important to us that we consulted widely – we included data managers, media managers, publication and archiving experts, and many more as we developed the policy. Close attention was paid to the complexities of natural history data. The policy serves not only as an internal standard but as a strategic tool for enabling long-term data stewardship within research and collection-based projects.

This presentation will share insights into the development and publication of the policy, focusing on both the collaborative process and the practical challenges of translating abstract RDM principles into actionable, institution-wide practices. We hope to demonstrate how a flexible, regularly updated policy can help museums adapt to the evolving landscape of open science, digital infrastructure, and global biodiversity data networks.

We hope our experience may be used as a model for other natural history institutions who are looking to embed sustainable data practices within their research cultures.

Session: 6788879-2**7014953**

23/10/25 | 11:37

Room: Caldas

ORAL • EN

From HOMED to FORSAID: sustaining forest health research across Horizon projects

Presenter

Peter Bozakov

Authors

Andrea Battisti (University of Padova, DAFNAE • Italy)

Davide Nardi (University of Padova, DAFNAE • Italy)

Andree Cappellari (University of Padova, DAFNAE • Italy)

Hervé Jactel (INRAE, University of Bordeaux • France)

Peter Bozakov (Pensoft • Bulgaria)

Abstract

Forests play a key role in achieving the objectives of the European Green Deal. However, pests (insects and pathogens) increasingly threaten European forests, which are already suffering from abiotic disturbances such as storms, fire, and drought. Among pests, invasive alien species are of great concern because they can strongly impact forest biodiversity and the economy, and many efforts are being made to regulate them in the European Union. Ongoing research is essential to maintain the main forest functions by enabling early detection of invasive pests, monitoring their spread, and informing phytosanitary measures that can mitigate their impacts.

The Horizon 2020 project *HOMED*, led by INRAE (France), adopted a holistic and multi-actor approach to develop tools and new methods for detecting and managing invasive forest pests, synthesized in the special issue of the journal *NeoBiota* (<https://blog.pensoft.net/2023/05/19/new-neobiota-special-issue-tackling-invasive-alien-forest-pests-in-europe/>). Building on this foundation, the Horizon Europe project *FORSAID*, led by UNIPD (Italy), continues and expands this work with a stronger focus on developing smart technologies and using Earth Observation data. *FORSAID* integrates several outputs from *HOMED*, including remote sensing methods, ground detection approaches, and citizen and stakeholder engagement. For instance, data on pest distribution collected in *HOMED* now serve as a baseline for *FORSAID* remote sensing activities, and generic attractants tested globally in *HOMED* will also be applied to smart traps as part of the *FORSAID* project. Furthermore, stakeholder surveys conducted during *HOMED* revealed a strong demand for tools such as pest identification apps, detection devices, satellite and drone-based monitoring, and eDNA-based methods, all elements that now form the core of *FORSAID* design.

By ensuring the continuity and reuse of data, tools, and engagement strategies, *FORSAID* exemplifies how the legacy of research can be sustained across projects. This approach demonstrates the importance of open data and participatory science in building long-term, impactful research efforts.

Session: 6788879-2**7015724**

23/10/25 | 11:50

Room: Caldas

ORAL VIRTUAL • EN

Continuity in data management plan: examples of the Horizon projects PoshBee and WildPosh

Presenter

Denis Michez

Authors

Denis Michez (University of Mons • Belgium)

Jordan Benrezkallah (University of Mons • Belgium)

Sara Reverté (University of Mons • Belgium)

Mark J.F. Brown (Royal Holloway University of London • United Kingdom)

Abstract

Biodiversity is under multiple threats resulting from human activities. To document population trends and their drivers, multiple initiatives are organised at various spatial and taxonomical scale. The European initiative for pollinator conservation is an inspiring example of multiple actions, including research, aiming to monitor and mitigate pollinator decline. One of the challenges of multiple projects is to manage data following FAIR principle along projects. We present here the example of data management of two articulated European projects funded under the Horizon program: PoshBee and WildPosh. PoshBee and WildPosh are both multi-actor, transdisciplinary projects whose overarching mission are to significantly improve the evaluation of the risk to domesticated and wild pollinators of pesticide exposure and enhance the sustainable health of pollinators in Europe. The collected data sustain the results and are the base for the communication and dissemination over the scientific, social and political spheres to maximise the impact of the project. An effort was done and will be done to streamline the processing of data collection (e.g. shared protocols, template and associated meta-data), data sharing (e.g. cross-WP workshops, data repository to upload the files), data manipulation (e.g. process to download the data), data analysis and ensuring data security (e.g. potential embargo) and ethics (e.g. acknowledgement of rights). EU Pollinator Hub is the repository for the WildPosh project. This hub was created to improve and centralise the efforts done on pollinator health and protection, and it is focused on data related to pollinators and the agricultural sectors. It aims to become the central place to go for stakeholders involved in pollinator health, to maximise the impact of the datasets. It provides open access to metadata, secured authentication for users, a streamlined procedure for data access and upload, versioning will be available, and a secured request procedure for data download.

Session: 6788879-2**7002742**

23/10/25 | 12:01

Room: Caldas

ORAL VIRTUAL • EN

Sustaining Knowledge Across Borders: The IP4OS Framework for Biodiversity Data Continuity and Policy Impact

Presenter

Katharina Miller

Authors

Katharina Miller (Miller International Knowledge (MIK) • Spain)

Frantzeska Papadopoulou Skarp (Sweden)

Vanessa Guzek (Miller International Knowledge (MIK) • Spain)

Abstract

The IP4OS (Intellectual Property for Open Science) project bridges gaps between open data initiatives and sustainable policy-making by introducing a resilient legal and ethical framework designed to support long-term knowledge continuity across international biodiversity research efforts. Anchored in principles of transparency, reproducibility, and co-creation, IP4OS extends the life cycle of biodiversity data far beyond individual project funding periods.

This presentation will showcase IP4OS as a flagship example of integrated policy, governance, and infrastructure design aimed at promoting data reusability and institutional memory. Drawing from the expertise of IP4OS partner Miller International Knowledge (MIK), we will highlight precedents from previous EU-funded projects and how these have informed the development of IP4OS tools and protocols, such as open licensing strategies, stakeholder co-ownership models, and regulatory harmonization for cross-border data flows.

In the context of biodiversity, these tensions are further complicated by international legal frameworks such as the Convention on Biological Diversity (CBD) and the Nagoya Protocol, which emphasize the sovereign rights of states over genetic resources and the equitable sharing of benefits arising from their use. The interface between these obligations and the open sharing of biodiversity data, genetic sequences, or traditional ecological knowledge—central to conservation science—is an interesting and complicated one. The presentation will explore legal uncertainty that may arise when open-access databases contain digital sequence information (DSI) derived from genetic resources.

Focusing on legacy and continuity, the talk will demonstrate how IP4OS facilitates the alignment of scientific outputs with legal frameworks, ensuring that open science efforts become embedded in broader societal structures. This ensures their longevity and relevance for future initiatives tackling biodiversity loss, climate action, and sustainable development.

Finally, we will reflect on the broader implications of embedding data ethics and inclusive governance in biodiversity data infrastructures, contributing to both agenda-setting processes and effective science-policy interfaces.

Session: 6788879-2**7020261**

23/10/25 | 12:13

Room: Caldas

ORAL VIRTUAL • EN

Ensuring continuous open data flow on the state of Open Science. GATE's service for reliable research and optimum Open Science

Presenter

Vanessa Guzek

Authors

Marie Alavi (Kiel University • Germany)

Anika Müller-Karabil (Miller International Knowlegde | Open Science Learning GATE • Germany)

Julia Priess-Buchheit (Kiel University • Germany)

Vanessa Guzek (Miller International Knowledge (MIK) • Spain)

Abstract

As new challenges in biodiversity research and advancing scientific methodologies arise, the research landscape is evolving. In response, the GATE initiative aims to advance research by fostering continuous knowledge exchange among communities and vivid open data flow within the Open Science (OS) framework.

This presentation will explore how GATE facilitates the definition and dissemination of OS foundations critical for advancing reliable biodiversity studies, emphasising the importance of community-agreed OS guiding thoughts, principles, and values such as FAIR, reproducibility, data quality, safety and co-creation (supporting topic 1).

GATE therefore empowers research communities – including researchers, knowledge creators (informing and educating on OS), funders, policymakers, and data infrastructures – to engage in an ongoing dialogue about the guiding thoughts of OS and Open Data, rather than to rely on static definitions. It fosters communication among research actors through a community-based feedback loop, continuously capturing and sharing their OS guiding thoughts ensuring research communities stay informed about the latest developments in OS, including the impact of artificial intelligence on research and data ethics.

This session will showcase GATE's innovative and sustainable approach to optimising OS capacity building, practices and policies through sharing knowledge among communities. Through annual GATE Reports and continuous community engagement, GATE enhances the visibility of open data repositories and cultivates a community dedicated to reliable OS and continuously engaged in knowledge exchange. By connecting OS stakeholders, and informing them on the current and evolving state of the art of OS, GATE promotes sustainable access to knowledge and resources about responsible conduct of OS, ultimately bridging the gap between science and policy (supporting topic 2).

Join us as we discuss how GATE's multi-level approach to knowledge sharing can transform scientific results into trustworthy innovation, thereby accelerating progress toward global biodiversity goals and fostering equitable participation in the OS ecosystem.

Session

6796861

Symposium

23/10/25 | 10:45

Room: Valle

Biodiversity data for One Health: Integrating open data to address global health challenges

Organizers

Quentin Groom

Timothée Poisot

Collin Schwantes

Description

The One Health approach recognizes the intricate connections between human, animal, and environmental health. Biosurveillance has traditionally focused on detecting known pathogens and disease outbreaks. However, translating biodiversity monitoring data into actionable insights for disease surveillance, pathogen spillover prediction, and public health remains a challenge.

This session will explore how biodiversity data can enhance pathogen surveillance, disease ecology, and One Health applications. Experts in biodiversity informatics, data science, and public health will discuss the role of biodiversity monitoring, the integration of databases (e.g., GBIF, GloBI, NCBI Virus, OBIS, Mammal Diversity Database), and best practices for data standardization. Key topics include data mobilization challenges, FAIR principles, automated workflows, and community engagement. By fostering cross-sector collaboration, this symposium aims to support the development of integrated biodiversity monitoring into the One Health frameworks, advancing data-driven decision-making for global health and conservation.

This session, presented in collaboration with the GEOBON One Health working group, explores how integrating biodiversity data into biosurveillance networks, and vice versa, can enhance our understanding of disease and biodiversity dynamics, ultimately leading to better prevention. We welcome abstracts examining successful case studies where biodiversity monitoring has helped identify disease emergence risks, discussing tools to link data across fields, examples of data-driven actions, and proposing frameworks for incorporating ecological data into existing biosurveillance systems.

Session: **6796861****7020942**

23/10/25 | 10:45

Room: Valle

ORAL • EN

Predictive mapping of a global, zoonotic parasite using climate, land-cover, and host traits

Presenter

Anna Willoughby

Authors

Anna Willoughby (University of Georgia • United States)

Daniel Suh (The Virginia Polytechnic Institute and State University • United States)

Ania Majewska (University of Georgia • United States)

Claire Teitelbaum (University of Georgia • United States)

Robert Richards (Georgia Institute of Technology • United States)

Kaylee Arnold (Washington University in St. Louis • United States)

Michelle Evans (United States)

Annakate Schatz (United States)

Joy Venkatachalam-Vaz (Switzerland)

Abstract

Gastrointestinal parasites of mammals often have large geographic ranges, impacting human and animal health globally. Understanding the determinants and boundaries of parasites' geographic ranges can help predict disease risk, yet mapping these distributions is challenging due to multi-taxa host interactions, periods of dormancy outside the host, and uneven sampling across political boundaries. Here, we study the distribution of *Echinococcus multilocularis*, a zoonotic helminth with a complex life-cycle that circulates between definitive carnivore hosts and intermediate small mammal hosts. We compiled a geodatabase of *E. multilocularis* presences and absences from >400 helminth parasitological studies in >70 countries. Using a species distribution modeling (SDM) approach, we tested how publically-available climate, landcover, and host diversity covariates performed in predicting the locations of *E. multilocularis*. Our best-fit spatial model not only recovered known *E. multilocularis* endemic areas in North America, Eastern Europe, and Southwest China, but also identified new areas of probable parasite presence in central Asia, northeastern Russia, and northern Turkey. Climate and landcover variables were the most important predictors, while host variables were the least important to model performance. These findings suggest global species distribution models built from fine-scaled species occurrences and coarse-scale environmental covariates effectively predict the range of complex life-cycle parasites. Though our model was not improved by host species richness measures, future integration of host trait datasets— particularly those capturing competence and abundance— could refine our model. We expect our *E. multilocularis* distribution map to be both actionable and flexible in planning local and regional surveillance campaigns. Additionally, our geodatabase of host-parasite interactions and the curated corpus of primary sources are available for future investigations. By implementing the gold-standard of presence and absence occurrence data and utilizing open ecological datasets, our case study reveals that SDMs offer valuable insights into the patchy and often elusive distributions of parasitic species.

Session: 6796861**7020171**

23/10/25 | 10:55

Room: Valle

ORAL • EN

Monitoring biodiversity for human, animal, and environmental health

Presenter

Francis Banville

Authors**Francis Banville** (Université de Montréal • Canada)**Colin Carlson** (Yale University • United States)**Timothée Poisot** (Université de Montréal • Canada)**Abstract**

The One Health approach promotes collaboration across disciplines to enhance the health of humans, animals, and the environment. The Quadripartite organizations, which include the Food and Agriculture Organization of the United Nations (FAO), the United Nations Environment Programme (UNEP), the World Organisation for Animal Health (WOAH), and the World Health Organization (WHO), developed the One Health Joint Plan of Action (OH JPA, 2022–2026) to support countries in achieving One Health. This plan consists of six action tracks, each consisting of a set of actions and activities for implementing One Health at the local, national, regional and global levels. By requiring knowledge of zoonotic host species, two of these tracks directly concern biodiversity: action tracks 2 (reducing the risks from emerging and re-emerging zoonotic epidemics and pandemics) and 3 (controlling and eliminating endemic zoonotic, neglected tropical and vector-borne diseases). Our research examines the extent to which all six tracks are covered by the Kunming–Montreal Global Biodiversity Framework (KM-GBF) of the Convention on Biological Diversity (CBD). We assess how much the biodiversity indicators of the KM-GBF are linked to disease surveillance and the monitoring of human, animal, and environmental health, evaluating the usability of these indicators for implementing the OH JPA. We found that a large proportion of biodiversity indicators are associated with disease surveillance and public health. The relevance of the KM-GBF indicators to One Health highlights the need for shared data, policy, and governance practices between the CBD Secretariat and the Quadripartite organizations. Overall, our work aims to strengthen collaboration and coordination between these organizations by finding synergies in their goals and practices.

Session: 6796861**7013603**

23/10/25 | 11:05

Room: Valle

ORAL • EN

GBIF Task Group on Vectors of Human Disease

Presenter

Quentin Groom

Authors

Quentin Groom (MEISE BOTANIC GARDEN • Belgium)**Lindsay Campbell** (Florida Medical Entomology Laboratory, Department of Entomology & Nematology, IFAS, University of Florida • United States)**Theeraphap Chareonviriyaphap** (Department of Entomology, Faculty of Agriculture, Kasetsart University • Thailand)**Josiane Etang** (Faculty of Medicine and Pharmaceutical Sciences, University of Douala • Cameroon)**Florence Fouque** (UNICEF|UNDP|World Bank|WHO Special Programme for Research & Training in Tropical Diseases (TDR), World Health Organization • Switzerland)**Sylvie Manguin** (HSM, Université de Montpellier • France)**Dmitry Schigel** (Global Biodiversity Information Facility • Denmark)**Paloma Shimabukuro** (Fundação Oswaldo Cruz • Brazil)

Abstract

The GBIF Task Group on Vectors of Human Disease was convened in 2020 to explore how biodiversity data can better support research, surveillance, and policy on vector-borne diseases. Bringing together expertise from medical entomology, public health, ecology, and biodiversity informatics, the group aimed to assess current capabilities, identify gaps, and promote the mobilization and use of open-access data on vectors and disease.

Now in its final phase, the Task Group has delivered concrete outputs that underscore the relevance of biodiversity data to health. In collaboration with WHO-TDR and GigaScience Press, it facilitated three successful calls for data papers, resulting in the publication of over 675,000 new occurrence records on GBIF.org and more in the pipeline. These records span key vectors, including mosquitoes, sand flies, ticks, and kissing bugs, with an emphasis on underrepresented regions of Africa, Asia, and Latin America. To support long-term sustainability, the Task Group prioritized outreach and capacity building at the 20th International Congress for Tropical Medicine and Malaria, the Asia Pacific Conference on Mosquito and Vector Control in Thailand, and the West African Aedes Surveillance Network conference in Ghana. Two of these events included targeted training on vector data mobilization.

The Group also provided guidance on data standards and highlighted critical challenges, particularly around integrating species interaction data and linking biodiversity data with epidemiological and biomedical sources. These findings feed into broader efforts to align biodiversity infrastructures with global policy, including the Sustainable Development Goals, and the One Health agenda.

As the Task Group concludes its work, its legacy includes not only a richer pool of open data, but also a strengthened foundation for collaboration between the biodiversity and health communities. The need remains urgent: open, FAIR biodiversity data are essential for anticipating and responding to emerging disease risks in a rapidly changing world.

Session: 6796861

7018609

23/10/25 | 11:15

Room: Valle

ORAL • ES

Hacia una vigilancia entomológica integral: sistematización de datos sobre Triatominos (Hemiptera: Reduviidae) mediante redes científicas, colaboración interinstitucional y ciencia participativa

Presenter

Soledad Ceccarelli

Authors

Soledad Ceccarelli, María Eugenia Vicente, Agustin Balsalobre, Emiliano Bruno, Barbara Dibene, Emilia Barboza, Gerardo Marti

(Centro de Estudios Parasitológicos y de Vectores (CEPAVE - CONICET, UNLP, asociado a CIC) • Argentina)

Abstract

El Chagas es una problemática de salud socio-ambiental en la cual interviene el parásito *Trypanosoma cruzi* (Kinetoplastida, Trypanosomatidae) como agente etiológico. Si bien existen otras vías de transmisión (vertical, por transfusiones de sangre o trasplantes de algunos órganos, y a través de alimentos y/o bebidas contaminados), este parásito se transmite principalmente a través de la materia fecal de Triatominos (Hemiptera: Reduviidae). A todas las especies de triatominos se las considera como vectores potenciales; por lo tanto, su distribución geográfica e información ecológica complementaria deben ser una guía fundamental para los programas de vigilancia y control del Chagas. Actualmente, hay alrededor de 150 especies descritas; más de 130 se distribuyen en las Américas (17 con registros en Argentina) y 16 especies entre África, Asia y Oceanía.

En esta oportunidad, se presenta un relato de experiencia del proceso de integración de datos sobre triatominos producto de revisiones exhaustivas de información pública, combinado con una importante colaboración interinstitucional con entidades gubernamentales y científicas. Además, se suma el aporte de datos proveniente de un proyecto enmarcado en la ciencia participativa (GeoVin) que utiliza una aplicación para dispositivos móviles como herramienta principal de reporte y articula con entidades de Salud.

Como resultado de esta integración de información, contamos con conjuntos de datos (+35000 registros), que representan tanto la biodiversidad de triatominos asociados a la problemática de Chagas en América, como también de aquellas especies presente en regiones que podrían convertirse en una problemática emergente (ej. sudeste asiático).

Consideramos que esta experiencia colaborativa para la integración de datos contribuye, no solo a mejorar el conocimiento sobre la biodiversidad de las especies de triatominos a nivel mundial, sino también al diseño de mejores estrategias para la promoción de la salud y el control de estos vectores por parte de los sistemas de vigilancia nacionales y regionales.

Session: 6796861**7013119**

23/10/25 | 11:25

Room: Valle

ORAL • EN

Biodiversity science and biosurveillance are fellow travelers

Presenter

Timothée Poisot

Authors

Timothée Poisot (Université de Montréal • Canada)

Abstract

The One Health approach sees advances in the health of ecosystems, humans, plants, and animals as mutually beneficial. In recent years, the One Health community has been calling for more integration of environmental expertise in what was traditionally a veterinary medicine–dominated field. In parallel, the field of biodiversity monitoring has made substantial progress, in response to both a mounting biodiversity crisis and the adoption of the Kunming–Montréal Global Biodiversity Framework (which focuses on integrating monitoring of biodiversity as a core component of our global ability to take evidence-driven policy decisions). Therefore, a tight integration between the fields of biodiversity monitoring and biosurveillance is not only achievable, but also mutually beneficial. In this presentation, I will review important lessons learned in establishing the Kunming–Montréal Global Biodiversity Framework, and how they directly translate to the surveillance of zoonotic diseases. I frame these advances in terms of concrete steps that can be taken to further integrate the two fields.

Session: 6796861**7020855**

23/10/25 | 11:35

Room: Valle

LIGHTNING TALK VIRTUAL • EN

WDDS: A Data Standard for Integrated Host-Pathogen Biodiversity Monitoring

Presenter

Collin Schwantes

Authors

Collin Schwantes (Yale University • United States)

Abstract

Biodiversity monitoring data are critical to our understanding of host-pathogen interactions and ability to respond to outbreaks of novel disease in humans, animals, or plants. The domains of micro- and macro-biodiversity data have separate, mature data repositories with robust and commonly used data standards. However, when a researcher has to link those domains to better understand disease dynamics, there is a paucity of unifying frameworks. The Wildlife Disease Data Standard (WDDS) brings those mature systems together in a user friendly and extensible format. Designed by a diverse set of members of the Verena Institute, the data attributes in WDDS draw on the mature data standards from each domain (e.g. Genbank, Darwin Core) to place equal emphasis on micro- and macro-biodiversity data attributes, as well as reporting of both presence and absence of a host-pathogen relationship. This combination facilitates the creation of FAIR data sets with high utility for practitioners across the One Health spectrum.

Session: 6796861**7014643**

23/10/25 | 11:40

Room: Valle

ORAL VIRTUAL • EN

Why Taxonomic Splits Matter for Bat Biodiversity and Viral Risk Analyses

Presenter

Nathan Upham

Authors

Nathan Upham (Arizona State University • United States)

Aja Sherman (Bat Eco-Interaction Project • United States)

Nancy Simmons (American Museum of Natural History, • United States)

Kendra Phelps (Veterinary and Biomedical Sciences, University of Minnesota • United States)

Anna Willoughby (Odum School of Ecology, University of Georgia • United States)

Quentin Groom (Meise Botanic Garden • Belgium)

Donat Agosti (Plazi • Switzerland)

DeeAnn Reeder (Department of Biology, Bucknell University • United States)

Jorrit Poelen (Ronin Institute for Independent Scholarship • United States)

Connor Burgin (Department of Biology, University of New Mexico • United States)

Abstract

Taxonomy is generally viewed as external to ecology, a fixed framework rather than a variable that needs tuning to understand its impact on inferences. However, since taxonomy is a human-imposed perspective rather than something innate, biodiversity scientists have the responsibility to quantify its impact on derived knowledge. Here we study how the 35% increase in recognized bat species (Chiroptera) since 1993 has impacted our knowledge of bat-virus interactions and, in turn, inferences of viral spillover risk to humans. We focus on change in the geographic concepts of bat species globally due to taxonomic splits between two periods: (i) 2008-2020 using IUCN range maps (based on Mammal Species of the World, 3rd edition) relative to Mammal Diversity Database (MDD) v1.2 range maps; and (ii) 2020- 2023 comparing MDD v1.2 to newly produced v1.11 maps. We then intersect these conceptual changes with known bat-virus interactions from databases to assess their impact upon risks of cross-species viral transmission. We find that taxonomic splits affected 248 bat species across both periods (185 and 63 species, respectively), which has impacted 16.9% of currently recognized bat species globally. Those taxonomic splits have rendered ambiguous 3,249 bat-virus interactions – 21.9% of all digitally known observations – since these data are indexed by host species name rather than observation location, which leads to ambiguity when species are split. We discuss high-throughput solutions for accurately translating the taxonomy of these data, and the impact of inaction upon estimates of viral spillover risk.

Session: 6796861**7020181**

23/10/25 | 11:50

Room: Valle

ORAL • EN

A community-of-practice-built database to globally support the integration, management, and sharing of wildlife health surveillance data

Presenter

Luz Dary Acevedo Cendales

Authors

Diego Montecino Latorre (Wildlife Conservation Society • United States)

Mathieu Pruvot (Wildlife Conservation Society • United States)

Paloma H F Shimabukuro (Brazil)

Christopher M Barker (United States)

Steve Gallo (Wildlife Conservation Society • United States)

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Suzan J Kutz (University of Calgary • Canada)

Claire Cayol (World Organisation of Animal Health • France)

Fernanda Dorea (Italy)

Sarah H Olson (United States)

Liz P Noguera Zayas (University of Calgary • Canada)

Abstract

Wildlife health (WH) surveillance systems rely on highly diverse data collected by multiple actors using varied methodologies. This leads to scattered and inconsistently structured information that lacks a standardized vocabulary. Additionally, the security and safety of WH data are usually poor. Consequently, WH data are lost, not usable, and their integration and sharing are inefficient or unfeasible. These limitations weaken comprehensive health risk assessments, restrict the integration of the environmental sector into One Health systems, and reduce the effectiveness of responses to environmental, animal, and human health crises.

Well-designed databases are essential to addressing these challenges. Yet, access to comprehensive databases remains a significant barrier in WH surveillance. Existing platforms are often private, costly, limited in scope, or accessibility, whilst underfunding of WH surveillance hampers the development of digital infrastructure.

To address this gap, Wildlife Conservation Society is leading the development of a WH surveillance purpose-built database with a comprehensive hierarchical data structure designed by a globally distributed and diverse group of experts (the Wildlife Health Intelligence Network). The database can harmonize and centralize diverse data from multiple sources, keep data secured in the long-term, and facilitate accessibility and sharing to selected receivers. Interoperability with platforms holding WH surveillance data (e.g., dead animal reported in iNaturalist) or interested on these data for monitoring purposes (e.g., parasites into GBIF) will be supported, allowing on-the-fly WH data integration and ensure participation of stakeholders in WH surveillance by continuing the use of their preferred systems (e.g., rangers using SMART Mobile).

Conceived as a global public good, the database proposes a collaborative model driven by continuous user feedback and shared maintenance costs, while protecting data safety and ownership through strict compartmentalization within and among organizations. Scheduled for 2025, the database is coming to fill a longstanding gap in the management of WH surveillance data.

Session: 6796861**7020665**

23/10/25 | 12:00

Room: Valle

LIGHTNING TALK VIRTUAL • EN

Targeted biodiversity conservation and habitat restoration to prevent the next pandemic

Presenter

Leonardo Teixeira Viotti

Authors

Leonardo Teixeira Viotti (University of Pittsburgh • United States)

Rachael Kramp (United States)

Garo Batmanian (Brazil)

Franck Berthe (Senegal)

Diego Herrera (United States)

Abstract

Diseases originating from wildlife pose a significant threat to global health, leading to substantial human and economic losses each year. Biodiversity plays a dual role: it serves both as a reservoir for infectious diseases and as a barrier to their transmission to humans.

Considerable evidence suggests that healthy ecosystems can reduce the likelihood of zoonotic spillover events—either by decreasing human-wildlife contact, making transmission less likely, or both. However, disease prevention has largely been neglected in conservation and restoration efforts. A significant constraint is the lack of reliable, spatially explicit information on where to effectively direct these efforts. Given the increasing rate of new disease emergence in recent decades—accelerated by climate change and biodiversity loss—identifying priority areas for mitigating the risk of disease transmission has never been more urgent. We present a methodology to pinpoint areas for targeted ecological countermeasures that reduce the likelihood of zoonotic spillover. Our approach compiles data on well-documented risk factors, protection status, restoration potential, and costs to map areas with high cost-effective intervention potential. The resulting high-resolution (1 km) layers, covering tropical regions globally, are freely available alongside an interactive no-code platform that allows users to adjust parameters to identify priority areas at multiple scales. We identify 191,000 km² in 56 countries of disturbed areas with elevated spillover risk and high restoration potential, and 300,000 km² of unprotected, standing forest under threat with elevated risk of future zoonotic spillover. Our preliminary cost analysis suggests that these efforts combined could cost as little as 1/35th of the damage caused by zoonotic diseases annually. Ecological countermeasures can be a cost-effective strategy for reducing the emergence of new pathogens, however, our study shows the extent to which conservation efforts currently fall short of this goal.

Session

6960773-5

Symposium

23/10/25 | 10:45

Room: Cauca

Applied Research & Policy Integration: Conservation Applications (Contributed Oral Presentations)

Organizers

Andre Zerger

Francisco Pando

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-5**7020526**

23/10/25 | 10:45

Room: Cauca

ORAL • ES

Aportar a la biodiversidad desde los datos abiertos en estudios de impacto ambiental

Presenter

Laura María Ramírez Hernández

Authors

Laura María Ramírez Hernández (INERCO Consultoría Colombia • Colombia)

Roberto Cárdenas Grajales (INERCO Consultoría Colombia • Colombia)

Abstract

La información recolectada en líneas base de estudios de impacto ambiental cuenta con un potencial superior al del cumplimiento normativo, gracias a que las empresas del sector privado recolectan datos de lugares en los cuales no se cuenta con información de biodiversidad. Por lo tanto, una línea base de sectores como el minero-energético, de infraestructura, hidrocarburos, entre otros, puede aportar información primaria de flora, especies vasculares (bromelias y orquídeas) y no vasculares (antocerotales, briofitos y líquenes) de hábito epífito y otros hábitos, así como fauna (aves, mamíferos, reptiles y anfibios) y comunidades acuáticas (fitoplancton, zooplancton, perifiton, macroinvertebrados bentónicos, macrófitas e ictiofauna). Por ejemplo, Inerco Consultoría Colombia ha participado en la elaboración y publicación de seis conjuntos de datos, que a mayo de 2025, han sido citados 1.361 veces, en artículos científicos, secciones de libros, reportes y tesis, que se centran en temas como ecología (27,7%), conservación (18,81%), cambio climático (17,63%), especies invasoras (12,93%) y, en menor proporción, en estudios de evolución, biogeografía, ciencia ciudadana, taxonomía, filogenética, servicios ecosistémicos, salud humana, entre otros, con un crecimiento exponencial en el número de citas año a año. Se evidencia que los datos de biodiversidad de las empresas, en la medida en que son abiertos, no solo aportan al conocimiento de la biodiversidad, sino que dicha información puede ser de utilidad en diferentes aspectos como la formulación y validación de medidas de manejo y planes de compensación, selección de especies carismáticas para trabajos con comunidades, verificación de ganancias netas de biodiversidad, verificación de determinantes ambientales, modelos de distribuciones de especies, entre otros.

Session: 6960773-5

7020837

23/10/25 | 10:55

Room: Cauca

ORAL • ES

Modelamiento de distribución de *Chinchilla chinchilla* en el desierto de Atacama mediante algoritmos de aprendizaje supervisado

Presenter

Stephanie Orellana Bello

Authors

Francisca Muñoz Narbona (Cienciambiental • Chile)

Álvaro Ly (Cienciambiental • Chile)

Valentina Romero (Cienciambiental • Chile)

Rodrigo Ibaceta (Cienciambiental • Chile)

Marcela Torres-Gómez (Cienciambiental • Chile)

Darío Moreira (Cienciambiental • Chile)

Antonio Tironi (Cienciambiental • Chile)

Alex Oporto (Cienciambiental • Chile)

Sergio Moraga (Cienciambiental • Chile)

Stephanie Orellana Bello (Cienciambiental • Chile)

Abstract

La Chinchilla (*Chinchilla chinchilla*), especie endémica en estado de amenaza, habita sectores áridos y rocosos del norte de Chile.

Este estudio modela su distribución potencial en una zona del desierto de Atacama, utilizando técnicas de aprendizaje supervisado implementadas en el paquete biomod2 de R. Se emplearon registros de presencia y ausencia recopilados por la organización entre los años 2022 y 2025, distinguiendo entre observaciones directas (visuales, cámaras trampa) e indirectas (fecas, madrigueras, reportes locales). Para reflejar el distinto nivel de certeza, se aplicó una estrategia de ponderación que replicó los registros directos, aumentando su peso en la calibración del modelo.

Las variables ambientales utilizadas abarcan dimensiones climáticas, edáficas, topográficas y satelitales. Su selección fue guiada por análisis multivariado (PCA), validación en terreno y literatura especializada. Todas las capas fueron armonizadas espacialmente a una resolución de 30 metros.

Se entrenaron tres algoritmos (GLM, MaxEnt y Random Forest) con validación cruzada aleatoria. A partir de los modelos con TSS = 0.7, se generó un modelo ensamblado mediante EMmedian, alcanzando un desempeño robusto (TSS = 0.868, ROC = 0.983, Kappa = 0.867). Los mapas de aptitud ambiental obtenidos, en formato continuo y discretizado, identifican áreas clave para la conservación.

Actualmente, este modelamiento se encuentra en proceso de perfeccionamiento, incorporando nuevas especies con distribución potencialmente complementaria o competitiva, como *Lagidium viscacia* y *Adesmia atacamensis*. Esta ampliación busca enriquecer el análisis ecológico del paisaje y fortalecer las bases para la gestión territorial.

El trabajo demuestra el valor de combinar evidencia local, ponderación informada y métodos reproducibles para modelar especies de difícil detección en ecosistemas extremos como el desierto de Atacama.

Session: **6960773-5****7020490**

23/10/25 | 11:05

Room: Cauca

ORAL • EN

Open data for conservation: identifying ecological corridors for threatened species along a fragmented landscape

Presenter

Nestor Galindo-Ruiz

Authors

Nestor Galindo-Ruiz (Terrasos S.A.S. • Colombia)

Felipe Diaz Salazar (Terrasos S.A.S. • Colombia)

Abstract

The Colombian biogeographic Chocó harbors severely transformed ecosystems and threatened species. Identifying areas for their conservation is a priority to prevent species population declines and the expansion of agricultural frontiers. In this context, the use of Open Data has become a key tool to support decision making when aiming for biodiversity conservation. This analysis presents how open-access data from GBIF was used to implement structural connectivity models aimed at identifying areas within the distribution of threatened species that could benefit from targeted conservation actions. We used occurrence records for three species cataloged under IUCN threat status: Colombian spider monkey (*Ateles fusciceps*), Cotton-headed tamarin (*Saguinus oedipus*), and the Sapphire-bellied hummingbird (*Chrysuronia lilliae*). For the connectivity models we employed the CircuitScape tool integrated with ArcMap, along with GBIF records

(2010-2025), land use covers from CORINE Land Cover (IDEAM, 2022), and available literature about species' biology and behavior. With these inputs, we evaluated which areas within the potential distribution of the species are most likely to support their presence and where the implementation of ecological corridors would be most beneficial. Additionally, we highlight that forest fragmentation has led to isolated population patches, limiting key ecological processes such as gene flow and local dispersal. Our results suggest that the three species face anthropogenic barriers (e.g., agricultural lands and urban areas) that increase resistance to movement across their range. We propose specific ecological corridors for each species, which could significantly improve connectivity if conservation strategies are implemented along these routes. These findings underscore the value of integrating open data into biodiversity conservation planning.

Session: **6960773-5****7015832**

23/10/25 | 11:15

Room: Cauca

ORAL • EN

Data-driven restoration: Mexico's national information system, SNIRA

Presenter

Patricia Koleff

Authors

Patricia Koleff (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO) • Mexico)**Victoria Contreras Ruiz** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad • Mexico)**Diego Yafte Hernández Avalos** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)**Wolke Tobón Niedfeldt** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)**Tania Urquiza-Haas** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)

Abstract

Achieving the ecosystem restoration targets outlined in the Global Biodiversity Framework Kunming-Montreal, particularly Target 2 on restoring 30% of degraded ecosystems, requires not only ambitious action but also robust data and information systems to guide restoration efforts. In Mexico, a megadiverse country facing rapid land-use change and biodiversity loss in all environments, the availability and integration of biodiversity data have become essential for prioritizing and orienting restoration interventions.

This presentation showcases the development and application of the National Information System on Environmental Restoration (SNIRA), a pioneering platform led by CONABIO. SNIRA integrates and standardizes data from more than 1,300 restoration initiatives across the country, providing a synthetic overview addressing fundamental questions, such as who is involved, when and where actions are being implemented, what are the main objectives and barriers for implementation of restoration practices. SNIRA is also connected to Mexico's National Biodiversity Information System (SNIB), which is linked to GBIF and aligned with FAIR data principles, to identify the species used or monitored in restoration projects.

The SNIRA platform also includes a geospatial tool to enable the visualization of restoration projects across Mexico, integrating data on biodiversity, including forecasts of the potential distribution of restoration-relevant species under climate change scenarios to support evidence-based planning and future actions. The geospatial tool will provide a general picture of restoration progress by linking socioecological and spatiotemporal information in a single platform. SNIRA is an open-access platform with the potential to interoperate with other national and international systems, making it a strategic tool to support monitoring and reporting on the targets of the Kunming-Montreal Global Biodiversity Framework.

Session: 6960773-5**7014654**

23/10/25 | 11:25

Room: Cauca

ORAL • EN

Application of Wise Ancestors model in Antioquia : Co-development of conservation projects for the protection of biodiversity

Presenter

Katie Jones

Authors

Katie Jones (Wise Ancestors • United States)

Solenne Correard (Wise Ancestors • United States)

Mailyn Adriana González Herrera (Instituto Humboldt • Colombia)

Gustavo Bravo (Instituto Humboldt • Colombia)

Abstract

Guided by local knowledge from the Paisa communities of Antioquia, researchers with the Alexander von Humboldt Biological Resources Research Institute and the Montañerito Paisa Conservation Initiative, led by NGO Neotropical Innovation, are partnering with Wise Ancestors to generate genomic data for the critically endangered Antioquia Brushfinch (*Atlapetes blancae*), known in Spanish as the “Montañerito Paisa,” and an enigmatic antpitta in the genus *Grallaria*.

Wise Ancestors, a non-profit organization affiliated with the Earth Biogenome Project, operates by braiding biotechnology, Indigenous science, and Traditional Ecological Knowledge to conserve biodiversity. Its model relies on a decentralized and collaborative system, where projects are co-developed with local scientists and/or Indigenous Peoples and Local Communities (IPs & LCs) before being posted to an online platform (<https://platform.wiseancestors.org/>). There, collaborators who can perform the technical work (labs, sequencing facilities, biobanks, etc) are recruited and work together to complete Conservation Challenges.

The set of Antioquia Conservation Challenges will lead to the generation of annotated reference genomes for the two birds, as well as population genomic studies and diet studies fostering a holistic approach to conservation that strengthens local conservation efforts and enables future studies. Central to Wise Ancestors model is the inclusion of funds for a local initiative, in this case, it is the Antioquia Biomonitoring Program. This program supports a network of local experts providing training on sampling techniques, taxonomic identification, genomic technologies, biodiversity monitoring and propagation of key food resources for the focal species offering western scientific tools and resources that complement local knowledge and stewardship practices for effective habitat conservation in this critical biodiversity hotspot.

Session: 6960773-5**7020979**

23/10/25 | 11:35

Room: Cauca

LIGHTNING TALK • EN

Fungal Biodiversity in the Caatinga: Spatial Analysis, Data Gaps, and Conservation Priorities

Presenter

Taimy Cantillo

Authors

Taimy Cantillo (Universidade Estadual de Feira de Santana • Brazil)

Luís F.P. Gusmão (Universidade Estadual de Feira de Santana • Brazil)

Abstract

The Caatinga biome hosts a significant but underestimated portion of Brazil's biodiversity. However, biodiversity data for this region remain fragmented and inconsistent, especially for fungi. This study aims to identify spatial knowledge gaps and inform conservation strategies using publicly available data. We focused on fungal records from the Global Biodiversity Information Facility (GBIF), filtered within Caatinga boundaries using RStudio and QGIS. After removing duplicates and incomplete entries, we obtained 4,104 records comprising Ascomycota (2,892 species across 281 families), Basidiomycota (1,137 species across 127 families), Glomeromycota (44 species), and basal fungi (31 species). Lichenized fungi and wood saprobes were the most frequently represented ecological groups.

Our spatial analysis revealed a strong collection bias, with most records concentrated in areas surveyed by the previous PPBio Semiárido initiative (2010–2014). Notably, the absence of precise geographic coordinates and standardized metadata in many records hampers their usefulness for monitoring and conservation. No species in the dataset were associated with an IUCN threat category.

We recommend prioritizing underrepresented regions and taxa in future fieldwork, increasing the involvement of specialists in poorly studied groups, and adopting the Darwin Core Archive (DwC-A) standard for in situ specimen collection. Integrating morphological and molecular data is essential to improve taxonomic resolution. We also advocate for conserving areas with high fungal diversity and propose the development of a user-friendly tool for capturing coordinates, metadata, and specimen images. This tool will be accompanied by basic training to empower local communities to contribute to biodiversity data collection and conservation, initially, mostly focused on macromycetes.

Session: 6960773-5**7019964**

23/10/25 | 11:40

Room: Cauca

LIGHTNING TALK • EN

Hidden in the Data: Unlocking the Potential of Brazil's Sociobiodiversity for a Sustainable Bioeconomy

Presenter

Ana Carolina Mendes dos Santos

Author

Ana Carolina Mendes dos Santos (Universidade Federal de Minas Gerais - Brazil)

Sonia Maria Carvalho (Universidade Federal de Minas Gerais - Brazil)

Abstract

Brazil harbors the greatest biodiversity on the planet and holds extraordinary potential for developing a sustainable, sociobiodiversity-based bioeconomy. This concept has been emerging as a way to integrate traditional knowledge on the use of native species from Brazilian biodiversity into the broader bioeconomy agenda. However, the potential remains largely untapped due to the lack of official data on existing value chains for native species, where at the municipal level the data gap is even more alarming. Despite growing academic and political interest in sociobiodiversity, there is no systematic monitoring of its use, production, or market flows. This study analyzes secondary data from official government sources (IBGE, SisGen, Conab) and compares them with field data collected in the northern region of Minas Gerais to assess how sociobiodiversity data is currently applied – and neglected – in supporting public policies for the bioeconomy. Our findings reveal that, among the 18 native species collected by agroextractivists in the region and the 25 native species most frequently accessed for research and technological development, only 4 have official production data (umbu, mangaba, pequi, and buriti), and 5 of them (including macaúba) are covered by public procurement policies. Even pequi, the main extractive product of the Cerrado biome and one with the most consolidated value chains, is officially registered in only 36% of the municipalities where its production occurs—and in 4 of the top-producing municipalities, there are significant discrepancies between official records and actual production. Our research highlights the need for public policies investing in territorialized data systems and strengthen local monitoring capacities. Doing so is not only a matter of improving data quality, but of enabling informed decision-making, equitable benefit-sharing, and the design of place-based policies for conservation, development, and resilience.

Session: 6960773-5

7020389

23/10/25 | 11:45

Room: Cauca

ORAL • EN

The FUNACTION project: pioneering aquatic fungi conservation

Presenter

Isabel Fernandes

Authors

Isabel Fernandes (Institute of Microbiology, University of Applied Sciences and Arts of Southern Switzerland (SUPSI) • Switzerland)

Andreas Bruder (Institute of Microbiology, University of Applied Sciences and Arts of Southern Switzerland (SUPSI) • Switzerland)

Abstract

Freshwater habitats support rich biodiversity and essential ecological services. Huge efforts to document and protect biodiversity are underway across Europe (e.g. EU Biodiversity Strategy for 2030, European Green Deal, Nature Restoration Regulation). However, aquatic fungi (AF), which are ecologically diverse organisms (decomposers, endophytes, symbionts, predators, parasites, pathogens) ensuring the health, function, and resilience of aquatic ecosystems, have been entirely neglected in all major conservation plans and policies. The FUNACTION project, supported by the Biodiversa+ EU Biodiversity Partnership, is addressing this gap by building the first comprehensive knowledge base on the taxonomic, phylogenetic, and functional diversity of AF at a pan-European scale. Its objectives are to: 1) produce data essential for AF-aware conservation, 2) co-develop monitoring and planning tools with stakeholders, and 3) raise awareness of AF's diversity and ecological roles. By combining eDNA metabarcoding and metagenomics with measures of ecosystem functioning (e.g., organic matter decomposition) and extensive metadata from a pan-European sampling campaign, FUNACTION is mapping and modeling AF biodiversity and their functions in relation to environmental and human pressures. A key question we aim to address is whether existing protected areas effectively conserve AF biodiversity and AF-driven ecosystem functioning. Already, ca. 300 sites have been sampled, across 9 case studies from 6 countries ranging from the Mediterranean to the Arctic. More than 2500 samples have been collected for eDNA, water chemistry and ecosystem functioning. To date, FUNACTION has also introduced hundreds of stakeholders to the importance of AF, established an IUCN Species Survival Commission Aquatic Fungi Specialist Group, and begun training the next generation of scientists and conservationists. By integrating science and policy, FUNACTION aims to embed AF into conservation practice—ensuring the protection of these critical yet neglected components of freshwater biodiversity.

Session: 6960773-5

7016001

23/10/25 | 11:55

Room: Cauca

ORAL • ES

Contribución del Jardín Botánico José Celestino Mutis al conocimiento sobre biodiversidad urbana y su aplicación en restauración ecológica y conservación

Presenter

Johanna Velásquez

Authors

Johanna Velásquez (Jardín Botánico de Bogotá José Celestino Mutis • Colombia)

Abstract

El Jardín Botánico José Celestino Mutis (JBB), como centro de investigación científica, desempeña un papel fundamental en la generación de conocimiento sobre biodiversidad urbana. Su misión lo posiciona como un referente nacional en botánica y ecología urbana, con una contribución significativa a la comprensión de la biodiversidad en entornos transformados. En los últimos cinco años, el JBB ha publicado más de 126.000 datos abiertos, lo que representa cerca del 50 % de la información disponible para Bogotá Distrito Capital, en el nodo nacional SiB Colombia.

El reconocimiento a su labor como proveedor de datos ha sido visible en diferentes escenarios: la inclusión de una imagen del JBB en la portada de GBIF en julio de 2024; su mención en los destacados del SiB Colombia en noviembre del mismo año; y su ubicación en la posición 21 del ranking de publicadores con mayor número de registros compartidos para el nodo Colombia.

Estos datos abiertos no solo enriquecen los repositorios globales, sino que también han sido fundamentales para orientar estrategias de restauración ecológica y conservación de la biodiversidad, tanto *in situ* como *ex situ*. El uso de esta información ha permitido identificar conectividades e interacciones ecológicas, modelar dinámicas de transformación del paisaje urbano y diseñar intervenciones basadas en evidencia para el restablecimiento de funciones y estructuras ecológicas.

La experiencia del JBB demuestra el valor de los datos vivos como insumos para la gestión adaptativa de la biodiversidad urbana y resalta el potencial de los jardines botánicos como actores estratégicos en la articulación entre ciencia, política pública y acción local frente al cambio global.

Session: **6960773-5****7019981**

23/10/25 | 12:05

Room: Cauca

ORAL • EN

A FAIR and Open approach for the study and integrated management of Invasive Alien Species in Italy

Presenter

Cristina Di Muri

Authors

Cristina Di Muri (National Research Council of Italy (CNR), Research Institute on Terrestrial Ecosystems (IRET) • Italy)**Ernesto Azzurro** (National Research Council of Italy (CNR), Institute for Marine Biological Resources and Biotechnology (IRBIM) • Italy)**Pierluigi Strafella** (National Research Council of Italy (CNR), Institute for Marine Biological Resources and Biotechnology (IRBIM) • Italy)**Ilaria Rosati** (National Research Council of Italy (CNR), Research Institute on Terrestrial Ecosystems (IRET) • Italy)

Abstract

The adoption of FAIR (Findable, Accessible, Interoperable, Reusable) principles and Open Science practices greatly enhance data integration and reuse of multi-disciplinary research products obtained by different monitoring approaches and data collection methods.

The opportunity to test the advantages provided by the implementation of FAIR and Open Science practices within a multi-disciplinary, multi-ecosystem, and multi-taxonomic context was provided by the USEit project.

USEit focuses on the study of Invasive Alien Species (IAS) in Italy and combine expertise from scientists studying IAS in different ecosystems (aquatic and terrestrial) by finding synergies across different data collection methods, ultimately, outlining operational and technical guidelines suitable for adoption within and beyond the project.

The operational guidelines for IAS data collection were developed following a structured, multi-step process. Initially, they were informed by an analysis of responses to a national survey. This was followed by a structured discussion involving 90 national experts on biological invasions. The resulting guidelines were then quantitatively evaluated using a SWOT analysis.

In addition, technical guidelines on IAS data management were defined collaboratively and shared within a Data Management Plan describing standards and schemas used for a diverse array of (meta) data (*i.e.*, occurrences, stable isotopes, elemental composition, remote sensing, DNA metabarcoding, citizen science, acoustic telemetry).

Overall, data, services and related metadata are published into canonical repositories and/or available within the LifeWatch Italy Data Portal and Metadata Catalogue. All research products are assigned with persistent identifiers, described by clear metadata and enriched with controlled vocabularies to enable a facilitated interpretation, reuse and interoperation of products and their outcomes.

These results could more readily be used to develop practical solutions for managing IAS, demonstrating how the adoption of community- shared FAIR practices in multi-disciplinary contexts can lead to an improved capacity to manage natural resources and create novel opportunities for growth.

Session: 6960773-5**7020848**

23/10/25 | 12:15

Room: Cauca

ORAL • EN

Enhancing Impact Assessments and Early Detection of Invasive Alien Species through Georeferenced Data and International Cooperation

Presenter

Ane Marlene Myhre

Authors

Ane Marlene Myhre (Norwegian Biodiversity Information Centre • Norway)**Olga Hilmo** (Norwegian Biodiversity Information Centre • Norway)

Abstract

The transportation and introduction of alien species by human activities are causing the number of invasive alien species (IAS) worldwide to rise alarmingly fast. At the same time, preventing introductions and responding rapidly are key factors for successful management. In Norway, the Norwegian Biodiversity Information Centre (NBIC) holds the national mandate to assess the negative ecological impact of alien species on nature and evaluate their introduction pathways. The species evaluated range from the well-established and expanding IAS to species that haven't crossed the Norwegian border yet.

Georeferenced data is a central piece to the puzzle. They support key assessment parameters such as species viability and expansion speed, helps evaluate species distribution and ecosystem affiliation and plays an important role in the process of horizon scanning. A primary source for georeferenced data is Norway's Species Map Service, which is jointly developed by the NBIC and GBIF Norway. At present, it contains more than 800 000 records of over 1 600 assessed alien species and subspecies. Data generated through impact assessments are fed back into the Species Map Service, continuously improving data quality and making the platform an essential tool for national management agencies and policymakers. Furthermore, checklist data from the assessments are shared through GBIF, expanding accessibility for international audience.

In line with international and national guidelines, NBIC is increasingly focusing on IAS that are still abroad or recently introduced. However, gathering information on IAS from neighbouring countries can be challenging. We believe that a stronger international cooperation would help preventing introductions of IAS, facilitate early detection and rapid response, as well as increase the knowledge base on the little-known invasive alien species.

Session: 6960773-5**7014928**

23/10/25 | 12:25

Room: Cauca

ORAL • EN

Horizon scanning for future potential non-native species at a biome scale

Presenter

James Speed

Authors

James Speed (Norwegian University of Science and Technology • Norway)**Tor Henrik Ulsted** (Norwegian University of Science and Technology • Norway)**Wayne Dawson** (University of Liverpool • United Kingdom)**Kristine Westergaard** (Norwegian University of Science and Technology • Norway)

Abstract

Invasive species can cause substantial disruption to ecological communities and ecosystems. The terrestrial Arctic has to date avoided the worst impacts from non-native species. However, increasing human activity raises the potential for introductions, and a warming climate increases the likelihood of establishment of more species. These processes make the development of a risk list of potential non-native species in the Arctic a priority.

In this study we develop a data-based horizon scanning approach for identifying potential non-native species across the terrestrial Arctic. We integrate the Global Naturalizing Flora database with species occurrence records from GBIF to identify suitable climate for naturalizing plant species currently absent from the Arctic. We use hypervolume analyses to identify species which have suitable climate that overlaps with the climate space within the Arctic.

We identify a total of 2554 potential non-native species that have the climatic potential to establish in the Arctic. Hotspots of potential species richness are found in Alaska and Greenland. We identified source regions for potential non-native species, with species with current ranges at higher absolute latitude found to have a greater climate overlap. Our horizon scan, leaning on GBIF data, produces regionally-targeted lists of species with establishment potential, which should be of value for environmental management across the vulnerable Arctic.

Session: 6960773-5

7016108

23/10/25 | 12:35

Room: Cauca

LIGHTNING TALK • ES

Uso de datos abiertos para la actualización Plan Nacional de especies exóticas, trasplantadas e invasoras de Colombia

Presenter

Ángela María Bedoya Blandón

Authors

Carolina Avella (Ministerio de Ambiente y Desarrollo Sostenible • Colombia)

Dairo Escobar (ANDI • Colombia)

Ángela María Bedoya Blandón (Ministerio de Ambiente y Desarrollo Sostenible • Colombia)

Federico Mosquera (Colombia)

Adrian Vasquez (Colombia)

Paula Sanchez (Colombia)

Abstract

A nivel global se han identificado cinco motores de transformación y pérdida de la biodiversidad, entre los que se encuentran las invasiones biológicas. Esta amenaza a la biodiversidad es retomada por el Marco Mundial de Biodiversidad que para el 2030, en su Meta 6, se ha propuesto eliminar, minimizar o reducir las especies exóticas invasoras o mitigar sus impactos en la biodiversidad y los servicios ecosistémicos. Desde 1978 Colombia ha venido abordando el tema de las especies exóticas, buscando mitigar el impacto ambiental, social y económico. En 2011 se publicó el Plan nacional para la prevención, control y manejo de las especies introducidas, trasplantadas e invasoras que incluyó el listado de especies continentales (terrestres y acuáticas) y marinas y costeras con 355 registros. El ejercicio de actualización de este instrumento en su etapa diagnóstica ha identificado 1.974 taxones que son registrados como exóticos, exóticos potencialmente invasores y exóticos invasores en el territorio colombiano. El proceso de consolidación incluyó la revisión de los registros del Sistema de Información sobre Biodiversidad de Colombia - SiB Colombia, instancia que integra los datos abiertos de diversos publicadores, incluidas grandes plataformas como GBIF, OBIS, iNaturalist, eBird, Xenocanto, SiBM, así como redes nacionales temáticas como invBasa. La información consolidada indica que el 97 % de los taxones se encuentran a nivel de especie y el 3 % a nivel de género, subespecie, variedad y forma. El mayor número de taxones exóticos se encuentra en la región Andina, seguido por las regiones Pacífico, Caribe, Orinoquía, Amazonía e insular, respectivamente. Las plantas son el grupo taxonómico con más especies exóticas registradas, seguidas por los peces. La siguiente etapa del ejercicio es depurar la información con los expertos de los grupos taxonómicos y consolidar una versión de referencia oficial que pueda ser publicada y actualizada a través del tiempo.

Session

6798859

Symposium

23/10/25 | 14:00

Room: Ballroom A

Advancing Sustainable Geo- and Biodiversity infrastructures, communities, and ideas

Organizers

Chuck Cook

Libby Ellwood

Vincent S. Smith

Yvan Le Bras

Anton Güntsch

Tanja Weibulat

David Fichtmueller

Ely Wallis

Jutta Buschbom

Gil Nelson

Deborah Paul

James Macklin

Nicky Nicolson

Description

Geo- and bio-diversity science communities have grown rapidly over recent decades, served by large, interconnected open data infrastructures. These have largely been supported by short- to mid-term funding streams intended to promote innovation, but long-term support is required to ensure continuity of service for users and society. Innovation is important, but the priorities are to maintain data holdings and software; keep communities active; provide outreach and training; and retain staff. Managers of data resources struggle to address these priorities while navigating funding uncertainties—they need long-term strategies that recognize maintaining infrastructures as a primary goal.

This challenge is particularly acute for the thousands of interconnected biodata resources that life scientists depend on, including National Biodiversity Data Infrastructures (NBDIs) that serve crucial roles connecting local efforts to global initiatives. Despite their importance, funding and relevant networks remain fragmented, limiting the ability to make long-term plans and respond to emerging opportunities and new ways of working.

As a global community, how can we build resilience? Can we join forces to streamline efforts and share funding to meet common goals? How does working across political, project, and domain boundaries help to keep us informed and improve our chances of success? What can we learn from the ten key roles recently defined for NBDIs (<https://doi.org/10.1093/biosci/biae109>) to strengthen cooperation at both technical and organizational levels?

Join representatives from the Global Biodata Coalition, International Partners for the Digital Extended Specimen, and various NBDIs as we think creatively about sustainability: how we can fund our activity, how we work together, how we specialise and allocate responsibilities—and discuss the opportunities and challenges that we face.

Session: 6798859**7017181**

23/10/25 | 14:00

Room: Ballroom A

ORAL • EN

Principles for sustaining the global biodata infrastructure

Presenter

Guy Cochrane

Authors

Chuck Cook (Global Biodata Coalition • United Kingdom)

Guy Cochrane (Global Biodata Coalition • United Kingdom)

Abstract

Life scientists are crucially dependent on a global infrastructure of thousands of interconnected biodata resources that provide access to archived and curated data across many data types, including biodiversity data resources. National Biodiversity Infrastructures (NBDIs) are an integrated component of this global biodata infrastructure. All life scientists have a shared interest in understanding this infrastructure and ensuring it is developed and sustained to meet the needs of the research community. We will briefly outline the Global Biodata Coalition's effort to understand the biodata infrastructure through our work to create an inventory of global biodata resources and to identify Global Core Biodata Resources that are of central importance to the infrastructure.

Despite their importance as an infrastructure, funding for these resources is fragmented and uncoordinated. Individual biodata resources are primarily funded through short-term and competitive grants, limiting their ability to implement long-term planning, to recruit and retain skilled staff, and to respond to emerging technological and scientific needs—such as the rapid emergence of AI and machine learning.

The Global Biodata Coalition is working to develop more sustainable ways to fund biodata resources and the infrastructure as a whole. The GBC has published a White Paper [<https://doi.org/10.5281/zenodo.14727223>] setting out nine principles for support of biodata resources that can act as a framework for developing sustainable long-term funding models. We will briefly outline these principles and discuss some proposed funding models. The challenges of sustainably funding data resources are shared by all researchers in all fields, including NBDIs, and we look forward to discussions with the biodiversity data resource community on its approaches to ensuring sustainability for data resources.

Session: 6798859**7020444**

23/10/25 | 14:10

Room: Ballroom A

ORAL • EN

Keeping the integrity of platforms with a worldwide scope in the current complex geopolitical landscape

Presenter

Mergen Patricia

Authors

Mergen Patricia (Meise Botanic Garden and Royal Museum for Central Africa • Belgium)**Meeus Sofie** (Meise Botanic Garden • Belgium)**Leliaert Frederik** (Meise Botanic Garden • Belgium)

Abstract

There is an ever growing pressure on global platforms in the current difficult geopolitical context that is threatening international collaborations across continents and to tackle acute challenges that need to be addressed at planetary level such as climate change or biodiversity loss. If the integrity of such platforms is not guaranteed anymore, if they become fragmented with only data from a continent, region or country, if access from outside the place where it is hosted becomes restricted, scientific research as we know it including international collaborations will be seriously jeopardized. Additionally to the arguments of strategic autonomy or competitiveness, the countries or for example EU authorities are becoming terrorized and unfortunately for good reasons by cyber-attacks and impose ever stricter cybersecurity rules that hamper or at least seriously slow down the pace of international collaborative scientific research. Notably when it comes to IT related activities such as testing new technologies not yet fully secured or working with cross-border developed software. There are measures discussed for example in Europe to support such platforms considering hosting and mirroring or at least backupper the content. Shockingly, some authorities want to address only the European content hosted outside Europe and potentially at risk, but do not want to invest into keeping the integrity of the global systems or backupper the non-EU content as well, ignoring that the users need access to data in a worldwide scope for their studies. This presentation will notably show as example the risky situation of the Biodiversity Heritage Library (BHL), which has to find a new host by January 2026. Additionally, we show examples of how the EU AI Act and the Flemish Research Foundation have found workable solutions to address the risks, while impacting international collaboration as minimally as possible.

Session: **6798859****7013902**

23/10/25 | 14:20

Room: Ballroom A

ORAL • EN

Beyond Boundaries: Strengthening NBDIs Through Shared Roles and International Collaboration

Presenter

Anton Güntsch

Authors

Anton Güntsch (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)

Vincent Smith (Natural History Museum • United Kingdom)

Yvan Le Bras (Concarneau Marine Station, French Museum of Natural History • France)

David Fichtmueller (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)

Tanja Weibulat (Staatliche Naturwissenschaftliche Sammlungen Bayerns • Germany)

Abstract

Inspired by a symposium at the TDWG conference 2022 in Sofia, 9 national biodiversity data infrastructures (NBDIs) worldwide have jointly developed and published a definition of their tasks in relation to international services and initiatives. As a result, ten roles were defined and published that represent key activities of national infrastructures and their importance for science, policy and practice (Güntsch et al. 2025). These roles comprise the following tasks:

1. provision of base infrastructure,
2. facilitating data mobilization,
3. facilitating concerted national digitization efforts,
4. promoting the application of standards,
5. providing local helpdesk functions for using international data infrastructures,
6. facilitating the linking regional biodiversity assessments and taxonomies,
7. providing a data hub for national citizen science activities,
8. mediating legal questions,
9. providing platforms for quality control, data integration and analysis, and
10. acting as an instrument for lobbying and structuring national funding.

The formulation of these roles provides a valuable foundation for the strategic development of national infrastructures. It supports the planning of future activities, the identification of funding priorities, and the alignment of national initiatives with broader international efforts. Building on this shared understanding, we now seek to identify specific areas where closer collaboration between NBDIs and between NBDIs and international infrastructures can lead to more effective outcomes.

By enhancing coordination, we aim to increase efficiency, avoid duplication of effort, and develop more robust, sustainable services that serve the national and global biodiversity communities. To achieve this, we propose the establishment of a dedicated collaboration framework, ideally under the umbrella of TDWG, that facilitates ongoing exchange, joint planning, and shared development. We invite all members of the biodiversity informatics community to join this emerging effort to strengthen the global biodiversity data ecosystem.

Reference

Güntsch, A. et al, 2025, National biodiversity data infrastructures: ten essential functions for science, policy, and practice, Bioscience, Volume 75, Issue 2, <https://doi.org/10.1093/biosci/biae109>

Session: 6798859**7020941**

23/10/25 | 14:30

Room: Ballroom A

ORAL VIRTUAL • EN

Embedding community participation across the data lifecycle: a case study from Mexico

Presenter

Irene Ramos

Authors

Irene Ramos (UNAM • Mexico)

Alicia Mastretta-Yanes (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

Sustaining biodiversity data infrastructures requires strategies that embed community engagement, which is the foundation for addressing local needs and for building a user base that can advocate for the continued relevance of services. This presentation explores how interventions toward more participatory approaches in data-centric projects can strengthen such engagement.

We showcase co-production strategies within the Agrobiodiversity Information System (SIAgroBD, <https://siagro.conabio.gob.mx>), developed by the National Commission for the Knowledge and Use of Biodiversity (CONABIO), GBIF's Mexican node. SIAgroBD, funded by GEF and with FAO as the implementing agency, supports food security and conservation policies by collecting and providing access to information on native crops in traditional agriculture. It serves a national community of practice working on sustainable food systems.

Co-production strategies within SIAgroBD included capacity building, participatory tool design, and inclusive data governance. These approaches responded to emergent challenges as data and stakeholder diversity increased. Training workshops on FAIR data principles empowered contributors to use the data they helped collect and increased their awareness of open data as a collaborative effort, extending their involvement beyond the data generation stage. The co-design of digital surveys and participatory assessment of data collection tools through focus groups ensured the relevance of these tools to local needs. SIAgroBD also piloted the participatory development of data management plans that reflect the collective interests of data donors and protect sensitive information.

Involving stakeholders across the data lifecycle improved data quality, facilitated mobilization, and ensured that the results were applicable in policy. At the same time, SIAgroBD illustrates that co-production spans a spectrum of involvement, and requires substantial time, coordination, and resources. As biodiversity data networks seek to coordinate across domains and borders, participatory explorations like SIAgroBD offer a model toward infrastructures that both support and are sustained by collaboration.

Session: 6798859**7016474**

23/10/25 | 14:40

Room: Ballroom A

ORAL • EN

From Data to Discovery: Building Biodiversity Websites the Simple Way

Presenter

Morten Høfft

Authors

Morten Høfft (GBIFS • Denmark)**Tim Robertson** (GBIF • Denmark)**Daniel Van Der Meijden** (GBIF • Denmark)**Mélanie Raymond** (Denmark)**Thomas Stjernegaard Jeppesen** (Denmark)

Abstract

The Global Biodiversity Information Facility (GBIF) offers a free and accessible solution to showcase biodiversity data: hosted portals. Recognizing the past challenges of duplicated website development and the short lived nature of project-funded sites, these portals empower communities to focus on data publishing rather than web development.

These hosted portals provide a simple website builder with integrated widgets, enabling users to create engaging sites featuring any subset of the vast data amounts mediated and enriched by GBIF – occurrences, datasets, literature, and more. Whether for national nodes, regional initiatives, taxonomic interest groups, academic journals, or museum collections, hosted portals facilitate the creation of focused websites tailored to specific needs.

Built on a robust technical foundation (Jekyll, React), these portals offer powerful functionalities like filtered occurrence search, interactive maps, media galleries, and download options, all configurable through simple layouts and configurations. Site owners manage content independently via GitHub, while GBIF provides hosting, infrastructure and support.

With over 50 sites live and another 50 in development, the adoption of hosted portals demonstrates their value in streamlining biodiversity data communication and sharing. The process is flexible, allowing participants to launch sites in days or months, without requiring developers or incurring any costs beyond their own time. GBIF ensures the longevity and continuous improvement of these portals through ongoing technical updates and the integration of new features from GBIF.org.

This presentation will introduce the concept, demonstrate its functionality, and showcase diverse examples of how hosted portals are being used. By simplifying the process of creating dedicated biodiversity websites, GBIF aims to empower the community to prioritize data sharing and usage.

Session: 6798859**7020059**

23/10/25 | 14:50

Room: Ballroom A

ORAL • EN

Working across scales: Shared building-blocks of a sustainable infrastructure environment for bio/geodiversity data

Presenter

Jutta Buschbom

Authors

Jutta Buschbom (Statistical Genetics • Germany)**James A Macklin** (Agriculture and Agri-Food Canada • Canada)**Deborah L Paul** (University of Illinois | Species File Group • United States)**Alina Freire-Fierro** (Universidad Regional Amazónica Ikiam • Ecuador)**Wouter Addink** (Naturalis • Netherlands)**Teresa J Mayfield-Meyer** (United States)**Breda M Zimkus** (Museum of Comparative Zoology, Harvard University • United States)**Kerstin Lehnert** (Lamont-Doherty Earth Observatory of Columbia University • United States)**Katie Pearson** (University of Kansas • United States)**Elizabeth R Ellwood** (iDigBio • United States)

Abstract

The bio/geodiversity community aims to create digital infrastructures that provide quality, well-structured and highly interlinked data at a scale that allows big data analyses to support the conservation and management of Earth's rich diversity. In response to global crises, bio/geodiversity informaticians, scientists and managers face the challenge of globally accelerating and upscaling open data availability. Upscaling requires fostering strong, bidirectional connections between global and national repositories, and local providers, data stewards and users of data that are grounded in location, time and community. Communities ranging from local experts to global platforms are engaged, motivated and productive, but they struggle with managing the ever-increasing amount of data being amassed, developing standards and best practices, and handling the pace of technical innovations. This resource-limited situation does not support reliable and efficient upscaling, rather it threatens the robustness of rich community networks and the long-term sustainability of existing infrastructures.

The International Partners for the Digital Extended Specimen (IPDES) network includes participants from a broad spectrum of backgrounds who contribute to information exchange and alignment of ongoing efforts to extend and enrich data associated with collection objects. The rich responses and insights generated by the US-based BIOFAIR project (<https://bcon.aibs.org/biofair/>) allowed us to take stock of strengths and gaps, both those that are unique to different levels of organization and those that are shared across scale. We will be looking at community and network structures, capacity needs, and economic options to explore building blocks of a long-term sustainable community and infrastructure environment. On this basis we will begin to define next steps in a living roadmap focused on building and sustaining bio/geodiversity data infrastructures.

Session: 6798859**7019803**

23/10/25 | 15:00

Room: Ballroom A

LIGHTNING TALK • EN

Connecting the scientific data infrastructure of Natural History Collections with State Archives for long term preservation: An example from Germany

Presenter

Tanja Melanie Weibulat

Authors**Tanja Melanie Weibulat** (Staatliche Naturwissenschaftliche Sammlungen Bayerns, IT Center • Germany)**Stefan Seifert** (Staatliche Naturwissenschaftliche Sammlungen Bayerns, IT Center • Germany)**Lina Hörl** (Generaldirektion der Staatlichen Archive Bayerns • Germany)**Michael Puchta** (Generaldirektion der Staatlichen Archive Bayerns • Germany)**Dagmar Triebel** (Staatliche Naturwissenschaftliche Sammlungen Bayerns, IT Center • Germany)**Abstract**

The preservation of structured content of database applications outside of the running relational in-house systems is challenging. Nevertheless it is regarded as pre-requisite to ensure long term accessibility and preservation of structure and content following national laws as well as the requirements and concepts of the OAIS (Open Archival Information System) reference model for a dynamic, expandable archive information system (ISO standard 14721:2025).

The involved partner organisations are the Bavarian Natural History Collections (SNSB) with their collection management system Diversity Workbench (DWB; and the Bavarian State Archives (GDA) with their digital archive, both acting under the same legislation and connected by service tasks. The cooperation was initiated by the National Research Data Infrastructure (NFDI) and established by its consortium NFDI4Biodiversity with the GFBio Data Center SNSB. The SNSB will realise a complete export of the database content (bio- and geodiversity data directly related to their historic collection objects) without loss of semantic content and relations. On the part of GDA an integration of the digital objects in the sustainable infrastructure of Bavarian Main State Archive with FAIR solutions for reuse is mandatory.

The project presents a solution based on SIARD (= Software Independent Archival of Relational Databases) format and SIARD software suite. SIARD is creating information packages (SIPs) that conform to the ISO standards Unicode, XML and SQL:2008, as well as URI internet standard and ZIP industry standard (Markus et al. 2024:8). The solution might be appropriate as a blueprint to realise cooperative national infrastructures for preservation of archival worthy digital objects. The established access portals of the state archives in Germany will protect sensitive archived data (protected by personal rights, environmental laws, etc.) and eventually make them available for historical research under restricted access rights. The approach for preservation supplements the open data publication pipelines of the SNSB.

Session: 6798859**7019946**

23/10/25 | 15:05

Room: Ballroom A

LIGHTNING TALK • EN

Empowering data integration and semantic interoperability across environmental domains to address the biodiversity crisis and related environmental challenges

Presenter**Cristina Di Muri****Authors****Cristina Di Muri** (National Research Council of Italy (CNR), Research Institute on Terrestrial Ecosystems (IRET) • Italy)**Davide Raho** (National Research Council of Italy (CNR), Research Institute on Terrestrial Ecosystems (IRET) • Italy)**Alexandra N. Muresan** (National Research Council of Italy (CNR), Research Institute on Terrestrial Ecosystems (IRET) • Italy)**Martina Pulieri** (University of Salento • Italy)**Ilaria Rosati** (National Research Council of Italy (CNR), Research Institute on Terrestrial Ecosystems (IRET) • Italy)**Abstract**

Addressing the ever-increasing biodiversity crisis requires the access, integration and reuse of big data.

Essential variables for monitoring biodiversity trends include biological and ecological data as well as co-occurring environmental data that, in some instances, drive changes in biodiversity at different spatio-temporal scales.

The use of standards and semantic artefacts (SAs; i.e. ontologies and controlled vocabularies) is vital to enable an efficient search, retrieval, integration and interoperability of such information. To perform these tasks, a terminology service was conceived and developed by taking advantage of a national project, i.e. ITINERIS (Italian Integrated Environmental Research Infrastructure System), involving 22 environmental Research Infrastructures, focusing on the study of four sub-domains, i.e. atmosphere, marine, biosphere and geosphere.

The conceptualisation of the terminology service was driven by an analysis of SAs and SA catalogues used and/or managed by ITINERIS Research Infrastructures. This analysis was broadened to generate an extensive list of significant SAs and catalogues for environmental sciences, followed by an assessment of their FAIRness and other key properties (e.g. SAs management, catalogue governance and accessibility). Based on such requirements, a terminology service was developed as a unique access point to enable the federated search of class/concepts of SAs available across diverse catalogues (N = 30). The service integrates a semi-automatic mapping tool for enhancing semantic interoperability and monitors available SAs' updates within the connected catalogues. In addition, the service was designed as a flexible tool to be integrated into (meta)data management systems for semantic annotation, and it can be also adapted to different domains and applications within and beyond the panorama of national and European environmental Research Infrastructures.

In the era of big data, the exploitation of such services is essential to enhance interoperability and to find integrated responses to current and expected biodiversity and environmental changes.

Session: 6798859**7016866**

23/10/25 | 15:10

Room: Ballroom A

LIGHTNING TALK • EN

ELIXIR Biodiversity Community: a consolidated effort to support biodiversity research in Europe

Presenter

Joana Paupério

Authors**Joana Paupério** (EMBL-EBI - European Bioinformatics Institute • United Kingdom)**Anne-Françoise Adam-Blondon** (Université Paris-Saclay, INRAE, BioinfOmics, URGI • France)**Valeria Di Cola** (SIB Swiss Institute of Bioinformatics • Switzerland)**Toni Gabaldón** (Institut de Recerca Biomedica • Spain)**Matúš Kalaš** (Centro Nacional de Supercomputacion • Norway)**Henrik Lantz** (Department of Informatics, University of Bergen • Sweden)**Patricia M. Palagi** (Department of Medical Biochemistry and Microbiology|NBIS, Science for Life Laboratory • Switzerland)**Robert Waterhouse** (SIB Swiss Institute of Bioinformatics • Switzerland)**Biodiversity Community ELIXIR** (SIB Swiss Institute of Bioinformatics • United Kingdom)**Abstract**

ELIXIR is the European research infrastructure consortium for bioscientific data, bringing together scientists and coordinating bioinformatics resources across Europe. ELIXIR's goal is to enable collaboration and to help scientists access, analyse, and share life science data to address key societal challenges. The ELIXIR Biodiversity Community includes scientists from various disciplines united by the need to address challenges associated with biodiversity research. The community started its work focusing on the current challenges and opportunities and defining a roadmap to build on ELIXIR expertise and available tools and engage with the wider range of biodiversity focussed science infrastructures.

Here we present the work developed by this community that puts into action the main priorities identified. To support the application of standards and promote data management best practices, we have collated existing data and metadata standards, guidelines and repositories in a Biodiversity collection in FAIRSharing. We also developed data management recommendations and created a "Biodiversity" page in the Research Data Management Toolkit (RDMKit) focused mostly on biodiversity genomics. To promote tools and workflows that facilitate reliable and reproducible data analysis, we catalogued and reviewed existing resources, created a curated subdomain in Bio.tools and identified relevant collections in Galaxy and WorkflowHub. To enhance ELIXIR's network we engaged with several stakeholders and projects in the biodiversity domain by promoting discussions with the community in order to identify synergies and align resources. Finally, we curated a collection of biodiversity-relevant training resources and developed learning pathways with the concerned communities, made available through a dedicated collection in ELIXIR's Training eSupport System (TeSS).

Overall, these efforts represent a step forward in addressing some of the key challenges identified and pinpointing the pressing needs in the development and interoperability of resources to support biodiversity research and data management.

Session

6796407

Symposium

23/10/25 | 14:00

Room: Ballroom B1

Marine Biodiversity Data Mobilization and Applications

Organizers

Joana Soares

Isabel Sousa Pinto

Frank Muller-Karger

Description

Knowledge about marine biodiversity is fundamental to sustainable development and managing, conserving, and enhancing ecosystem services. Emerging technologies make it possible to routinely incorporate biology and ecology into ocean surveys and monitoring programs at local and regional scales. A better understanding of CARE and FAIR principles and legal frameworks, advances in standardization of data formats and storage, databases that protect intellectual property and data rights and provide specific products openly, all contribute to critical regional to global assessments of how biodiversity is changing and why. Publication of accepted best practices is important for information to be implementable by local groups, intercomparable, and scalable.

This session invites contributions that promote the local and regional integration of BioEco observations into coastal and ocean observing systems and monitoring programs. Increased coordination, capacity development, and implementation efforts are required for standardisation, or at least interoperability of collection, analysis, and delivery of biodiversity observations.

Experts and stakeholders are invited to present co-design strategies conducted in collaboration with the Marine Biodiversity Observation Network (MBON), the Global Ocean Observing System (GOOS), and the Ocean Biodiversity Information System (OBIS). Our goal is demonstrate how to satisfy national needs and reporting requirements in order to meet the targets of Sustainable Development Goals (SDGs), the Kunming-Montreal Global Biodiversity Framework (GBF), and other multinational environmental agreements.

Session: 6796407**7020203**

23/10/25 | 14:05

Room: Ballroom B1

LIGHTNING TALK • EN

Mobilizing Ocean Observations for Marine Ecosystem Sustainability & Resilience

Presenter

Erin Satterthwaite

Authors**Erin Satterthwaite** (Scripps Institution of Oceanography, UCSD • United States)**Ben Best** (EcoQuants • United States)**Rasmus Swalethorp** (Scripps Institution of Oceanography, UCSD • United States)**Brice Semmens** (Scripps Institution of Oceanography, UCSD • United States)**Abstract**

Collecting and effectively using ocean observations is crucial for advancing ocean sustainability and resilience efforts. A robust data pipeline is essential to ensure that observations are efficiently processed, managed, and mobilized to inform research, policy, and sustainable resource management. This presentation will explore strategies to enhance the mobilization, integration, and utility of ocean data, using the California Cooperative Oceanic Fisheries Investigations (CalCOFI) program as a case study. CalCOFI's long-standing, comprehensive data collection—particularly its high-resolution biological, chemical and physical sampling—offers a powerful foundation for advancing marine ecosystem science and policy.

We present an approach to strengthen the data pipeline from collection to use by developing an integrated database infrastructure that ensures reproducibility, transparency, and usability. Key aspects include: automated ingestion of raw tabular data using R scripts and the calcofi4r package; the establishment of a robust documentation process; implementation of a robust API for seamless, language-agnostic access to customized data subsets and visualizations; and generation of standardized metadata and data packages for discovery across multiple platforms such as ERDDAP, OBIS, DataOne, and NCEI. We also are beginning to explore new data management and system technologies such as DuckDB and observable file formats for efficient data querying and visualization. We illustrate how these efforts contribute to improved data stewardship and facilitate collaborative research initiatives.

By sharing our experiences and insights, we hope to showcase the importance of aligning technology with community needs and collaborative governance. It also aims to foster dialogue on best practices in marine data stewardship and showcase how well-designed systems can support more effective research, management, and decision-making for ocean sustainability and resilience.

Session: 6796407**7013335**

23/10/25 | 14:10

Room: Ballroom B1

LIGHTNING TALK • EN

Deployment of Essential Ocean Variables through APMBON and Their Application to Biodiversity Indicators for CBD and TNFD Frameworks

Presenter

Masahiro Nakaoka

Authors

Masahiro Nakaoka (Akkeshi Marine Station, Hokkaido University • Japan)

Takehisa Yamakita (Japan Agency for Marine-Earth Science and Technology • Japan)

Abstract

Sustainable management of marine ecosystems requires the long-term and integrated observation of biodiversity and environmental changes. This presentation introduces the efforts to monitor Essential Ocean Variables (EOVs) as defined by the Marine Biodiversity Observation Network (MBON) and the Global Ocean Observing System (GOOS), in comparison with Essential Biodiversity Variables (EBVs) used in terrestrial systems. While marine EOVs are selected based on feasibility for regular acquisition, capturing the qualitative changes in ecosystem status may require more sophisticated and higher-resolution data.

We will present ongoing efforts in deploying EOVs, highlighting Japan's national monitoring network (Monitoring Sites 1000), as well as related initiatives in East and Southeast Asia under the Asia-Pacific Marine Biodiversity Observation Network (APMBON), including the use of deep learning applied to satellite imagery for mapping seagrass and macroalgae habitats. Regional characteristics and challenges in implementation will be discussed.

Finally, we will explore how such observational data can contribute to global biodiversity frameworks. This includes their potential integration into indicators for the Kunming-Montreal Global Biodiversity Framework (KMGBF) under the Convention on Biological Diversity (CBD), as well as applications in marine ecosystem assessments such as the Ocean Health Index (OHI). Furthermore, we will examine the relevance of these data to the Taskforce on Nature-related Financial Disclosures (TNFD), particularly in assessing nature-related risks and financial dependencies. We aim to discuss current challenges, required technological innovations, and the importance of international collaboration and policy integration to advance marine biodiversity observation systems.

Session: 6796407**7017010**

23/10/25 | 14:15

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

The marine biodiversity data knowledge gaps in the SW Pacific and the Indian Ocean

Presenter

Hanieh Saeedi

Authors

Hanieh Saeedi (Senckenberg Research Institute and Natural History Museum • Germany)

Abstract

Digital marine biodiversity data is essential for supporting the objectives of the UN Ocean Decade. Here we have mapped the current biodiversity patterns of fauna in two underrepresented areas, the SW Pacific (SWP) and the Indian Ocean (IO), to identify the knowledge gaps and their drivers. The generated knowledge is useful for science-policy interfaces, facilitating informed decision-making processes. All occurrence data (Animalia) were extracted from the Ocean Biodiversity Information System (OBIS) and the Global Biodiversity Information Facility (GBIF). The occurrence records were quality-controlled (QC) following the OBIS manual. More than 60% of the occurrence data, which had reported depth information, belonged to the shallow waters, highlighting the knowledge gaps in the deep sea. The occurrence records decreased with depth in all taxa in both oceans. The higher latitudes of the SWP (0 - 25°S) were less sampled or the data were not reported, compared to the lower latitudes. Mid latitudes of the SWP (30 - 45°S) had the highest distribution records, mostly related to Chordata, followed by Arthropoda and Mollusca. However, 10 - 25°S latitudes of the SWP had the highest reported species records, mostly associated with Chordata, followed by Mollusca and Arthropoda. The mid latitudes of the IO (5 - 30°S) were less sampled or the data were not reported, compared to the upper and lower latitudes. The exception is the Chordata occurrence records with a peak at 10 - 25°S latitudes showing the highest distribution records, followed by Arthropoda. Also, 10 - 20°S latitudes of the IO had the highest number of species records, mostly related to Chordata, followed by Arthropoda and Mollusca. All this information is crucial in boosting biodiversity monitoring assessments and providing easy and fast access to information for policymakers to establish urgent conservation plans for underrepresented and endangered ecosystems before it is too late.

Session: 6796407**7015148**

23/10/25 | 14:20

Room: Ballroom B1

LIGHTNING TALK • EN

GBR Data Management System: A one-stop shop to Great Barrier Reef data.

Presenter

Eduardo Klein Salas

Authors

Eduardo Klein Salas (Integrated Marine Observing System • Australia)

Abstract

The Great Barrier Reef Data Management System (GBR-DMS) is a central data repository that supports the management of the Great Barrier Reef. As a one-stop shop for GBR relevant data, the GBR-DMS integrates more than 170 diverse datasets from multiple sources, providing stakeholders with efficient access to crucial information required for evidence-based decision making. Developed by the Integrated Marine Observing System (IMOS), the GBR-DMS consolidates fragmented data streams into a cohesive, accessible platform. This system not only delivers biodiversity monitoring data but also incorporates remote sensing observations, oceanographic measurements, and socioeconomic indicators relevant to reef management.

The cloud-native architecture of GBR-DMS implements standardized metadata schemas and cloud-optimised data formats, ensuring consistency across datasets while maintaining the integrity of original information. The platform leverages modern cloud infrastructure to handle large-scale spatial data processing, making it particularly valuable for remote sensing applications and large biodiversity datasets and long time series over vast geographic areas.

Stakeholders benefit from a comprehensive metadata catalogue and metadata API service. The DMS provides programmatic access through APIs that support scientific workflows in R, Python, and other analytical environments. This accessibility democratizes data use across research institutions, management agencies, and conservation organizations working to protect the reef. By making authoritative datasets on coral cover, oceanographic indicators, species distribution, and human impacts FAIR, the GBR-DMS facilitates comprehensive ecosystem assessment and more responsive adaptive management strategies. As climate change intensifies pressures on reef systems worldwide, this integrated data approach provides a model for how coordinated information management can enhance resilience planning and conservation outcomes for vulnerable marine ecosystems globally.

Session: 6796407**7015007**

23/10/25 | 14:25

Room: Ballroom B1

LIGHTNING TALK • EN

Advancing Marine Biodiversity Knowledge: Integrating Norwegian Marine Data into Global Observing Systems

Presenter

Vanessa Pitusi

Authors**Vanessa Pitusi** (The Arctic University Museum of Norway - UiT • Norway)**Andreas Altenburger** (The Arctic University Museum of Norway - UiT • Norway)**Abstract**

Knowledge about marine biodiversity is essential for sustainable development, effective conservation, and the management of ecosystem services. Emerging technologies and advances in data standardization now enable the routine incorporation of biological and ecological data into ocean surveys and monitoring programs at local, regional, and global scales. To support these efforts, the Arctic University Museum of Norway has joined the Ocean Biodiversity Information System (OBIS) network and is actively working to publish all Norwegian marine biodiversity data, including marine data from museum collections to OBIS. We aim to simultaneously publish marine data to both OBIS and the Global Biodiversity Information Facility (GBIF), ensuring broader accessibility and interoperability.

This presentation highlights our efforts to integrate Norwegian marine biodiversity data into global observing systems, aligning with the CARE (Collective Benefit, Authority to Control, Responsibility, Ethics) and FAIR (Findable, Accessible, Interoperable, Reusable) principles. By leveraging advances in data standardization, legal frameworks, and open-access databases, we aim to contribute to critical regional and global assessments of biodiversity change. Our work emphasizes the importance of publishing best practices to ensure that biodiversity data are implementable, intercomparable, and scalable across local and global contexts.

This case study demonstrates how coordinated efforts in data standardization, capacity development, and interoperability can strengthen marine biodiversity observation systems. By sharing our experiences, we hope to inspire new collaborations and strategies that advance the integration of marine biodiversity data into global frameworks, ensuring that biodiversity knowledge informs sustainable ocean management and conservation efforts.

Session: **6796407****7012006**

23/10/25 | 14:30

Room: Ballroom B1

LIGHTNING TALK VIRTUAL • EN

Lessons learned in developing the Information System MORSE - Marine Organisms Resources Storage system to ensure ABS regulation

Presenter

Brendan HENNEBAUT

Authors

Brendan HENNEBAUT (IFREMER - Institut Français de Recherche pour l'Exploitation de la Mer • France)

Sylvie VAN ISEGHEM (IFREMER - Institut Français de Recherche pour l'Exploitation de la Mer • France)

Abstract

The national APA coordination within Ifremer's direction recommended the implementation of an information system capable of managing, over time and space, the traceability of biological samples in order to meet the regulatory requirements of the Nagoya Protocol (Access and Benefit-Sharing Clearing-House - ABSCH). European funding programs also increasingly require a high level of traceability and sharing with the scientific community.

This first Information System MORSE has been built between 2020 and 2024 within SISMER Data Center. It is accredited as a French National Oceanographic Data Center (NODC) by UNESCO's International Oceanographic Commission (IOC) as part of the "International Oceanographic Data and Information Exchange" (IODE) program.

Illustrated with examples from Ifremer's laboratory data, we propose an approach that can serve as a model for research data management that allows researchers to disseminate their data by satisfying the main FAIR (Findable, Accessible, Interoperable, Reusable) criteria without insurmountable efforts.

The MORSE information system is designed to harvest information directly from Ifremer's data systems without the need for re-entry, allowing each laboratory to manage its data according to its specific needs.

The main objectives of the **MORSE** information system are as follows

1. To comply with regulatory requirements (APA, CITES, Customs obligations);
2. To store essential traceability information and manage the lineage between samples;
3. To import existing traceability data from Ifremer's standard data storage systems without re-entry;
4. To reliably identify and locate a biological sample;
5. To identify samples owned by Ifremer;
6. To share collections internally and externally in compliance with applicable legislation;
7. To easily search for a series of samples.

Lessons learned from this project are presented in terms metadata best practices, common vocabularies and methodologies to answer regulatory requirements.

Session: 6796407**7020542**

23/10/25 | 14:35

Room: Ballroom B1

LIGHTNING TALK • EN

Applying FAIR principles to plankton metabarcoding time series data from the Southeast US Marine Biodiversity Observation Network

Presenter

Luke Thompson

Authors**Luke Thompson** (Northern Gulf Institute, Mississippi State University • United States)**Enrique Montes** (Cooperative Institute for Marine and Atmospheric Studies, University of Miami • United States)**Sammy Harding** (Northern Gulf Institute, Mississippi State University • United States)**Katherine Silliman** (Northern Gulf Institute, Mississippi State University • United States)**Bayden Willms** (Northern Gulf Institute, Mississippi State University • United States)**Ian Smith** (Cooperative Institute for Marine and Atmospheric Studies, University of Miami • United States)**Rachel Cohn** (Cooperative Institute for Marine and Atmospheric Studies, University of Miami • United States)**Francis Serrano** (Cooperative Institute for Marine and Atmospheric Studies, University of Miami • United States)**Clement Coclet** (Northern Gulf Institute, Mississippi State University • United States)**Frank Muller-Karger** (College of Marine Science, University of South Florida • United States)**Abstract**

Substantial progress in genomics is leading to the development of tools for mobilizing eDNA-based marine biodiversity data. The tools include bioinformatics workflows that track exact sequence variants, metadata checklists and templates, machine-readable protocol formats, software to assist exploring and publishing data to biodiversity repositories, and data portals. These tools open up new possibilities for exploring biodiversity, allowing us to ask questions that were previously out of reach. They help mobilize information into the hands of researchers and policymakers, and ensure the use and reuse of data for decades to come. The Southeast US Marine Biodiversity Observation Network (SEUS MBON) has collected eDNA and plankton imaging data on South Florida Ecosystem Restoration cruises since 2015. Nearly 4000 eDNA samples from 2015 to 2024 have been collected, extracted, and metabarcoded for bacteria and archaea (16S rRNA V4-V5), and protists and metazoa (18S rRNA V9). We present preliminary results of analyses that combine eDNA, morphological and taxonomic image-based plankton observations, hydrographic and biogeochemistry measurements, and satellite remote sensing data. Our goal is to evaluate how shifts in seasonal to interannual environmental conditions affect the abundance and composition of primary producers (including harmful algal blooms or HABs), zooplankton, and food web dynamics. We demonstrate how these data are shared openly through the Making eDNA FAIR (FAIRe) metadata checklists and templates, applying the Better Biomolecular Ocean Practices (BeBOP) protocol format, and using edna2obis software to publish to global biodiversity repositories (OBIS and GBIF). We showcase these data on the Ocean DNA Explorer (<https://oceandnaexplorer.org>), a data portal used to host, explore, and visualize data from SEUS MBON and other DNA-based marine biodiversity surveys.

Session: 6796407**7020263**

23/10/25 | 14:40

Room: Ballroom B1

LIGHTNING TALK • EN

Empowering Coastal Communities through Marine Citizen Science: Taiwan's Approach to Biodiversity Data Mobilization and Application

Presenter

Ning Yen

Authors

Ning Yen (Taiwan)

Abstract

In recent years, Taiwan has initiated a comprehensive national strategy to integrate marine citizen science into its biodiversity observation and data mobilization framework. Partnering with the Ocean Conservation Administration, our team co-developed the “Taiwan Marine Citizen Science Strategy,” aiming to enhance data interoperability, foster local capacity, and improve biodiversity monitoring at coastal and regional scales.

Through in-depth interviews with local NGOs, we identified a spectrum of needs: some groups were just beginning and required scientific support to design monitoring methods; others had amassed 10–20 years of data yet lacked the digital tools or expertise to analyze them; while a few were already aligned with global standards, publishing in journals or contributing data to platforms such as GBIF. In response, we designed tailored capacity-building programs, including workshops on FAIR/CARE data principles, data cleaning, dashboard-based visualization, and digital tools for field monitoring.

We also facilitated a small seminar among stakeholders, including government representatives, scientists, media representatives, and NGOs, to enhance data workflows and promote open science. A national citizen science platform now showcases local teams and their contributions, complemented by public outreach campaigns and a marine data-thon that connected NGOs with data engineers to transform legacy datasets into accessible visual stories.

These efforts demonstrate a scalable, inclusive model for integrating citizen science into national and international biodiversity frameworks, contributing toward the Kunming–Montreal Global Biodiversity Framework and SDG targets.

Session

6803213-1

Symposium

23/10/25 | 14:00

Room: Ballroom B2

Modern challenges of classic taxonomy, how to connect and keep catalogues up to date (Part 1)

Organizers

Olaf Bánki

Vijay Barve

Camila Plata

Description

Taxonomy, the fundamental framework of biological sciences, provides a shared understanding of every organism. Traditionally, curated taxonomic name lists were disseminated through print publications and later transitioned to online platforms. However, these resources often become rapidly outdated after publication, with limited capacity of maintenance by their original creators. Developing and maintaining taxonomic name resources is challenging, and entails innovative solutions and new ways of collaboration. These taxonomic data sources are crucial to represent biodiversity data in general, and link these to fundamental science and societal efforts. In this session we would like to bring together both providers and users of taxonomic resources to understand their challenges and how they have addressed these successfully -or not. In a collaborative environment we aim to share best practices, learn from one another's experiences, and better understand the need to connect local, national and regional taxonomic lists and derived species lists to a global effort.

Session: 6803213-1**7020608**

23/10/25 | 14:00

Room: Ballroom B2**ORAL • EN**

World Flora Online: a global catalogue for land plants supported by the international botanical taxonomic community

Presenter

Lauren Raz

Authors

Lauren Raz (Instituto de Ciencias Naturales • Colombia)**Mark Watson** (Royal Botanic Garden Edinburgh • United Kingdom)**Peter Wyse Jackson** (Missouri Botanical Garden • United States)

Abstract

World Flora Online (WFO), is a growing consortium of 55 botanical organizations worldwide. Its mission is to support the conservation, restoration and sustainable use of plants by providing accurate and up-to-date scientific information on all known species of vascular plants and bryophytes, using FAIR principles. At the heart of WFO is a consensus classification (taxonomic backbone) of 380,000 accepted names of species and their synonyms, which is maintained by the global taxonomic community. This is used to generate the WFO Plant List (<https://wfoplantlist.org>): an archived, citable global checklist published at six-month intervals. Updating the consensus classification is achieved through an innovative community-based, consensus model in which curation of specific taxonomic groups (usually a family) is devolved to Taxonomic Expert Networks (TENs) approved by WFO Council. WFO currently has 55 TENs covering 53% of accepted species, with over 900 taxonomists participating. Full accreditation is given to original sources, allowing users to refer back to the primary data. A TEN Manager, in collaboration with members of the WFO Technical and Taxonomic Working Groups, manages the workflows using a custom editing platform: Rhakhis. New names are continuously imported from the International Plant Names Index (IPNI) and Plazi, and are subject to TEN review. How to curate names not yet covered by a TEN is an ongoing challenge.

These gaps are currently filled with updates from the World Checklist of Vascular Plants (WCVP), however, work is underway to undertake this by a general curation team within WFO, incorporating WCVP workflows. WFO is also developing a new data infrastructure and data pipelines to support a portal which will enable more sophisticated interrogation of the data, including integrating more geographic information and the generation of regional and national lists. Data consumers will also be able to become data providers, for example, by contributing national checklists.

Session: 6803213-1**7015502**

23/10/25 | 14:11

Room: Ballroom B2**ORAL • EN**

Beyond classical taxonomy - Standardizing plant cultivar names to address modern challenges

Presenter

Richard Dodd

Authors

Richard Dodd (Royal Botanic Gardens, Kew • United Kingdom)

Udayangani Liu (Royal Botanic Gardens, Kew • United Kingdom)

Reinis Rozkalns (Royal Botanic Gardens, Kew • United Kingdom)

Robert Turner (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

Cultivars denote species varieties that have been generated in cultivation and their naming conventions follow the rules of the International Code of Nomenclature for Cultivated Plants (ICNCP), not the standard code (ICN) used for wild plants. Cultivar names are often tied to plant breeders' rights or patents; unique and registered names helping to protect the intellectual property of breeders. Whilst wild plant taxonomy benefits from established platforms like Plants of the World Online (POWO), World Flora Online (WFO), and Global Biodiversity Information Facility (GBIF), cultivated plants lack a centralised system for naming, tracking, and confirming their existence. Therefore, although they are essential for horticulture, agriculture and botanical science, cultivated names are often underrepresented in online resources. The lack of centralised cultivated plant name backbone creates significant challenges for managing plant living collections, especially in botanic gardens, where capturing accurate plant names is essential for curation, conservation, research, and education.

Without a centralised name backbone, data integration and record-keeping for cultivars becomes fragmented, institutes struggle to compare or share data effectively, duplicate records are difficult to detect and historical records risk becoming ambiguous or misleading. Here, we share our experience, insight, best practice and knowledge on how we handle key challenges of standardising cultivar names beyond classical taxonomic principals within Royal Botanic Garden, Kew's Integrated Collections Management System, using EarthCape Oy software. We discuss how we capture aspects of a cultivar's name, including group, grex, series and trade designation. In the absence, currently, of a comprehensive, open-access cultivar name backbone, we look at the steps we are taking to introduce some standardisation within our own collection management system and consider what might be done to facilitate global collaboration in plant conservation, sustainable horticulture, research and education, to strengthen plant conservation stewardship worldwide.

Session: 6803213-1**7012971**

23/10/25 | 14:22

Room: Ballroom B2**ORAL • EN**

Integrating biodiversity data by name matching to shared reference lists

Presenter

Leen Vandepitte

Authors

Roger Hyam (Royal Botanic Garden Edinburgh • United Kingdom)**Liesbeth Lyssens** (Flanders Marine Institute (VLIZ) • Belgium)**Bart Vanhoorne** (Flanders Marine Institute (VLIZ) • Belgium)**Leen Vandepitte** (Flanders Marine Institute (VLIZ) • Belgium)

Abstract

The process of combining biodiversity data from multiple sources currently starts with matching of the Latin name strings for the organisms used in each dataset. Datasets often contain names that cannot be unambiguously matched. The reasons for this are complex. They arise from the nomenclatural codes that have evolved over many decades as well as human and computer error. In smaller studies these issues can be resolved manually but in the larger studies, such as plot monitoring networks, or when combining data from very different domains, such as ecological and molecular phylogenetic data, they become a major hurdle.

The solution is to match each dataset to a reference name list. Through a process of name matching the Latin name used in the data is augmented with an unambiguous identifier supplied by the list. The name matching process only has to be done once and then the data can be combined with any other data set that has been matched to the same reference list. Unfortunately each reference list has its own implementation of how to do the name matching.

The Flanders Marine Institute (VLIZ) and Royal Botanic Garden Edinburgh manage large reference lists including the World Register of Marine Species (WoRMS), PESI and the World Flora Online. We have been working on a shared name matching standard that could be implemented by other reference lists. This should make it easier for researchers to align data with any reference list without having to learn a new system and it would facilitate tooling in the future.

We will present the results of our work on the Taxonomic Name Linking Services (TNLS) which was funded as part the Horizon Europe Research and Innovation programme within the framework of the TETTRIs (Grant Nr. 101081903).

Session: 6803213-1**7019764**

23/10/25 | 14:32

Room: Ballroom B2**ORAL • EN**

Where to go with my name? Recommendations for checking scientific organism names as a key to data integration

Presenter

Walter G. Berendsohn

Authors

Walter G. Berendsohn (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Markus Döring** (GBIF Secretariat • Denmark)**David Fichtmueller** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Anton Güntsch** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Roger Hyam** (Royal Botanic Garden Edinburgh • United Kingdom)**Liesbeth Lyssens** (Vlaams Instituut voor de Zee • Belgium)**Andreas Müller** (Freie Universität Berlin, Botanic Garden and Botanical Museum Berlin • Germany)**Bart Vanhoorne** (Vlaams Instituut voor de Zee • Belgium)

Abstract

Scientific names of organisms form part of local data across diverse fields including systematics, forestry, agriculture, oceanography, ecology, conservation, medicine, government regulations, and laws. To enable data linkage (Vaccaro & Swerts 2022, <https://doi.org/10.24449/FG-2022-00018>), these names must be as accurate as possible. Traditionally, taxonomists played a key role in validating and connecting names from various sources. Today, this task is often delegated (sometimes uncritically) to automated tools provided by “taxonomic aggregators” (TETTRIs 2024+, https://wiki.bgbm.org/tettris/Global_or_regional_aggregators) that match names against global, regional or thematic taxonomic checklists.

However, users outside taxonomy face an overwhelming array of online sources and name-matching services. The EU-funded TETTRIs project developed a step-by-step guide to help users choose appropriate solutions for their specific needs.

This presentation will outline the key considerations for selecting a name-checking approach for a specific dataset:

- Does the dataset have a specific taxonomic or geographic scope?
- Is the primary goal to check orthography, taxonomic validity, or classification of the name(s)?
- Are there just a few names to check, or a large dataset?
- Is a resolvable identifier or persistent link required as output? (In order to enable overarching linkage)
- What is the user’s technical capacity? (E.g., is API access needed for automation, can tools like OpenRefine be used?)

Drawing on use cases examined in the course of the project (Berendsohn 2023, <https://doi.org/10.3897/biss.7.109666>) and taken from literature (e.g., Islam et al. 2024, <https://doi.org/10.3897/rio.10.e121871>; Osawa 2019, <https://doi.org/10.1111/1440-1703.12023>; Güntsch & al. 2024, <https://doi.org/10.1093/biosci/biae109>), recommendations for selecting appropriate datasets and matching services have been developed.

Given the rapid evolution of these resources, some recommendations may quickly become outdated. To address this, TETTRIs will make the matrix used to evaluate services publicly available online in a form that allows future updating.

Session: 6803213-1**7020777**

23/10/25 | 14:44

Room: Ballroom B2

ORAL VIRTUAL • EN

infraFADA: Upgrading the taxonomic backbone of global freshwater animal biodiversity research infrastructures

Presenter

Géraldine Mertens

Authors

Géraldine Mertens (RBINS • Belgium)

Astrid Schmidt-Kloiber (BOKU University • Austria)

Koen Martens (RBINS • Belgium)

Abstract

The Freshwater Animal Diversity Assessment (FADA) comprises an extensive set of global taxa lists for freshwater animal groups. At present, more than 125,000 described freshwater animal species in more than 11,000 genera have been documented. However, taxonomy is a living scientific discipline, where new taxa are continuously being described, and existing taxa are being placed in new taxonomic positions. Therefore, after a period of relative inactivity, the BELSPO (Belgian Science Policy) project “infraFADA” (2023–2026) re-establishes the global FADA consortium of taxonomic experts, so that all taxa lists will be brought up to date, both technically and in terms of content. infraFADA is developing a living, updated, and global FADA database, fully in open access and according to the FAIR principles. On the one hand, the infraFADA database helps the experts to curate their data (using FADAtims; see separate poster), on the other hand it is intended for use and consultation by the scientific freshwater community or interested stakeholders, for example, freshwater ecosystem managers, biodiversity conservationists, and others. Most importantly, FADA will also serve as a taxonomic backbone for other global biodiversity data infrastructures, such as the Catalogue of Life (CoL), the Global Biodiversity Information Facility (GBIF), the Freshwater Information Platform (FIP), and others. As such, FADA will provide a digital and living heritage of freshwater data, building bridges between science and society and helping to sustainably maintain freshwater resources.

Session: 6803213-1**7020691**

23/10/25 | 14:55

Room: Ballroom B2**ORAL • EN**

Flexible Taxonomic Viewpoints through Structured Name Usage: Implementing the 'Build Classification' Tool in TaiCOL

Presenter**Sz-Yi Tsai****Authors****Sz-Yi Tsai** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Jin-Ying Lee** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Kuo-Fang Chung** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Abstract**

The use of structured data for scientific names plays a crucial role in preserving the continuity of taxonomic knowledge. As taxonomy evolves, new perspectives emerge not in isolation but by building upon existing classifications. This cumulative approach enables the integration of historical viewpoints, ensuring that valuable insights from past literature remain accessible and reusable.

TaiCOL (Catalogue of Life in Taiwan) provides an online scientific name management tool that allows taxonomists to manage names, references, and taxonomic data from literature or checklists. Recently, we developed a new feature, Build Classification, designed to help taxonomists integrate and edit past taxonomic viewpoints. This feature supports the publication of new literature while preserving associated taxonomic concepts in a structured system of name usages, allowing them to circulate and be reused.

The Build Classification workflow incorporates three methods for filtering taxa: by higher taxonomy, by selecting relevant literature, or by regional distribution. After choosing the taxa and references to include, the system compiles the relevant name usages using the same logic applied in TaiCOL checklist, determining name validity based on literature priority. The results are output to a draft checklist area, where users can review and refine their concepts. This process allows users to build personalized taxonomic perspectives on the foundations of previous classifications. Finalized concepts can be exported—either as document files or in data exchange formats—for publication or sharing.

By implementing this feature, we fulfill the core vision of TaiCOL's data structure: storing and managing taxonomic data based on name usages. Rather than generating a single consensus taxonomy, the system now supports the flexible creation of multiple taxonomic viewpoints, each grounded in documented name usages—reinforcing a dynamic and transparent taxonomic data infrastructure.

Session: 6803213-1**7019777**

23/10/25 | 15:05

Room: Ballroom B2**ORAL • EN**

Beyond classical Linnaean taxonomy: how temporary names are being integrated into the World Register of Marine Species (WoRMS)

Presenter

Leen Vandepitte

Authors

Leen Vandepitte (Flanders Marine Institute (VLIZ) • Belgium)

Tammy Horton (National Oceanography Centre • United Kingdom)

Muriel Rabone (Natural History Museum London • United Kingdom)

Shane T. Ah Yong (Australian Museum • Australia)

Rüdiger Bieler (Field Museum of Natural History, Chicago, USA • United States)

Christopher B. Boyko (Department of Biology, Hofstra University • United States)

Simone N. Brandão (Division of Invertebrate Zoology, American Museum of Natural History • Brazil)

Gustav Paulay (Universidade Federal Rural de Pernambuco • United States)

Erik Simon-Lledo (Unidade Acadêmica de Serra Talhada • Spain)

WoRMS Data Management Team (Florida Museum of Natural History, University of Florida • Belgium)

Abstract

Species are fundamental units of biodiversity and underpin communication in biology. Current advances in the fields of molecular biology and the growing use of image-based identifications have resulted in an explosion of temporary or informal species names globally, increasing the rate of discovery of undescribed species and cryptic species complexes. Given the pressure the ocean is under and the urgent need to estimate how many marine species actually live in our ocean, new species discoveries are currently being recognised and ‘named’ outside of the conventions of the classical Linnaean taxonomic system that has existed since 1753; these are often referred to as ‘temporary names’.

We recently defined two categories of temporary names: Type 1 names that are delineated in a local context but not further assessed; and Type 2 names that have been taxonomically assessed and recognised as either new or part of an unresolved species complex. The current challenge is to manage these temporary names in a robust and standardised manner, making them part of major data flows so they can contribute to global species registers, as well as including them in existing quality control procedures on taxonomic names. The temporary names can then be linked to formal Linnean names.

Aphia, the infrastructure underlying the World Register of Marine Species (WoRMS), has recently developed the possibility to document Type 2 temporary names, so these names can become part of nomenclatural databases, and thus contribute to endeavors to objectively estimate the number of existing species. Practical recommendations are available to all Aphia-WoRMS editors on how such names should be selected for entry and how they can be entered in a standardised way. These recommendations are a small step forward, but their broad adoption would support the robust integration of informal and formal taxonomies.

Session

6803221

Symposium

23/10/25 | 14:00

Room: Tolima

Experiences & lessons of managing community-based biodiversity data in ethnic & local communities

Organizers

Ricardo Ortiz Gallego

Keila Macfadem Juarez

Description

Biodiversity monitoring is a key pillar for its conservation. In this regard, community-based data gathering generated from the traditional knowledge of Indigenous Peoples, ethnic groups, and local communities has become a crucial aspect to monitoring the conservation status of their territories. Indigenous-led monitoring initiatives deliver essential insights by weaving time-honored ecological knowledge with advanced Earth observation technologies. Indigenous communities have long been stewards of their lands, contributing invaluable perspectives on ecosystem health, species behaviors, and climate resilience. However, questions and challenges arise due to the asymmetries between the knowledge systems from which we produce this information and how we can support them in a way that is accessible and benefits stakeholders and rights-holders involved.

The symposium will focus on the data governance from ethnic groups and local communities, exploring topics ranging from the full identification of data generated from traditional practices, appropriate standards, principles and licenses for publication, biodiversity monitoring and management experiences, and the preservation of knowledge systems. The goal is to build a baseline that provides perspectives for biodiversity information systems globally, outlining the roadmap to follow in the context of global commitments and local interests.

Session: 6803221**7020874**

23/10/25 | 14:05

Room: Tolima

ORAL • EN

A model for data mobilisation that supports and upholds Sámi data governance

Presenter

Susanna Ragnhild A. Siri

Authors

Susanna Ragnhild A. Siri (UiT The Arctic University of Norway • Norway)

Máret J. Hætta (The Saami Council • Norway)

Per Axelsson (Várdduo Centre for Sámi Research, Umeå University • Sweden)

Veronika A. Johansson (Department of Bioinformatics and Genetics, Swedish Museum of Natural History • Sweden)

Abstract

Sápmi (also referred to as Sábmme or Saepmie) denotes the traditional territory of the Indigenous Sámi people, encompassing northern regions of Norway, Sweden, Finland, and the Kola Peninsula in Russia. Despite the extensive collection of unique biodiversity data from this region within the Global Biodiversity Information Facility (GBIF), the Indigenous origins and cultural significance of the area are frequently unacknowledged. Including cultural context to GBIF data provides a unique opportunity for multiple governing tasks related to monitoring changes in landscapes, the use of nature, and the biodiversity surrounding us. Importantly, these data are also part of cultural stories wherein terminologies, descriptions and names document long-term relationships through traditional use and knowledge of the lands, waters and ecosystems.

This pilot study explores how Sámi interests and needs can be more fully integrated into GBIF's data ecosystem, aligning with both the FAIR (Findable, Accessible, Interoperable, Reusable) and CARE (Collective Benefit, Authority to Control, Responsibility, Ethics) principles. By focusing on Sámi significant biodiversity items, the study will assess the extent to which Sámi taxonomies, names, and traditional knowledge are currently represented—or missing—in GBIF records. Furthermore, the study will examine key data types (for example, data annotations and tags provided by *Local Context*) and metadata (e.g., traditional names, provenance, temporal context of use) necessary for ensuring Sámi interests in data infrastructures, along with technical solutions and governance pathways for upholding Sámi data sovereignty. Finally, we will evaluate if and how new Sámi datasets including traditional knowledge, could be incorporated into GBIF's data infrastructures. This research seeks to develop a model for respectful and reciprocal inclusion of Sámi biodiversity data available in GBIF and provide a template for future data mobilisation to uphold Sámi data governance.

Session: 6803221**7013572**

23/10/25 | 14:15

Room: Tolima

ORAL • EN

Embedding Indigenous Data Governance in Global Biodiversity Infrastructure

Presenter

Cas Sedran-Price

Authors

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Abstract

The Global Biodiversity Information Facility (GBIF) is a leading international network and open data infrastructure funded by governments around the world. GBIF provides free and open access to biodiversity data and is committed to aligning its practices with FAIR data principles (Findable, Accessible, Interoperable, and Reusable). However, efforts to date have paid limited attention to Indigenous Data Governance frameworks, particularly the CARE Principles (Collective Benefit, Authority to Control, Responsibility, and Ethics), which support Indigenous rights to their data and guide the ethical access and (re)use of Indigenous data.

In a significant step towards advancing Indigenous data rights within global biodiversity infrastructure, GBIF has established a dedicated Indigenous Task Group. This group comprises leading international experts in Indigenous Data Governance and biodiversity knowledge systems. The Task Group's mandate is to develop actionable recommendations to guide GBIF in adopting and implementing Indigenous governance mechanisms across its network and infrastructure.

The group's work includes reviewing existing biodiversity data currently mobilized through GBIF that relates to Indigenous and local knowledge systems; consulting with GBIF national nodes to support case studies and best practices on partnerships with Indigenous Peoples and local communities; assessing the implications of adopting the CARE Principles within the GBIF framework; and exploring options for the technical implementation of mechanisms such as Local Context Notices and Labels.

This is a foundational step toward embedding Indigenous rights, perspectives, and governance into global biodiversity data infrastructure. It acknowledges the longstanding role of Indigenous Peoples as knowledge holders and stewards of Indigenous data. The Task Group's recommendations will support the integration of Indigenous-led governance mechanisms into GBIF, ensuring that biodiversity data systems uphold equity, traceability, accountability, and Indigenous Data Sovereignty.

Session: 6803221

7020376

23/10/25 | 14:25

Room: Tolima

LIGHTNING TALK • ES

El poder de lo local: aportes del monitoreo comunitario a la gestión de la biodiversidad.

Presenter

Maria Helena Olaya Rodriguez

Authors

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Maria Camila Parra Guevara (Instituto Alexander von Humboldt • Colombia)

Maria Alejandra Molina (Instituto Alexander von Humboldt • Colombia)

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Abstract

El monitoreo comunitario de biodiversidad se ha convertido en un espacio de encuentro donde diferentes sistemas de conocimiento conversan, recogiendo datos y produciendo información con el potencial de apoyar procesos para la gestión de la biodiversidad. Pero, ¿cómo podemos conectar los ejercicios de monitoreo a escala local con los sistemas de información a nivel regional y nacional para generar una mayor incidencia en las decisiones ambientales?

A partir de varias experiencias de ejercicios de monitoreo de la biodiversidad, se propone el Ciclo de Monitoreo como un marco guía para producir datos e información útil a partir de la planeación e implementación de estrategias de monitoreo que respondan a las necesidades e intereses de los actores involucrados e integrando diferentes sistemas de conocimiento.

Como resultado se presentarán tres experiencias de implementación del ciclo en territorios colombianos: 1) en páramos con comunidades campesinas y pueblos indígenas que están monitoreando especies priorizadas para aportar a la gestión integral de sus ecosistemas; 2) en la Amazonía, monitoreando cómo responde la biodiversidad a las estrategias de conservación que están implementando comunidades campesinas y grupos étnicos para frenar la deforestación; y 3) en el Caribe, en un territorio que históricamente ha sido minero, monitoreando el avance de la restauración a través de una red de diversos actores locales. Todas estas iniciativas tienen el potencial de generar datos que se pueden compartir de forma abierta, dando visibilidad a las redes de monitoreo y destacando su relevancia en el cumplimiento de las metas de país en el Plan de Acción de la Biodiversidad.

Session: 6803221

7021025

23/10/25 | 14:30

Room: Tolima

LIGHTNING TALK • ES

Restauración con identidad: Monitoreo comunitario en el Resguardo Indígena Llanos del Yará -- Yaguara II

Presenter

Bibiana Gómez Valencia

Authors

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Paola Isaacs (Instituto Humboldt • Colombia)

Alejandra Castaño (Instituto Humboldt • Colombia)

Bibiana Gómez Valencia (Instituto Humboldt • Colombia)

Mónica Hernández (Instituto Humboldt • Colombia)

Ana Belén Hurtado (Instituto Humboldt • Colombia)

Daniela Martínez (Instituto Humboldt • Colombia)

Eliana Barona (Instituto Humboldt • Colombia)

Abstract

Frente al avance de la deforestación y su impacto en la biodiversidad, la comunidad del Resguardo Indígena Llanos del Yará – Yaguara II, se ha desarrollado una estrategia de **monitoreo participativo** que acompaña los procesos de restauración ecológica, productiva y social. El objetivo principal es el seguimiento a la efectividad de la restauración, al tiempo que se fortalece el conocimiento local para la **toma autónoma de decisiones** sobre la gestión del territorio y el retorno de las familias desplazadas. La metodología implementada se basa en el **ciclo de monitoreo del Instituto Humboldt**, que abarca las fases de planificación, recolección de datos, análisis e interpretación. Se realiza seguimiento a **51 parcelas restauradas**, utilizando indicadores clave como: **Vegetación:** altura, DAP, cobertura, supervivencia.

Fauna: abundancia relativa mediante cámaras trampa, con análisis automatizado en la plataforma *Wildlife Insights* y paisajes sonoros. **Aspectos sociales:** número de familias que han retornado, mecanismos comunitarios de resolución de conflictos y fortalecimiento de la vida colectiva. La **gestión de datos es liderada por la comunidad**, con roles definidos para la recolección, sistematización, análisis y divulgación. Se emplean tanto formatos locales como plataformas digitales, adaptadas al contexto. Los resultados se comparten en redes sociales y espacios de diálogo interno, alimentando procesos de gobernanza. Los indicadores, definidos desde la mirada del territorio, permiten evaluar conectividad ecológica, diversidad biocultural, sostenibilidad agroecológica y cohesión social. Este caso muestra cómo las comunidades indígenas no solo participan, sino que lideran la producción y uso de datos, generando información viva que guía decisiones colectivas. La apropiación tecnológica —como el uso de cámaras trampa e inteligencia artificial— combinada con el **diálogo de saberes**, fortalece la autonomía territorial y promueve una **restauración con identidad**.

Session: 6803221**7020456**

23/10/25 | 14:35

Room: Tolima

LIGHTNING TALK • EN

Self-Determination and Data: Indigenous Experiences and Perspectives in the Regulation of Biodiversity Research

Presenter

Mabel Fernandes

Authors**Mabel Fernandes** (Articulation of the Indigenous Peoples of Brazil (APIB) • Brazil)**Alberto França Dias** (Articulation of the Indigenous Peoples of Brazil (APIB) • Brazil)**Cristiane Gomes Julião** (Articulation of the Indigenous Peoples of Brazil (APIB) • Brazil)**Lais Alves Moreira Brasileiro** (Articulation of the Indigenous Peoples of Brazil (APIB) • Brazil)**Keila Macfadem Juarez** (SiBBR - RNP • Brazil)**Clara Baringo Fonseca** (Sibbr - RNP • Brazil)**Abstract**

The sovereignty of Indigenous Peoples and traditional communities over their territories, knowledge, and ways of life is a fundamental right guaranteed by various legal instruments. Among them are Convention 169 of the International Labour Organization (ILO) and Brazil's Decree No. 7.747/2012, which regulates Free, Prior, and Informed Consent (FPIC) in the country. The right to FPIC must be respected whenever there is the possibility of direct impacts on these peoples, including the conduct of scientific research in their territories.

Given its importance, several communities have already developed their own consultation protocols, representing significant progress in the exercise of their self-determination. In the specific case of Indigenous Peoples in Brazil, another key governance instrument stands out: the Territorial and Environmental Management Plans (PGTAs). A PGTA is a document created by Indigenous Peoples to plan, protect, and manage their territories, respecting their knowledge, ways of life, and rights. Thus, Consultation Protocols and PGTAs document Indigenous perspectives on governance and offer valuable lessons on how to operationalize Indigenous data governance systems aligned with their vision of sovereignty.

Biodiversity research protocols are currently under debate in Brazil, and respect for Indigenous rights and sovereignty must be central to these discussions. A careful analysis of existing consultation protocols and PGTAs, through the lens of data sovereignty, is an essential step toward building specific guidelines for research involving data collection, associated traditional knowledge, and genetic resources. Based on the study of these Indigenous governance instruments, we will present pathways outlined by Indigenous Peoples in Brazil to ensure their sovereignty in the production of scientific knowledge.

Session: **6803221****7009148**

23/10/25 | 14:40

Room: Tolima

LIGHTNING TALK • EN

Embedding Indigenous Data Sovereignty in Environmental Research

Presenter

Cas Sedran-Price

Authors**Cas Sedran-Price** (University Centre for Rural Health, University of Sydney • Australia)**Rachel Ankeny** (Wageningen University • Netherlands)**Riley Taitingfong** (Native Nations Institute, Udall Center for Studies in Public Policy, University of Arizona • United States)**Jess Melbourne-Thomas** (CSIRO Environment • Australia)**Rose Barrowcliffe** (Department of Critical Indigenous Studies, Macquarie University • Australia)**Lydia L. Jennings** (Department of Environmental Studies, Dartmouth College • United States)**Stephanie Russo Carroll** (Native Nations Institute, Udall Center for Studies in Public Policy, University of Arizona • United States)**Abstract**

In ecology, climate science, and natural resource management, Indigenous data are increasingly used to develop models that guide decision-making for biodiversity conservation, sustainable agrifood systems, and emerging environmental technologies. Supporting Indigenous rights and integrating both Indigenous and Western Knowledges is essential for improving environmental outcomes in the management of Country. This inclusive approach benefits Indigenous Peoples and can enhance the development and application of ecological models. For instance, incorporating Indigenous Knowledge into species distribution modelling for threatened and culturally significant species in Australia has led to more accurate models and better-informed management strategies.

Widely promoted data principles enhanced data sharing, such as the FAIR Principles (Findable, Accessible, Interoperable, Reusable) while other principles that remind data users of the people and purpose orientation, such as CARE Principles (Collective Benefit, Authority to Control, Responsibility, Ethics), remain underutilised. Embedding the CARE Principles presents a critical opportunity for modellers and researchers to ensure that their work respects Indigenous knowledge systems, strengthens partnerships with Indigenous communities, supports fair and equitable benefits for those on whose Country they work, and benefits from the expertise of Indigenous Peoples intergenerational knowledge of their ecosystems and from where the data and associated modelling derive.

This presentation explores how operationalising the CARE Principles can support Indigenous rights, strengthen the ethical foundations of modelling practices, and ensure Indigenous communities maintain sovereignty over their data while receiving equitable benefits from research outcomes.

Session: 6803221**7014653**

23/10/25 | 14:45

Room: Tolima

LIGHTNING TALK • EN

Earth Data Relations: Implementing CARE Principles for Indigenous Data Governance across the data lifecycle for biodiversity research

Presenter

Katie Jones

Authors

Katie Jones (Wise Ancestors • United States)

Lydia Jennings (Dartmouth College • United States)

Abstract

Indigenous Peoples and Local Communities maintain relationships with and responsibilities to the many species that share lands they steward. The stories they hold are essential to understanding local and global patterns of biodiversity. However, community knowledge, priorities, and concerns are frequently excluded from research activities and are invisible in digital data frameworks. The CARE Principles for Indigenous Data Governance offer guidance for ethical practices for engaging with Indigenous data, honoring data sovereignty and integrating data governance into research design. The Earth Data Relations (EDR) recommendations activate the CARE Principles and offer suggestions for implementation across the data lifecycle. This presentation will highlight opportunities from the EDR working group to center community priorities in the planning, collection, storage, publication and re-use phases of biodiversity research in support of true co- development and community-led research practices.

Session: 6803221**7016064**

23/10/25 | 14:50

Room: Tolima

LIGHTNING TALK • ES

Entre saberes y tecnología: Gestión de información para la vida y el territorio Awá

Presenter**CAMILA SOLIS****Authors****RIDER PAY** (UNIDAD INDIGENA DEL PUEBLO AWA • Colombia)**CLAUDIA CARRION** (UNIDAD INDIGENA DEL PUEBLO AWA • Colombia)**CAMILA SOLIS** (UNIDAD INDIGENA DEL PUEBLO AWA • Colombia)**LIZETH GUERRERO** (UNIDAD INDIGENA DEL PUEBLO AWA • Colombia)**YEIMS BOTINA** (UNIDAD INDIGENA DEL PUEBLO AWA • Colombia)**CARLOS MIGUEL PAI** (UNIDAD INDIGENA DEL PUEBLO AWA "UNIPA" • Colombia)**Abstract**

La organización UNIPA, ubicada en el departamento de Nariño, Colombia, ha desarrollado diversas iniciativas territoriales orientadas a la defensa de la vida, la biodiversidad y los saberes ancestrales del pueblo Awá, frente a las crecientes amenazas del extractivismo, el cambio climático y la degradación ambiental. Estas acciones, guiadas por la visión propia del territorio, integran procesos de restauración ecológica, conservación comunitaria, monitoreo territorial y participación activa en escenarios de decisión ambiental. Gracias al liderazgo de las consejerías, se ha fortalecido el relacionamiento con actores nacionales e internacionales, posicionando marcos de conservación biocultural y promoviendo figuras como las OMEC, las KBA y las TICCA.

Estos avances han sido posibles por la creación y articulación del Sistema de Información Geográfica y el Observatorio de Derechos Humanos de UNIPA, que conforman una herramienta clave para la recolección, sistematización, análisis y difusión de información ambiental y territorial. El SIG organiza datos obtenidos mediante metodologías participativas como caracterizaciones biológicas, mapeos culturales, monitoreo comunitario y registros de biodiversidad, permitiendo la georeferenciación de sitios sagrados, áreas amenazadas, puntos críticos de deforestación y zonas de conectividad ecológica. Este proceso se fortalece con el uso de licencias de ESRI y sus aplicativos como Survey123 y Field Maps, que permiten la captura de datos geoespaciales desde el territorio.

Por su parte, el Observatorio documenta de manera rigurosa las afectaciones al pueblo Awá en el contexto del conflicto armado, así como delitos ambientales como derrames de crudo, tala, contaminación y afectaciones a zonas de importancia ecológica, articulando esta información con el SIG.

Ambos sistemas se nutren de datos generados por las autoridades tradicionales, la Guardia Indígena y las comunidades, garantizando legitimidad, pertinencia cultural y precisión técnica. Esta articulación fortalece la gobernanza territorial y la autonomía en la toma de decisiones frente a las amenazas que enfrenta el Gran Territorio Awá.

Session: 6803221**7020174**

23/10/25 | 14:55

Room: Tolima

LIGHTNING TALK • EN

Preliminary Results - CESP | Developing a data extension for documenting socio-biodiversity information

Presenter

Clara Baringo Fonseca

Authors

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Abstract

The CESP project “Developing a Data Extension for Documenting Socio-Biodiversity Information” aims to standardize data related to the uses, practices, and traditional knowledge. This effort addresses the urgent need to responsibly structure this data, safeguarding the rights of the communities who are the custodians of this knowledge.

In May of 2025, an in-person workshop was held with participants from Brazil, Colombia, and Argentina to discuss the core elements of the proposed data extension and relevant controlled vocabularies. This meeting marked a critical step toward collaboratively building solutions that support interoperability across regional and global biodiversity data platforms.

Standardizing socio-biodiversity data and adopting interoperable formats are essential for enabling the identification of information related to these knowledge systems, including their origin and context. This contributes to benefit-sharing policies and promote the misuse or misappropriation of knowledge. Regional collaboration is key to ensuring proper recognition and protection of this information across South America and beyond.

The project also includes three case studies designed to test and validate the proposed solutions, ensuring a robust and community-informed approach. By the time of the Datos Vivos 2025 event, the project expects to have advanced in the formal process within TDWG, making it essential to begin engaging additional countries in the discussion to promote wider adoption and alignment.

This presentation will share the main results achieved so far and open the floor for discussion with the broader community, aiming to refine the approach and encourage wider participation in the next steps.

Session: 6803221**7021018**

23/10/25 | 15:00

Room: Tolima

LIGHTNING TALK • EN

DSIS OF FLORA LOCATED IN BRAZILIAN Indigenous TERRITORIES: PRIOR CONSENT AS A GUARANTEE OF THE RIGHT TO INFORMATIVE SELF-DETERMINATION

Presenter

Denise Leal

Authors

Denise Leal (UnB (Brasília University) • Brazil)

Carina Costa de Oliveira (UnB • Brazil)

Fernanda Castelo Branco (Brazil)

Abstract

This research addresses the issue of DSIs of plants free communication in online-accessible databases, many of which disclose information on species originating from Indigenous territories without prior consent. National data repositories facilitate access to DSIs through international platforms such as GenBank and promote unrestricted and non-consensual use of this data, potentially violating rights related to ownership. Therefore, by examining the lack of specific legal protection over the communication of DSIs from Indigenous territories, this research proposes a critical legal analysis considering whether, in this context, the right to informational self-determination is guaranteed. It hypothesizes that this guarantee is possible through the complementarity of Indigenous territorial autonomy rights and Indigenous ownership of DSIs, based on a complementary analysis of instruments established in various legal norms. The adopted methodology combines the mapping of databases that disclose DSIs, bibliographic and documentary analysis, and critical hermeneutics, aiming to highlight normative and interpretative gaps in the protection of Indigenous collective data. The research is innovative in proposing the incorporation of the concept of Indigenous Data Sovereignty (IDS) into the Brazilian legal context, recognizing the right of Indigenous Peoples to control, decide on, and manage data related to their territories and knowledge, as recognized in many treaties. As a contribution, the research emphasizes the potential to harmonize existing legal structures to partially address regulatory gaps on the subject. It affirms the legal obligation of prior consent for the communication of DSIs, including in national databases, grounded in constitutional principles, socio-environmental norms, the Brazilian General Data Protection Law (LGPD), and international instruments for the protection of Indigenous Peoples and the environment. This approach would allow for greater control over data and the recognition of DSIs as both collective and personal data, safeguarding collective rights, Indigenous identity, and autonomy in the digital age.

Session

6802990

Symposium

23/10/25 | 14:00

Room: Caldas

Trust, Traceability & Transparency: Tackling biodiversity data provenance

Organizers

Dan Lear

Elizabeth Lawrence

Pieter Provoost

Description

Ensuring accurate data provenance is critical for biodiversity research, the development of defensible policy and the implementation of management measures, yet recording and tracking provenance presents significant technical and cultural challenges. Technically, lack of consistent use of persistent identifiers, lack of standardised tools and wider interoperability issues hinder seamless provenance tracking. Culturally, differing attitudes towards data sharing, ownership and attribution, and varying levels of data literacy create additional barriers. This session explores the complexities of recording and tracking data through complex and multiple transformations and aggregations, and through usage across diverse systems and stakeholders.

We welcome submissions from the research, policy and wider societal sectors highlighting exemplar implementations of provenance tracking, showcasing supporting tools and frameworks, and illustrating alignment and standards and current good practice to improve trust, reproducibility, and data reusability in biodiversity science.

Session: 6802990**7015389**

23/10/25 | 14:00

Room: Caldas

LIGHTNING TALK • EN

Leveraging AI-integrated, semantic modelling technology for a FAIR, scalable and collaborative biodiversity data-sharing and modelling strategy

Presenter

Ken Bagstad

Authors**Ferdinando Villa** (Basque Center for Climate Change (BC3) • Spain)**Stefano Balbi** (Basque Center for Climate Change (BC3) • Spain)**Alessio Bulckaen** (Basque Center for Climate Change (BC3) • Spain)**Megan Critchley** (Basque Center for Climate Change (BC3) • Spain)**Beñat Eguidazu** (Basque Center for Climate Change (BC3) • Spain)**Caterina Gilli** (Basque Center for Climate Change (BC3) • Spain)**Marta Pascual** (Basque Center for Climate Change (BC3) • Spain)**Ken Bagstad** (United States)**Abstract**

ARIES (ARTificial Intelligence for Environment & Sustainability) is an open-source technology platform designed to deliver FAIR and Open Data-aligned modelling capabilities through high-level semantic interoperability. Unlike approaches that rely solely on data format compatibility, ARIES enables machines to understand and appropriately reuse both data and models by encoding their meaning and usage conditions. This allows for automated selection and assembly of models tailored to specific contexts—by time, place, and scale—while maintaining full transparency through provenance reporting.

Through its semantic infrastructure, ARIES provides a unified framework for integrating heterogeneous data and models. This lowers technical barriers for users such as National Statistical Offices (NSOs), ministries, and researchers. It supports collaboration between data producers and decision-makers by enabling the rapid generation of meaningful, context-specific outputs.

ARIES technology is particularly well-suited to expand into biodiversity-related data and modelling services. This can play a crucial role in advances towards biodiversity conservation targets, such as by supporting the monitoring and reporting of key biodiversity indicators for the Kunming-Montreal Global Biodiversity Framework.

Realizing this potential requires close collaboration with domain-specific partners. Strategic partnerships will be essential to translating this technical capability into real-world impact. In this envisioned role, ARIES will act as a semantic orchestrator for diverse data and modelling services. This will enable biodiversity knowledge to be more accessible, reusable, and impactful across scales. Achieving this will make FAIR-aligned modelling and data more accessible worldwide, while expanding the reach and reuse of scientific models from leading institutions.

This vision outlines a path toward a next-generation interoperable biodiversity information infrastructure—one that is rapidly recompilable, globally comparable, and locally customizable.

Session: 6802990**7013886**

23/10/25 | 14:05

Room: Caldas

ORAL VIRTUAL • EN

A model for the provenance of marine biological samples and data

Presenter

Katrina Exter

Authors

Katrina Exter (Flanders Marine Institute (VLIZ) • Belgium)

Laurian Van Maldeghem (Flanders Marine Institute (VLIZ) • Belgium)

Christina Pavloudi (EMBRC • Belgium)

Ioulia Santi (EMBRC • Greece)

Cymon Cox (CCMAR • Portugal)

Abstract

We present our conceptual model for documenting provenance information for *biological material, observations, and their related and derived data*, with a focus on the marine biology domain. This model describes the provenance information necessary to describe the who, what, where, when, and how of collected/created/used biological material, the derived data, and observations. The model covers the activities carried out during typical marine biological field and experimental work, and is easily extendable to accommodate specialised areas of research (e.g. bioinformatics, AI-based analyses, complex imaging, etc.).

By providing this provenance information, one is providing: trustability; transparency and traceability; and reproducibility and reusability, thus ensuring FAIRness. Unfortunately, provenance metadata is not often provided at the level necessary to fully provide for “trust, trace, and reuse”; this can be due to lack of knowledge or neglect by individual scientists or due to the lack of standards’ implementation by data repositories.

EMBRC has constructed this model, its associated schemas, and examples in plain text, EML, and JSON-LD, to make it easier for data producers to create provenance metadata for the data they publish and share. This work started in the Horizon project EOSC-Life, and is completing its journey in the Horizon project MARCO-BOLO.

We will present the conceptual model and its schemata, and explain how this provides the necessary provenance. We will demonstrate this in action by going through some example experiments and their datasets, and showing the provenance metadata that should accompany the resulting data. These examples and associated templates, can be used as resources by other scientists when creating their own provenance descriptions.

Session: 6802990**7019901**

23/10/25 | 14:16

Room: Caldas

ORAL • EN

Tracking natural science objects and their physical and digital derivatives in DINA

Presenter

Jonas Grieb

Authors

Jonas Grieb (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)**James Macklin** (Agriculture and Agri-Food Canada • Canada)**David Shorthouse** (Agriculture and Agri-Food Canada • Canada)**Christian Bölling** (Museum für Naturkunde Berlin – Leibniz Institute of Evolution and Biodiversity Science • Germany)**Michaela Grein** (Übersee-Museum Bremen • Germany)**Etta Grotrian** (Übersee-Museum Bremen • Germany)**Volker Lohrmann** (Übersee-Museum Bremen • Germany)**Claus Weiland** (Senckenberg – Leibniz Institution for Biodiversity and Earth System Research • Germany)

Abstract

Provenance plays an important role in natural history collections, but capturing this information on a technical level accurately proved challenging for legacy digital collection management systems. DINA is being developed to address these limitations through a process-oriented data model that more effectively captures the complexity and context of provenance information. DINA is an open-source, robust sample and specimen-based collection management system in production and developed by an unincorporated international Consortium of technologists and practitioners of the Natural Sciences. Its governance and data models help to foster the adoption of FAIR principles and to integrate objects across science domains. DINA's innovative "samplistic" design model records the metadata on stepwise, branching processes that generate physical and digital derivatives from parent material samples. Each object in the provenance chain as well as first-class related objects like projects, collections, events, people, protocols, and storage exposes a system-defined global unique identifier. DINA integrates with external systems wherever possible, based on the linkage via persistent identifiers. Its application programming interface helps simplify data import and migration and can be used by scientific programming languages like Python or R to access data objects or their relationships. Flexible user- or project-defined "managed attributes" along with custom tooltips (e.g. categories of regulated taxa) are used to enhance object and derivative metadata when standards do not yet exist and to help guide users and their teams through the user interface. When standards like MIxS (Minimum Information about Any Sequence) or MIDS (Minimum Information about a Digital Specimen) do exist, these are seamlessly incorporated as field extensions.

We will provide examples and discuss how the DINA data model supports strong provenance tracking to foster reproducible science, and for potential use in regulatory or applied research environments where intellectual property and legal protections may be required.

Session: 6802990**7020085**

23/10/25 | 14:33

Room: Caldas**ORAL • EN**

Bridging the Gap: Simplifying Metadata Flows with an EOVS Application

Presenter

Elizabeth Lawrence

Authors

Elizabeth Lawrence (UNESCO | IOC Project Office for IODE Ocean Biodiversity Information System • Canada)

Abstract

Metadata is the backbone of trust and transparency in biodiversity data, yet it remains a challenging and often technical process to document effectively. The Ocean Data and Information System (ODIS) aims to facilitate connections between resources like the GOOS BioEco Portal and OBIS, but its technical requirements for submissions can be a barrier for many users. BioEcoOcean, a Horizon Europe project, has supported the development of an Essential Ocean Variable (EOV) Application to address this gap by providing a user-friendly, form-based interface designed for non-technical users to seamlessly record, submit, and update essential metadata about organizations, institutions, or other monitoring programs (“data producers”) that monitor biodiversity. By simplifying the process, the tool promotes greater accessibility and ensures metadata aligns with established data schemas, without burdening users with technical knowledge. Future development aims to incorporate EOV data schemas and conversions of field data templates to Darwin Core, further enhancing its utility for biodiversity data management. This presentation will showcase the app’s development, key features, and its role in advancing trust and traceability in biodiversity data management.

Session: 6802990**7020730**

23/10/25 | 14:46

Room: Caldas

LIGHTNING TALK VIRTUAL • EN

Embedding Provenance into Biodiversity Data: Team-Based Integration, Standards, and Preservation in Taiwan's LTSER

Presenter

De-Kai Kao

Authors**De-Kai Kao** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Chun-I Chang** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Mao-Ning Tuanmu** (Taiwan Biodiversity Information Facility, Biodiversity Research Center, Academia Sinica • Taiwan)**Abstract**

Accurate data provenance is essential for biodiversity research, defensible policy development, and effective management implementation. However, it requires more than just technical frameworks—it demands human-centered collaboration and long-term institutional support.

Within Taiwan's Long-Term Socio-Ecological Research (LTSER) platform, we work closely with individual data contributors to address the practical challenges of standardization, traceability, and data preservation across disciplines.

One persistent challenge is the inherent heterogeneity of biodiversity data, spanning diverse ecological, species observation, and socio-cultural contexts, which often hinders seamless cross-domain data integration. To address this, we facilitate the adoption of biodiversity data standards through tools that guide metadata structuring and ensure data quality. This includes a GPT-powered assistant to aid contributors in standard alignment and external toolkits for crucial data cleaning and validation before publication. Through one-on-one consultations, we promote awareness of metadata quality and standard adherence, fostering trust-based engagement vital for harmonizing disparate datasets.

For long-term preservation and transparent provenance, we primarily utilize the depositor platform, maintained by Academia Sinica. We support contributors in preparing metadata, assigning persistent ARK identifiers, and aligning with FAIR principles. Crucially, the depositor API enables powerful extensions: data are directly visualized on associated project websites, enhancing accessibility and reusability.

Furthermore, the API allows for managing and tracking the progress of data uploads, ensuring timely and consistent submissions while preserving provenance throughout the data lifecycle.

These overarching workflows and solutions were not developed in isolation but emerged through continuous dialogue and collaboration between researchers, data managers, and software developers.

Our experience highlights the value of hands-on, trust-based support in embedding robust provenance practices into real-world biodiversity data workflows. We offer this work as a practical example of how traceability, interoperability, and transparency can be achieved through ongoing engagement and shared responsibility in a complex socio-ecological context.

Session: 6802990**7020779**

23/10/25 | 14:51

Room: Caldas

LIGHTNING TALK • EN

Enhancing Provenance and Interoperability in Biodiversity Informatics Through Decentralized Aggregation: The Symbiota Model

Presenter

Edward Gilbert

Authors**Edward Gilbert** (University of Kansas • United States)**Nico Franz** (University of Kansas • United States)**Beckett Sterner** (Arizona State University • United States)**Abstract**

The generation and maintenance of biodiversity data remain inherently decentralized, scattered across thousands of local institutions and collections. Yet, researchers, policymakers, and conservationists depend on centralized, standardized data resources. Reconciling these conflicting needs—local control versus global integration—poses significant social and technical challenges, including data fragmentation, limited interoperability, and the absence of efficient bidirectional feedback between local collections and global aggregators.

Symbiota is a community-driven biodiversity data content management system that addresses these challenges through a novel, decentralized aggregation model. Unlike conventional top-down aggregators, Symbiota portals function as both data managers and publishers, offering tools that empower collections to maintain control over their data while contributing to broader data networks. Recent developments include an Application Programming Interface (API)-driven architecture enabling real-time, bidirectional data exchange between distributed portals, source collections, and potential external systems such as Specify and EMu.

This infrastructure allows annotations and updates to propagate dynamically across the network, improving data provenance, reducing latency, and enhancing trust. It also re-engages domain specialists, who remain the most qualified to detect and correct errors, by providing mechanisms to contribute directly to the data curation lifecycle. By supporting transparent record-level change tracking and live synchronization, the Symbiota model fosters a culture of shared responsibility and collaboration.

This presentation will highlight how API-enabled cross-portal integrations enhance data quality and provenance while advancing interoperability and reuse. Symbiota's architecture offers a blueprint for building dynamic, distributed biodiversity data infrastructures that balance local autonomy with global utility. It demonstrates how socially aware technical frameworks can overcome longstanding barriers to data sharing, supporting more reproducible science, responsive conservation action, and defensible policy development.

Session: 6802990**7020151**

23/10/25 | 14:56

Room: Caldas**ORAL VIRTUAL • EN**

Book Binding for the Digital Age - Format Agnostic Method to Review and Archive Biodiversity Data

Presenter

Jorrit Poelen

Authors

Jorrit Poelen (UC Santa Barbara Cheadle Center for Biodiversity and Ecological Restoration • United States)**Katja C. Selmann** (UC Santa Barbara Cheadle Center for Biodiversity and Ecological Restoration • United States)

Abstract

While traditional books offer stable, citable, and independently archived units of knowledge, digital data often lack these qualities. Books maintain consistent content over time, and bookbinding ensures content integrity because it is evident if a page has been torn out. In contrast, digital content on the web is ephemeral, susceptible to modification or loss without clear mechanisms for tracking what was changed. Here, we present a framework for treating biodiversity datasets as “digitally bound books”: immutable, read-only data packages that can be archived, verified, cited, and grouped into collections without altering their content or structure. This approach provides a durable and decentralized model for data stewardship, enabling biodiversity knowledge to be preserved, discovered, collected, shared and cherished much like traditional books.

Built on flexible and mature NIST and W3C standards, these “digitally bound books” or data packages, support rich provenance and exact content referencing. A data package can consist of single data records, entire datasets (a Darwin Core Archive), data portals, as well as larger collections of biodiversity data (GBIF & iDigBio datasets, BHL pdfs).

We show how our framework allows for packaging of heterogeneous data sources by applying it to three examples: (1) single specimen image, (2) darwin core archive from a natural history collection including associated images, and (3) packaging entire networks. We then demonstrate digitally binding these examples and depositing them to Zenodo, creating sharable and citable versions of the datasets for QC review (taxon name alignment) and analysis.

With these examples, we hope to demonstrate that this framework supports any data format and allows for packaging, citing and distributing these digital data similar to how books are bound, referenced and distributed. These digitally bound datasets are ready to be cited in published literature, and enable trustworthy, decentralized biodiversity data stewardship at multiple scales.

Session: 6802990**7020041**

23/10/25 | 15:07

Room: Caldas

LIGHTNING TALK VIRTUAL • EN

BioDash : an EBV-based dashboard of European biodiversity monitoring schemes

Presenter

Guillaume Body

Authors**Guillaume Body** (Patrinat (OFB-MNHN-CNRS-IRD) • France)**Mathieu Basille** (Patrinat (OFB-MNHN-CNRS-IRD) • France)**Petteri Vihervaara** (Finnish Environment Institute • Finland)**Thomas Bouix** (Patrinat (OFB-MNHN-CNRS-IRD) • France)**Loïse Vergnaud** (Patrinat (OFB-MNHN-CNRS-IRD) • France)**Morgane Maillard** (French Biodiversity Agency (OFB) • France)**Abstract**

Biodiversity monitoring schemes run on the long term, and are notably providing annual datasets and various data products, from raw data to indicators through Essential Biodiversity Variable products. In Biodiversa+, the European partnership aiming at improving biodiversity monitoring across Europe, we started to centralize information about the protocols and practises of monitoring schemes—information that is currently scattered across various papers and metadata sheets. We are developing a digital project, named BioDash, to directly describe monitoring schemes by their goals, protocols, ressources and EBV products, and linking them to the various datasets it produces to facilitate navigation through all this information. With BioDash, we will be able to evaluate the quality of monitoring schemes and of each EBV produced. By listing EBV products from monitoring schemes, we will also be able to synthetize the landscape of hundreds of biodiversity monitoring schemes. BioDash will provide decision-makers a key service currently missing to improve connections between existing and dispersed schemes, and engage scheme leaders to discuss harmonisation throughout Europe.

Session

6798921

Symposium

23/10/25 | 14:00

Room: Valle

Best practices to mobilize & integrate local & community-based data for scalable biodiversity impact

Organizers

Thore Engel

Florencia Grattarola

Diana Bowler

Laura Catalina Quintero Uribe

Tafadzwa Muzira

Cathrine Mashonganyika

Description

Biodiversity data is only as strong as the communities that generate it. With over 80% of the world's biodiversity found in local and Indigenous territories, engaging communities in biodiversity monitoring is crucial for accurate, policy-relevant, and actionable data. Citizen science (or community science) underpins most large-scale species monitoring and is already used for national indicators of biodiversity change. However, citizen science is incredibly diverse, with a broad range of types of data collected using diverse methods. With the proliferation of smart phone apps, many data streams from citizen science are being mobilized. However, there are many untapped opportunities, including local recording groups and community-based projects, that could fill information gaps in some parts of the world, especially in tropical and other undersampled regions. In this session, we invite contributions that mobilize and integrate such community-based biodiversity data.

We are interested in the diverse experiences of community-based projects that cover any of the various stages of data mobilization, from data collection and management to publication and use. This also includes the question how the FAIR and CARE data principles are applied in the context of citizen science. We are especially interested in case studies from Latin America and the global south and we encourage submissions from early career researchers and practitioners. We hope that a set of guidelines or best practices will emerge from the discussions, which will point towards ways to mobilize untapped data sources.

Session: 6798921**7020448**

23/10/25 | 14:00

Room: Valle

ORAL • EN

Building trust to mobilize local biodiversity data: community-based monitoring in Colombian páramos

Presenter

Ana Belén Hurtado-M

Authors

Ana Belén Hurtado-M (Instituto Humboldt • Colombia)

Sindy Martinez-Callejas (Instituto Humboldt • Colombia)

Viviana Salinas Vargas (Instituto Humboldt • Colombia)

Angela Sierra (Instituto Humboldt • Colombia)

Helena Olaya (Instituto Humboldt • Colombia)

de monitoreo Equipo locales (Instituto Humboldt • Colombia)

Abstract

Within the GEF-funded project *Páramos para la Vida*, we are working with Indigenous and peasant communities in six regions of Colombia to promote community-based biodiversity monitoring in páramos—ecosystems that are ecologically vital and inhabited by local communities who depend on and care for these landscapes. The goal is to generate local, actionable data on species of ecological, cultural, and conservation interest to inform restoration and sustainable management.

Eighteen local monitoring groups are currently collecting data on birds, mammals, and plants using a shared protocol adapted to the context and capacities of each region. The process has prioritized building trust and strengthening community capacities to enable participants not only to collect data but also to analyze it and use it in local decision-making. Special attention has been given to gender inclusion and youth participation, recognizing their key roles in territorial stewardship and intergenerational knowledge exchange.

Challenges such as limited literacy, restricted access to formal education, and concerns about data sharing have been addressed through continuous support and community engagement. This case highlights the importance of long-term partnerships and culturally rooted approaches for implementing monitoring systems that respect local values while generating reliable biodiversity information.

Our experience contributes to the discussion on how community-based science can align with the FAIR and CARE principles, offering practical insights for mobilizing untapped data sources from tropical and underrepresented ecosystems.

Session: 6798921

7008943

23/10/25 | 14:15

Room: Valle

ORAL • EN

From Data to Dialogue: A Participatory Approach to Landscape Sustainability

Presenter
Arturo Tovar

Authors
Arturo Tovar (Rainforest Alliance • Perú)
Hannah Grice (United Kingdom)

Abstract
In many landscapes around the world, sustainability challenges are complex, interconnected, and deeply tied to local context. LandScale is a system for assessing sustainability across environmental, social, and economic dimensions—designed not only to generate trusted data, but to foster inclusive processes that bring stakeholders together. This talk explores how landscape initiatives are using LandScale not just as a reporting tool, but as a catalyst for collaboration. Through consultations, data sharing, and collective analysis, local actors—from farmers to NGOs to policymakers—build a shared understanding of their landscape’s conditions and co-create solutions. We’ll share practical examples of how credible, holistic information—paired with a participatory process—can support more informed, transparent, and community-driven sustainability decisions.

Session: 6798921**7012812**

23/10/25 | 14:30

Room: Valle

ORAL • EN

A GBIF-hosted portal for Germany: Der Lebendige Atlas der Natur Deutschlands (LAND)

Presenter

Thore Engel

Authors

Thore Engel (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig • Germany)**Martin Friedrichs-Manthey** (Germany)**Jörg Holetschek** (Germany)**Robert Köpke** (Germany)**Pascal Scherreiks** (Germany)**Anton Güntsch** (Germany)**Birgitta König-Ries** (Germany)**Aletta Bonn** (Germany)

Abstract

Biodiversity data can be messy, scattered and hard to come by. As the national research data infrastructure for biodiversity (NFDI4Biodiversity) we set out to make German biodiversity data FAIR and open. One of our products is the “Lebendiger Atlas der Natur Deutschlands (LAND)”, a national biodiversity portal that provides species occurrence data in Germany to researchers, conservation authorities and the general public. To do so, we joined forces with the Global Biodiversity Information Facility (GBIF) as well as the national node GBIF.de and created the LAND-portal using the GBIF hosted portal service (<https://land.gbif.de/>).

The portal integrates species occurrence data from different sources, including monitoring initiatives, citizen science, natural history societies, museums and universities. To start with, we mostly stocked the portal with existing datasets from GBIF. Now we focus on mobilizing new datasets. To continue to improve the service and mobilize new datasets to GBIF and LAND, we organize annual community workshops with 50–80 stakeholders from different institutions. In this talk, we present the current state of the portal and its functionalities and discuss opportunities for data holders and researchers to get involved. Furthermore, we’re keen to connect with similar initiatives in other countries.

Session: 6798921**7018680**

23/10/25 | 14:45

Room: Valle

LIGHTNING TALK VIRTUAL • EN

Unpacking Data Quality in Citizen Science: An Analysis of City Nature Challenge India

Presenter

Ram Dayal Vaishnav

Authors

Ram Dayal Vaishnav (The Naturalist School • India)

Ashwin A (The Naturalist School • India)

Vijay Barve (India)

Chitra Shanker (India)

Lavanya Bhat (India)

Abstract

The City Nature Challenge (CNC) has rapidly expanded across India from 2023 to 2025, resulting in a surge of biodiversity observations on iNaturalist. While the volume of data is impressive, its long-term research and conservation value depends heavily on data quality – particularly the proportion of observations reaching “Research Grade” (RG). This study investigates patterns and barriers related to RG achievement in CNC India observations over three consecutive years.

We analyze RG percentages at regional, state and city scales, comparing initial post-event values from this year with those from previous years. In addition to temporal comparisons, we investigate spatial variations in data quality across India. Utilizing iNaturalist data, we identify taxa and locations with disproportionately high numbers of “Needs ID” observations. This analysis is conducted both horizontally across taxonomic groups and vertically by taxonomic rank (e.g., family vs. genus vs. species). This approach helps reveal where data curation is bottlenecked, whether due to identification challenges, observer behavior, or absences within the identifier community.

Our findings offer practical insights for enhancing community engagement, directing identification efforts and designing more effective support mechanisms for new observers. We also discuss implications for using CNC data in research and conservation, particularly in regions with emerging citizen science communities.

By providing a nuanced perspective on evolution of data quality within a massive, volunteer-driven dataset, this presentation contributes to broader discussions on sustaining and improving the living data ecosystems that support contemporary biodiversity science.

Session: 6798921**7014678**

23/10/25 | 14:50

Room: Valle

LIGHTNING TALK • EN

Ictio: the Amazon fish observation platform

Presenter

Sannie Brum

Authors

Sannie Brum (Wildlife Conservation Society - Andes, Amazônia & Orinoquia • Brazil)

Carolina Doria (UNIR • Brazil)

Gina Leite (WCS • Brazil)

Guido Miranda (WCS Bolivia • Bolivia (Plurinational State of))

Guillermo Estupiñan (Brazil)

Jonathan Valdiviezo-Rivera (INABIO • Ecuador)

Liliane Stedile de Matos (UFMT • Brazil)

Pablo A. Tedesco (Université de Toulouse • France)

Mariana Varese (WCS • Perú)

Fernando Anaguano (WCS Ecuador • Ecuador)

Abstract

Migratory fish are culturally, economically and ecologically important in the Amazon but are threatened. Their conservation requires monitoring and management at the appropriate scale - a major challenge for artisanal fisheries. The lack of data for fishery statistics is one of the biggest challenges for ichthyofauna conservation and the Citizen Science approach can be an important ally. In this sense, the Amazon Water Alliance created Ictio, a free platform to record fish observations. Ictio was initially developed by a group of experts who discussed the variables to be collected. The design of the app was then discussed with focus groups of fishers and the first version launched in July 2018. From then on, training sessions were held with interested fishers, as well as a communication campaign. Ictio App could be downloaded and used by anyone from the Google Play Store. Later, a spreadsheet upload platform was added. Between April 2018 and March 2025, 732 people and institutions shared 130,566 valid observations of 121 species or groups of fish species in 7 countries in the Amazon basin. With Ictio data, invasive species have been recorded, such as the Arapaima in the Madeira basin (Bolivia and Brazil) and tilapia in the Santiago River (Ecuador). Ictio increased the known range size of 8 prioritized species by an average of 26%. Ictio faces challenges such as limited internet access in the region and more participatory data analysis. Currently, data is made available quarterly on our website and we support data feedback, a crucial part of user involvement. We are also developing new collection tools based on other platforms such as Anecdata, SMART and EarthRanger. The experience with Ictio has been a success, demonstrating that it is possible to collect and store accurate data securely through a citizen science platform.

Session: 6798921**7020950**

23/10/25 | 14:55

Room: Valle

LIGHTNING TALK • ES

Integration of Technologies for Information Management and Participatory Conservation in the Regional Management District Cuchilla (RMD) del San Juan

Presenter

Manuel Rodríguez Rocha

Authors

Manuel Rodríguez Rocha (Wildlife Conservation Society • Colombia)

Carlos Baena (FECOMAR • Colombia)

Mario Santana (Wildlife Conservation Society • Colombia)

Styven Herrera (CARDER • Colombia)

Jorge Enrique Parra (Wildlife Conservation Society • Colombia)

Abstract

The RMD Cuchilla del San Juan, located in the Western Andes of Colombia, is the largest protected area in the department of Risaralda, covering 29,661.8 hectares. Classified as an IUCN Category VI protected area, it allows for the sustainable use of natural resources without compromising biodiversity conservation. In 2024, its Management Plan for the period 2024–2029 was formally adopted. The plan was developed through a participatory process involving local communities, institutions, and strategic partners (CARDER, FECOMAR, IAvH, WCS). It focuses on six priority management issues: forest management, agricultural development, nature and wellness tourism, regulation of environmental resource use, human-wildlife coexistence, and aquatic ecosystem management. This work presents the District's Information Management System, designed to support the implementation of the management plan and assess its effectiveness in achieving conservation objectives. The system integrates multiple technological platforms, including SMART (spatial monitoring and reporting tool), Global Forest Watch (deforestation alerts), eBird and iNaturalist (citizen science tools), and EarthRanger (real-time data visualization and analysis), thereby enhancing decision-making processes. To date, the system has consolidated socio-economic, cultural, and livelihood data from 514 families (1,504 individuals), alongside geospatial data on biodiversity, land use, and anthropogenic pressures. With over 10,000 records, the system enables the monitoring of deforestation alerts and key conservation targets, including ecosystems, carnivores, birds, pollinators, seed dispersers, and water resources. Furthermore, it has supported the implementation of more than 100 conservation actions across 4,000 hectares, grounded in community-based agreements. This information system strengthens community engagement as a cornerstone of adaptive management and guides decision-making at both local and protected area scales. Ultimately, it fosters technical and social cooperation to ensure the long-term sustainability of the protected area.

Session: 6798921**7007029****23/10/25** | 15:00**Room:** Valle**ORAL • EN**

Empowering young ocean scientists in Egypt: Enhancing Community Engagement for Sustainable Aquaculture and Biodiversity Conservation in Climate Change Mitigation

Presenter

Hadeer Elkhoully

Authors

Hadeer Elkhoully (Early Career Ocean Professionals • Egypt)

Abstract

This presentation highlights the pivotal role of Africa Ocean Scientist in Egypt in fostering community engagement to promote sustainable aquaculture and biodiversity conservation amidst the challenges of climate change. As Egypt's aquaculture sector expands to meet growing nutritional demands, it faces pressures from environmental degradation and biodiversity loss. ECOPs are uniquely positioned to bridge scientific knowledge and local communities, facilitating awareness, capacity-building, and participatory decision-making processes. Through tailored outreach initiatives, training programs, and collaborative projects, young professionals are actively involving local stakeholders in sustainable practices that enhance fishery resilience and ecosystem health. This presentation will showcase successful case studies illustrating how Egyptian ECOPs are contributing to community-led conservation efforts, integrating traditional knowledge with innovative solutions, and advocating for policies that support climate adaptation. Emphasizing the importance of empowering early career professionals, this talk underscores their potential to drive positive change, foster community ownership, and ensure the long-term sustainability of Egypt's aquaculture and marine biodiversity sectors in the face of climate change. The insights shared aim to inspire similar initiatives globally, demonstrating that empowered young ocean professionals are vital agents of environmental resilience and sustainable development.

Session

6799326

Symposium

23/10/25 | 14:00

Room: Cauca

Listen to the Future: Mobilizing Bioacoustic Data to Meet Conservation Goals

Organizers

Vanessa Reyes

Talía Speaker

Justin Kitzes

Description

Bioacoustics is transforming biodiversity monitoring by providing an efficient, scalable, and non-invasive tool for identifying species, assessing ecosystem health, and detecting human impacts across vast and remote areas. As recording technologies and AI-driven analytics become more accessible, the discipline is advancing rapidly. However, critical challenges remain in translating these innovations into effective conservation action, requiring clear priorities to guide progress.

This session will unveil and explore findings from our recent global horizon scan that identifies emerging innovations poised to shape bioacoustics over the next two decades. The study draws insights from 50 experts across disciplines, highlighting priority advancements in engineering, analytics, and coordination—from real-time acoustic monitoring with cutting-edge AI to abundance estimation tools to mobilizing bioacoustic data to meet conservation goals.

Attendees will gain insights into how the sector can leverage bioacoustics to monitor the impacts of climate change, track biodiversity trends, and evaluate ecosystem health. The discussion will highlight pathways for overcoming barriers to adoption and fostering interdisciplinary collaboration, ensuring bioacoustics can drive meaningful conservation action and data-driven decision-making.

Session: 6799326**7015925**

23/10/25 | 14:10

Room: Cauca

ORAL • EN

PiWild: Optimising the Raspberry Pi for acoustic monitoring of ecosystems

Presenter

Gabriel Kiarie

Authors

Gabriel Kiarie (Centre for Data Science and Artificial Intelligence (DSAIL), Dedan Kimathi University of Technology • Kenya)

Abstract

Advances in technology have resulted in the development of low-cost open-source boards that can be utilised to collect data remotely and continuously in ecosystems. The Raspberry Pi is among the most commonly used single-board computers due to its low cost, strong support community, and compatibility with various programming languages and machine learning frameworks. Its relatively high processing power also makes it suitable for edge-based machine learning.

Power supply is critical when deploying sensors off-grid. Improper shutdowns when using the Raspberry Pi, such as those caused by battery depletion, can corrupt its storage and result in data loss. To address this, PiWild, a power management board, was developed. It allows the Raspberry Pi to operate autonomously off-grid by enabling: (1) powering the acoustic sensor using a battery and a solar panel;

(2) battery monitoring and safe shutdown upon low charge; (3) user-defined operation windows, with the system shutting down outside these times; (4) scheduled wake-up using an onboard RTC before shutdown; (5) automatic shutdown after an operating window or on low battery; and (6) automatic wake-up at the start of an operation window or after recharging.

Using PiWild, Raspberry Pi-based acoustic sensors have been deployed in the central region of Kenya to monitor ecosystems. The acoustic sensor costs less than USD 250, making it relatively cheaper than commercially available alternatives. This makes it easier to scale, addressing the scarcity of data in the Global South, especially in Africa. The superior processing capabilities of the Raspberry Pi compared to microcontrollers also allow edge computing. This reduces the need for large computing resources needed to process the voluminous data collected by multiple sensors. The inferences are also transmitted using a low-power wide area network (LPWAN) such as LoRa, since the process requires less bandwidth. This setup supports real-time, energy-efficient ecosystem monitoring.

Session: 6799326**7020486**

23/10/25 | 14:18

Room: Cauca

ORAL • EN

Individual identification and call type classification with unsupervised learning

Presenter

Mélisande Teng

Authors

Mélisande Teng (Canada)

Julien Boussard (Mila, McGill University • Canada)

Hugo Larochelle (Mila • Canada)

David Rolnick (Mila, McGill University • Canada)

Abstract

Individual identification and call type classification are crucial for many ecological tasks, such as tracking individuals, classifying behaviour and estimating population. Recently, deep learning has proved to be a promising tool for bioacoustics, particularly for species classification, alleviating the need for manual annotation of long passive acoustic monitoring audio recordings. However, in the context of individual identification, there is little available data labelled at the individual or call level, restricting the applicability of supervised data-driven approaches to a few species and datasets. One approach is to segment the calls as sequences of syllables to facilitate individual ID or call type classification (TweetyNet, Cohen et al., 2022), but still relies on per-species syllable annotations. In this talk we present an unsupervised machine learning algorithm to decompose any call from any species into a sequence of syllables. We first separate the notes based on silences (Sainburg et al., 2019), then use hierarchical clustering to group these notes into clusters and extract templates -syllable representations- before performing matching pursuit to decompose each call as a sequence of syllables. We explore whether this approach can help identify an individual's unique vocabulary and vocal signature. We investigate whether the intra-species, per-syllable variability is sufficient for clustering and classifying individuals.

Session: 6799326**7013823**

23/10/25 | 14:26

Room: Cauca

ORAL • EN

Enabling large-scale acoustic biodiversity data mobilization through open and automated data flows

Presenter

Mao-Ning Tuanmu

Authors

Zhi Xian Hoh (Department of Computer Science and Information Engineering, National Taipei University of Technology • Taiwan)**Chia-Yun Lee** (Biodiversity Research Center, Academia Sinica • Taiwan)**Jin-Ying Lee** (Taiwan Biodiversity Information Facility • Taiwan)**Mao-Ning Tuanmu** (Biodiversity Research Center, Academia Sinica • Taiwan)

Abstract

Passive acoustic monitoring (PAM) has emerged in recent years as a cost-effective and scalable method for long-term, high-frequency collection of environmental and biodiversity data, offering distinct advantages over traditional survey approaches. However, the large volume and unstructured nature of audio recordings present significant challenges for data storage, mobilization, and subsequent information extraction and application. In response to these challenges, the Asia Soundscape Monitoring Network data portal (<https://soundscape.biodiv.tw/>), officially launched in 2024, provides open access to over 23 million minutes of audio recordings and associated derived data, including acoustic indices and species-specific call identifications. These recordings, collected since 2014 from multiple Asian countries—such as Taiwan, Vietnam, Thailand, and Malaysia—are made available through a user-friendly interface with clearly defined data licensing and citation information. To enhance the efficiency of data processing and mobilization, we have developed an end-to-end automated workflow encompassing recording verification and upload, acoustic index computation, AI-based animal sound recognition, and data publication to the portal. This workflow is integrated with a graphical user interface (GUI) to facilitate user oversight and parameter adjustment. Additionally, we have implemented a verification interface for AI-generated identification results, enabling taxon-specific experts to efficiently review and annotate species detections. This not only improves the quality and reliability of species identification results presented on the platform, but also generates high-quality training and validation datasets necessary for the continued optimization of AI recognition tools. The integration of these automated pipelines and expert-review interfaces significantly enhances the timeliness and accessibility of acoustic biodiversity data, thereby increasing its utility for a wide range of ecological and conservation applications.

Session: 6799326**7014612**

23/10/25 | 14:35

Room: Cauca

ORAL • EN

pamflow: Analysis and standardization for passive acoustic monitoring data

Presenter

Nicolas Betancourt

Authors

Nicolas Betancourt (Instituto de Recursos Biológicos Alexander Von Humboldt • Colombia)**Juan Sebastian Ulloa** (Instituto de Recursos Biológicos Alexander Von Humboldt • Colombia)

Abstract

A promising approach to improve ecological knowledge has been to involve local communities in passive acoustic monitoring (PAM). Processing the vast amounts of data resulting from these initiatives remains a significant bottleneck, limiting the adoption of this technology by local communities. Thus, community PAM projects demand the implementation of a simple, standardized and replicable data processing workflow. Available computational tools require more than minimal computational resources and internet connectivity, which is unrealistic for many communities inhabiting biodiversity hot-spots. Even after processing PAM data, an additional challenge is that currently available tools don't translate data into global standards for biodiversity information, impeding public availability of the resulting data.

We will introduce pamflow, an open-source and modular solution for processing large amounts of PAM data using minimal computational resources and for standardizing data. We will show the results of a PAM project with communities of La Macarena region, a biodiversity hotspot where the Orinoco Basin, the Amazon Jungle and the Andes meet. In this project we not only processed the resulting acoustic data but also standardized the metadata and the audios for feeding the observations to GBIF and storing the WAV files in Humboldt's Sound Collection. Having a data processing workflow connecting the outputs of monitoring projects to open and widely used information systems such as GBIF is critical and extends the impact of any PAM project. As an open-source project, we hope pamflow empowers researchers and local communities with easier access to cost-efficient tools, enabling them to better manage their natural resources and contribute essential data on the status and trends of biodiversity.

Session: 6799326**7018615**

21/10/25 | 14:42

Room: Cauca

ORAL • EN

Can we use the Camera Trap Data Package standard for bioacoustics data?

Presenter

Sanne Govaert

Authors

Sanne Govaert (Research Institute for Nature and Forest (INBO) • Belgium)**Julia Wiel** (Norwegian Institute for Nature Research (NINA) • Norway)**Peter Desmet** (Research Institute for Nature and Forest (INBO) • Belgium)**Benjamin Cretois** (Norwegian Institute for Nature Research (NINA) • Norway)

Abstract

Bioacoustics has seen a rapid usage growth in the last decade, allowing wildlife monitoring at an unprecedented scale. However, this rapid growth has created challenges regarding data management, classification, use, exchange and archival. The lack of an accepted bioacoustic standard is one of the main bottlenecks for making bioacoustic data easily exchangeable. This hinders global cooperation and impedes the publication of open data to platforms such as the Global Biodiversity Information Facility (GBIF).

This issue was recently tackled in the camera trap community, with the development and adoption of the Camera Trap Data Package (Camtrap DP). This community-developed open standard supports the FAIR exchange and archiving of camera trap data. The standard is now rapidly adopted by the camera trap community, creating an ecosystem of interoperable software tools for data management, analysis, visualisation and publication. While Camtrap DP is designed for traditional camera trap studies of medium-to-large mammals, it is theoretically suitable for other biodiversity studies using immobile devices that collect media files.

In the Safe and Sound project, we explored whether the recently developed Camtrap DP standard is a good fit for bioacoustic data. We interviewed bioacoustic researchers and investigated existing bioacoustic databases and formats to understand what data is typically collected and used. We then explored how these data can be expressed in Camtrap DP's model of deployments, media and observations and what changes are required for Camtrap DP to support the exchange of bioacoustic data. In this talk we will give an overview of our conclusions, ongoing developments, and how you can contribute to a new version of Camtrap DP that supports the exchange of bioacoustic data.

Session: 6799326**7015643**

23/10/25 | 14:50

Room: Cauca

ORAL • EN

Mobilizing bioacoustic data with WildTrax

Presenter

Elly Knight

Authors

Brandon Allen (Alberta Biodiversity Monitoring Institute • Canada)**Erin Bayne** (University of Alberta • Canada)**Corrina Copp** (Innotech Alberta • Canada)**Chad Klassen** (Alberta Biodiversity Monitoring Institute • Canada)**Alex MacPhail** (Biodiversity Pathways • Canada)**Mike Packer** (Alberta Biodiversity Monitoring Institute • Canada)

Abstract

Environmental sensors are quickly becoming the primary tool for monitoring vocalizing species like birds and amphibians. Their effective use requires a robust system to manage and share the enormous volume of acoustic data they collect. WildTrax is a web-enabled platform specifically designed to meet this need—supporting the management, storage, processing, sharing, and discovery of environmental sensor data, including acoustic recordings collected using autonomous recording units (ARUs).

WildTrax supports and encourages open data management, with many elements aligned with the intent and guidance of the FAIR and CARE principles. Data owners have control over their data, determining how it is stored, processed and shared, while the system ensures data standards are maintained for consistency, reuse and interoperability. Users from environmental non-profits to academics to government agencies have used WildTrax to share and harmonize datasets across wide geographic areas, enabling them to answer broad, novel ecological questions with their data. The centralized information in WildTrax contributes to the broader avian network, enhancing collaboration and data sharing for the conservation of birds in Canada, and beyond.

In this session, we highlight how WildTrax has lowered technical and logistical barriers to working with acoustic data in support of collaborative efforts to use bioacoustic data. Emphasizing that investments in data systems like WildTrax can support biodiversity monitoring, collaborations, data mobilization, and empower researchers, practitioners, and decision-makers alike.

Session: 6799326**7013770**

23/10/25 | 14:58

Room: Cauca

ORAL • EN

Fine-Scale Acoustic Monitoring: Grassland Bird Responses to Agricultural Disturbances

Presenter

John Quinn

Authors

John Quinn (Furman University • United States)

Abstract

Frequent disturbances from practices like harvesting, tillage, and chemical applications are inherent to arable land management. However, a critical data gap often exists regarding their fine-scale temporal impacts, as assessments are typically limited to a coarse annual basis. To address this, we employed data-intensive passive acoustic monitoring (PAM) to investigate the effects of these disturbances on grassland breeding bird populations from 2020 to 2022. Bird vocalizations were recorded hourly, 24/7, over a 7-month period at 33 farms, alongside farmer-reported dates for planting, harvesting, nitrogen fertilization, and pesticide applications. Our findings indicate that short-term agricultural activities trigger distinct, species-specific responses, providing crucial data for more comprehensive biodiversity assessments in these managed landscapes. While species such as Dickcissels and Eastern Meadowlarks exhibited significant declines in detections post-disturbance without recovering to baseline levels within a week, Horned Larks appeared to benefit from harvesting, with detection rates often surpassing pre-disturbance levels. This research underscores the timely, species-specific impacts of agricultural practices on grassland birds and highlights the critical need for fine-scale temporal considerations in agroecosystem management. Identifying vulnerable and adaptable species offers evidence-based, actionable insights for farmers and can inform policy aimed at integrating biodiversity conservation with agricultural productivity.

Session

6803172

Symposium

23/10/25 | 16:00

Room: Ballroom A

Connecting the Dots: Integrating Animal Movement Data into Global Conservation Frameworks

Organizers

Lacey Hughey

Talía Speaker

Andreas Bruder

Joana Soares

Description

Animal movement is a fundamental driver of biodiversity, influencing species distributions, linking disparate ecosystems, and underpinning healthy communities of people and wildlife. Accordingly, it is a key component of at least nine Sustainable Development Goals, fifteen targets of the Kunming-Montreal Global Biodiversity Framework (GBF), and multiple Global Ocean Observing System Essential Ocean Variables (EOVs) and Essential Biodiversity Variables (EBVs). Given its recognized importance, systematic approaches to integrating movement data into global conservation policy should be further developed.

We are launching the Animal Movement Biodiversity Observation Network (Move BON) Initiative in 2025 as a collaborative and open partnership that aims to align efforts across the animal movement community with Multilateral Environmental Agreements and processes. Move BON will foster a global community of practice to advance movement-informed conservation strategies.

This session will explore opportunities for integrating Move BON and associated workflows with the global community—through GEO BON and in partnership with groups such as GBIF, OBIS, GOOS, FW BON, and MBON—to support a more comprehensive and dynamic global biodiversity monitoring system. We will highlight the need for collaboration across geographic regions and taxonomic groups, emphasizing how movement data can fill critical gaps in biodiversity assessments and enhance conservation efforts worldwide.

Session: 6803172**7020166**

23/10/25 | 16:07

Room: Ballroom A

LIGHTNING TALK • EN

Motus Wildlife Tracking System: A Collaborative Network for Integrating Animal Movement Data into Global Biodiversity Monitoring

Presenter

Catherine Jardine

Authors

Stuart Mackenzie (Birds Canada • Canada)

Catherine Jardine (Birds Canada • Canada)

Abstract

The Motus Wildlife Tracking System is a global collaborative research network that uses automated radio telemetry to track the movements of small animals, including birds, bats, and insects. Since its launch in 2014, the Motus community of more than 1,000 individuals and organizations has tracked more than 55,000 animals of more than 450 species with an expanding network of more than 2,100 receiving stations across 34 countries. Motus enables high-resolution, long-term tracking of the behaviour and movements of typically small-bodied species that are underrepresented in global biodiversity monitoring efforts.

By generating data on species distributions, migratory connectivity, survival, and habitat use, Motus contributes directly to Essential Biodiversity Variables (EBVs) and informs conservation efforts across local to hemispheric scales. Its open data infrastructure and standardized protocols align well with FAIR data principles and facilitate integration with global platforms such as GBIF, OBIS, GEO BON, and the developing Move BON initiative.

By showcasing a model of community-driven, technology-enabled collaboration, Motus offers a scalable solution for integrating animal movement data into global conservation frameworks. Our presentation will outline key opportunities and challenges in aligning Motus with emerging global biodiversity observatory networks, and will invite new partners to help build an inclusive, interoperable movement ecology infrastructure for the Anthropocene.

We will highlight the relevance of Motus to multiple targets of the Kunming-Montreal Global Biodiversity Framework, and present case studies that demonstrate how Motus supports policy-relevant applications, such as the conservation of migratory species, identifying critical stopover habitats and cross-border conservation priorities, improving ecological connectivity, and enhancing biodiversity monitoring.

Session: 6803172**7019843**

23/10/25 | 16:14

Room: Ballroom A

ORAL • EN

Ready to move: mobilizing animal tracking data infrastructure to inform global conservation efforts

Presenter

Sarah Davidson

Authors

Sarah Davidson (Max Planck Institute of Animal Behavior • Germany)

Roland Kays (North Carolina Museum of Natural Sciences • United States)

Francesca Cagnacci (Fondazione Edmund Mach • Italy)

Christian Rutz (University of St Andrews • United Kingdom)

Abstract

Community data platforms for animal tracking serve as repositories and researcher networks for efficient global data mobilization (Davidson *et al.*, 2025, <https://doi.org/10.1038/s41559-024-02585-4>). They support the harmonization, curation, public discovery and sharing of data, and many include automated access protocols and real-time management. Just one of these platforms, Movebank, hosts over 8 billion occurrences describing movements of over 1,500 taxa across several decades, owned by nearly 5,000 users. Together, these users add millions of new species occurrence records daily, including those streaming through automated feeds from more than 30,000 electronic tags currently deployed on wildlife. Movebank has grown through meeting the needs of movement ecologists for thousands of research and conservation projects, and is also suited to support coordinated in-situ biodiversity monitoring across sites (Kays *et al.*, 2022, <https://doi.org/10.1111/2041-210X.13767>). Community tracking data platforms are used at regional scales by government monitoring programs and national parks, including countless collaborations for applied conservation. At an international scale, they have enabled the development of global migration atlases and designation of protected areas. The new Animal Movement Biodiversity Observation Network (Move BON) provides impetus to adapt these infrastructures to support the production of global biodiversity metrics and indicators. The creation of ‘study collections’ hosted on shared platforms provides a framework to connect data owners to policymakers. Because access to most animal movement data is restricted, a key challenge is to encourage open data practices and ensure long-term stewardship. Together with platform managers and the International Bio-Logging Society, we have identified next steps to operationalize data integration pipelines and expand the role of animal tracking in global biodiversity indicators and monitoring systems. These include a global data discovery portal, standard vocabularies and transfer protocols, and mobilization to GBIF. We encourage those implementing national and global policy frameworks to engage with Move BON to guide these efforts.

Session: 6803172**7005380**

23/10/25 | 16:26

Room: Ballroom A

LIGHTNING TALK • EN

How we plan to publish 1,000 bio-logging datasets to GBIF and OBIS

Presenter

Peter Desmet

Authors**Peter Desmet** (Research Institute for Nature and Forest (INBO) • Belgium)**Sanne Govaert** (Research Institute for Nature and Forest (INBO) • Belgium)**Pieter Huybrechts** (Research Institute for Nature and Forest (INBO) • Belgium)**Jonathan Pye** (Ocean Tracking Network (OTN) • Canada)**Claudia Meneses** (European Tracking Network (ETN) • Belgium)**Sarah Davidson** (Max Planck Institute of Animal Behavior • Germany)**Abstract**

Bio-logging data are data collected by animal-borne sensors, recording their movements, behaviour, physiology and/or environments. These data are used for movement ecology studies, wildlife management and conservation, but are underutilized as species occurrence data. Three platforms of bio-logging data—Movebank, the Ocean Tracking Network (OTN) and the European Tracking Network (ETN)— have collaborated to establish best practices and software for transforming and publishing these data as Darwin Core Archives to the Global Biodiversity Information Facility (GBIF) and the Ocean Biogeographic Information System (OBIS). In this talk we will cover:

- Our best practices for transforming bio-logging data, including which Darwin Core terms to include, how to acknowledge the source dataset and platform, why we downsample recorded positions, and how to include biometrics collected during capture and release.
- The open source software tools we developed for transforming data.
- How this approach works across different bio-logging techniques (GPS, acoustic telemetry) and realms (aerial, freshwater, aquatic).
- How the bio-logging data published on GBIF and OBIS can be used to create visualizations (from B-Cubed species occurrence cubes) or monitor marine species (by comparing with non-bio-logging species occurrence data, as is done in MBON's A-BioTrack project).

We believe that these best practices and prototypes can now be extended to more use cases and leveraged to scale the mobilization of bio-logging data. Want to join our collaborative goal of publishing 1,000 bio-logging datasets to GBIF and/or OBIS?

Session: 6803172**7020887**

23/10/25 | 16:33

Room: Ballroom A

LIGHTNING TALK • EN

Shrinking Wild Spaces: Connecting Home Ranges and Human Expansion to Conservation Targets

Presenter

Samara Manzin

Authors

Samara Manzin (McGill University • Canada)

Pollock Laura (McGill University • Canada)

Gonzalez Andrew (McGill University • Canada)

Abstract

The ability of animals to move through their environment is critical for the maintenance of ecological communities. However, human development can have extensive impacts on movement, often resulting in limited dispersal and reduced home ranges. With the recent advances in long term animal tracking data and movement ecology, our capacity to monitor and model animal home range use has been greatly expanded. However, it remains difficult to connect movement data to large scale conservation planning, especially for species or regions where we are data limited. Here, we aim to connect global trends of home range loss to conservation goals by predicting spatiotemporal changes in mammal home ranges caused by expansion of the human footprint. Leveraging summarised movement data, we estimate human induced changes in home range size through time. We identify terrestrial mammal species and regions globally where human induced habitat degradation could result in significant reductions in home range size. Finally, we evaluate whether species will be able to meet their conservation protection targets, based on the extent of their ranges already converted to high intensity human footprint. This approach offers a systematic way to link predicted changes in movement and space use with spatial conservation priorities. It allows us to break down patterns of home range loss through time and identify high risk species and regions, which can inform conservation planning and monitoring at multiple scales.

Session: 6803172**7019865**

23/10/25 | 16:40

Room: Ballroom A

LIGHTNING TALK • EN

Leveraging linear green infrastructure for biodiversity conservation in a rapidly changing world

Presenter

Job Aben

Authors

Job Aben (CentraleSupélec, Université Paris-Saclay • Belgium)

Carmen Bessa-Gomes (France)

Fernando Ascensão (Portugal)

Justin Travis (United Kingdom)

Didier Clouteau (France)

Abstract

Europe's biodiversity is under significant pressure from large-scale intensive agriculture, which reduces landscape heterogeneity and habitat quality. Insects are particularly affected, triggering cascading negative effects on birds and ecosystem services like pollination. These impacts are further exacerbated by climate warming, which threatens species persistence if populations cannot adapt or shift their distributions accordingly. However, heavily human-modified landscapes can hinder such range expansions.

In this context, anthropogenic linear green infrastructure (LGI), such as road and railway verges, may serve as crucial corridors for species responding to shifting climate envelopes. Despite this potential, LGIs remain largely overlooked in conservation planning, likely due to the complexity of integrating spatially explicit habitat data with species-specific dispersal behaviors.

The MINERVE project addresses this gap by evaluating the potential of railway verges to support species range expansion across France. Using the individual-based modelling platform *RangeShifter*, we simulated how species demography and dispersal interact with landscape structure to influence spatio-temporal dynamics. We modelled range expansion velocities for four grassland butterfly species-types across 270 10x10 km landscapes centred on railway tracks, comparing a baseline scenario (verges non-functional) with a scenario where verges act as habitat.

We then extrapolated these results to the entire SNCF railway network, using statistical models to predict expansion velocities under both scenarios. The value of railway verges was quantified by the reduction in expansion lag (difference between expansion velocity and climate change velocity) relative to the baseline. Verges were found to mitigate the negative impact of low habitat cover on the velocity of range expansion resulting in lag reductions up to 40%.

This work highlights how railway verges can contribute to climate-driven range shifts and biodiversity conservation, emphasizing the need to better integrate LGIs into land-use planning.

Session: 6803172**7020853**

23/10/25 | 16:46

Room: Ballroom A

LIGHTNING TALK • EN

Unlocking Animal Movement Data for Conservation in Peru: Towards a National Collaborative Monitoring System

Presenter

Ximena Velez-Zuazo

Authors

Vania Tejeda G. (Smithsonian National Zoo and Conservation Biology Institute • Perú)

Reynaldo Linares-Palomino (Smithsonian National Zoo and Conservation Biology Institute • Perú)

Alfonso Alonso (Smithsonian National Zoo and Conservation Biology Institute • United States)

Ximena Velez-Zuazo (Smithsonian National Zoo and Conservation Biology Institute • Perú)

Abstract

Understanding animal movement is key to conserving biodiversity, ensuring ecological connectivity, and achieving targets under the Kunming-Montreal Global Biodiversity Framework (GBF), Sustainable Development Goals (SDGs), and Peru's NBSAP 2050. In Peru, movement ecology studies have provided valuable insights into migration routes, habitat use, and species responses to environmental change. Yet, the national scope and accessibility of such data remain limited.

The Smithsonian National Zoo and Conservation Biology Institute's Center for Conservation and Sustainability (CCS) has led long-term monitoring of marine and terrestrial biodiversity in Peru. Since 2021, CCS has integrated movement data into its work, initially focusing on seabirds, sharks, and rays, to understand how infrastructure development influences species behavior and habitat use. Through this work, we identified key gaps in data availability, collaboration networks, and access to equipment and expertise—challenges that hinder the systematic use of animal movement data in conservation planning.

In alignment with the global launch of the Animal Movement Biodiversity Observation Network (Move BON), we propose the formation of a national community of practice to integrate and mobilize movement data across ecosystems and taxa. This initiative seeks to catalyze a unified monitoring system that supports national ecological connectivity goals and contributes to global networks and Peru's System of Information on Biodiversity.

We present an overview of 30+ movement studies across Peru and share preliminary results from a nationwide rapid survey aimed at mapping efforts and capacities. These findings will inform the design of a national workshop to coordinate priorities, share methodologies, and identify opportunities for linking local research with global biodiversity monitoring systems. This work sets the foundation for a more connected and conservation-relevant use of animal movement data in Peru.

Session: 6803172**7020438**

23/10/25 | 16:55

Room: Ballroom A

LIGHTNING TALK • EN

Bridging the Data-Policy Gap: Integrating Spatiotemporal Data to Advance International Migratory Bird Conservation in the Americas

Presenter

Bill DeLuca

Authors**Jill Deppe** (Migratory Bird Initiative, National Audubon Society • United States)**Abstract**

Migratory species present a complex conservation challenge: they traverse international borders, use geographically distant habitats, and are exposed to various threats across the year. Audubon and nine conservation science partners created the Bird Migration Explorer (ExplorAves in Spanish), a powerful, data-driven platform that can be integrated into conservation frameworks to enhance the protection of migratory bird species in the Western Hemisphere. Built on millions of tracking and connectivity data, abundance estimates, and distributional ranges generously shared by hundreds of scientists and institutions, the Explorer visualizes migratory routes, geographic connections, and exposure to conservation challenges across the full annual cycle of hundreds of bird species. This holistic, spatiotemporal perspective is essential for effective biodiversity conservation under global frameworks, such as the Convention on the Conservation of Migratory Species and the Convention on Biological Diversity.

The Explorer is an open-access, dual language (English and Spanish), interactive web-platform designed to make migration science accessible and relevant for conservation practitioners, decision-makers and policy advocates working to protect migratory birds and their habitat in the Americas. The platform is a “living data” system regularly updated with the most recent tracking, connectivity and abundance data.

Additionally, Audubon has collaborated with partners to develop customized, quantitative analyses that harness the power of movement data to answer specific conservation questions. A couple examples of conservation applications include: (1) integrating tracking and connectivity data with seasonal abundance to map migratory pathways and the network of important areas migratory birds depend on across the full annual cycle, and (2) combining tracking data with spatial patterns of environmental change to estimate risk of bird population declines across the Western Hemisphere. Movement data integrated into these outputs and tools enable countries to target investments for biodiversity conservation and foster international cooperation to support year-round migratory bird populations.

Session

6803199

Symposium

23/10/25 | 16:00

Room: Ballroom B1

Enhancing Data Policy & Biodiversity Monitoring: Quality, Gap Analysis & Environmental Integration

Organizers

Clara Baringo Fonseca

Keila Macfadem Juarez

Leonardo Lima Bergamini

Debora Pignatari Drucker

Silas Principe

Pieter Provoost

Maria Cornthwaite

Jonathan Pye

Description

Both public conservation policies and the development of indicators to assess progress toward global biodiversity targets—across marine, terrestrial, and freshwater ecosystems—rely on large volumes of data with accurate taxonomic, spatial, and temporal information. However, biodiversity data gaps exist across these dimensions, limiting the scope of possible analyses. At the same time, for many regions and taxonomic groups, data are being collected but remain fragmented, scattered across different organizations and not flowing to central systems.

Recognizing how these gaps affect data usability is essential for advancing strategies to maximize the value of available data. This includes modeling, integrating multiple data sources (e.g., biological collections, regional species lists, expert knowledge, remote sensing, and citizen science), and implementing initiatives to address these gaps through data mobilization, refinement, and targeted primary surveys.

This symposium will explore approaches that integrate biodiversity data to support public policy and monitor progress toward global biodiversity targets. Additionally, we will examine strategies for assessing data quality and identifying gaps. Through collaborative dialogue and case studies, we aim not only to identify barriers to data integration but also discuss actionable solutions—from new technologies for biodiversity data collection to coordinated efforts for increasing spatial and taxonomic coverage.

We invite researchers, policymakers, educators, and conservation professionals to join us in discussing biodiversity indicators and sharing knowledge, experiences, and best practices for improving data availability, quality, and usability, with special attention to reducing fragmentation and enhancing data flow to centralized systems.

Session: 6803199**7020919**

23/10/25 | 16:00

Room: Ballroom B1

ORAL • EN

Overcoming the disconnect between species interaction networks and biodiversity conservation and management

Presenter

Gabriel Dansereau

Authors

Gabriel Dansereau (Université de Montréal • Canada)

Abstract

Decision-makers and practitioners increasingly need multi-species and whole-ecosystem indicators for biodiversity conservation and management. Species interaction networks hold a promising potential to fill those needs, and yet, explicit and quantitative integration of network indicators into conservation is still lacking due to challenges with uncertainty and indicator accessibility to practitioners. The resulting gap between network science and management leads to decisions being made without considering available scientific knowledge. Here, we will argue that existing data and methodologies are sufficient to generate network information usable for conservation, and to begin overcoming existing barriers to the integration of network information and biodiversity decision-making. To do so, interaction network indicators must meet criteria important to decision-makers and be tied to specific conservation goals, which requires academics to better engage with practitioners. We will use network robustness as an example of an already applicable indicator, and showcase its potential with a reusable workflow to inform decision-making. Overall, we will show how we can start bridging network information into biodiversity management and towards application, building on existing metrics and available data as starting points to establish operational frameworks.

Session: 6803199**7020724**

23/10/25 | 16:12

Room: Ballroom B1

ORAL • EN

Machine-Actionable Metadata in Practice: Lessons from Automating FAIR Assessment in Plant-Pollinator Datasets

Presenter

Debora Drucker

Authors

Debora Drucker (Embrapa • Brazil)**Jorrit Poelen** (UC Santa Barbara Cheadle Center for Biodiversity and Ecological Restoration • United States)**Jose Salim** (Brazil)**Filipi Soares** (Brazil)

Abstract

As the biodiversity community advances towards FAIR data, machine-actionable metadata has emerged as a critical enabler for scalable data assessment, discovery, and reuse. However, while FAIR principles emphasize machine-readability, many datasets are still evaluated manually or lack structured metadata entirely, limiting their integration into global platforms. This study shares practical insights from the WorldFAIR Agricultural Biodiversity Case Study, where we operationalized machine-actionable FAIR metadata in the review of plant-pollinator interaction datasets.

We developed a semi-automated workflow using two bots – Nomer and Elton – to assist in evaluating datasets against the FAIR principles. These tools read structured metadata provided in standard vocabularies like Darwin Core (DwC), Ecological Metadata Language (EML), and the Plant-Pollinator Interactions (PPI) vocabulary. Nomer focuses on taxonomic alignment with several taxonomic catalogues, such as GBIF Backbone and Catalogue of Life. Elton extracts species interaction from datasets of many different structures and formats, including DwC-Archives.

By relying on machine-readable metadata, the bots were able to flag inconsistencies, suggest improvements, and generate repeatable reports across pilot projects in Argentina, Brazil, Kenya, Colombia, and the USA (for example, Elton, Nomer, & Preston, 2025). This helped researchers assess dataset interoperability without needing full access to the raw data, a crucial feature given legal and institutional access constraints.

Our results underscore the transformative role of machine-actionable metadata in biodiversity data governance. Automating FAIR assessments not only increases transparency and repeatability but also accelerates the integration of datasets into platforms like the Global Biotic Interactions (GloBI). While human expertise remains essential, tools like Nomer and Elton show that FAIR assessment can move beyond checklists to become dynamic, scalable, and embedded in the data lifecycle. Resources and code are openly available on Zenodo and GitHub, which are summarized in <https://globalbioticinteractions.org/worldfair>.

Session: 6803199**7015376**

23/10/25 | 16:23

Room: Ballroom B1

ORAL • EN

Hold the Data: A Call to Prevent Biodiversity Knowledge from Falling into Darkness

Presenter

Maite Telletxea

Authors

Maite Telletxea (University of Navarra, Biodiversity and Environment Institute BIOMA • Spain)**Rafael Miranda** (University of Navarra, Biodiversity and Environment Institute BIOMA • Spain)**Arturo H. Ariño** (University of Navarra, Biodiversity and Environment Institute BIOMA • Spain)**David Galicia** (University of Navarra, Biodiversity and Environment Institute BIOMA • Spain)

Abstract

Efficient biodiversity data management is essential for informing conservation policies and meeting legal reporting requirements. Under the Habitats Directive (92/43/EEC), member states are required to monitor targeted species and report on their conservation status every six years, including a distribution area (DA) ideally based on the best available evidence. Using the 31 targeted bat species in Spain as a case study, we evaluated how integrating Digital Accessible Knowledge (DAK) and mobilized Dark Data (DKD) could have improved the official estimation of their DA in the last sexennial report (2013–2018). We obtained over 46,000 GBIF-published occurrences, primarily generated between 2000 and 2018 but published with an average four-year lag. Records published before 2018 were considered DAK and thus available for compilation, while records published thereafter were considered DKD: already existing but likely undiscoverable and/or unavailable for the last sexennial report. Approximately 50% of the records were DKD, meaning many existing data were not readily available to inform the report. We estimated bat species DA under four scenarios: official report, sexennial report + DAK, sexennial report + DKD, and full data integration. Incorporating DAK and DKD contributed to the official DA of the bat species by an average of 27% and 16%, respectively, and all data integration increased the official DA by 33%. Even when accessible, many data were likely underused due to their lack of integration into official reporting procedures. This research shows the significance of efficient data management, including timely data publication and utilization of available information, in biodiversity reporting. Establishing procedures that minimize data latency and maximize the use of existing data for conservation policies is essential, because the integration of often-overlooked data into formal assessments can help us to more accurately address the species conservation status and improve decision-making, ultimately contributing to better biodiversity governance.

Session: 6803199**7016104**

23/10/25 | 16:36

Room: Ballroom B1

ORAL • EN

SISBia: An Optimized System for Ecological Data Management and Seamless GBIF Integration

Presenter**RODRIGO KOBLITZ****Authors****RODRIGO KOBLITZ** (Ibama • Brazil)**Ana Paula Cavalcante Da Cruz** (Ibama • Brazil)**Cecilia Cronemberger de Faria** (ICMBio • Brazil)**Ana Elisa de Faria Bacellar** (Ibama • Brazil)**Ivan Salzo** (ICMBio • Brazil)**Gabriel Mendes** (Brazil)**Brunna Stefanny Sangel De Oliveira** (Ibama • Brazil)**Vivianne Eilers** (Ibama • Brazil)**Alexandro Cardoso Costa** (Ibama • Brazil)**Frederico Queiroga Do Amaral** (Ibama • Brazil)**Abstract**

The Biodiversity Data Management System for Environmental Impact Assessment (Sistema de Gestão de Dados de Biodiversidade para Avaliação de Impacto Ambiental - SISBia), developed by Brazilian federal environmental agencies Brazilian Institute of the Environment and Renewable Natural Resources (Ibama) and Chico Mendes Institute for Biodiversity Conservation (ICMBio), is a dynamic platform for managing ecological data from Brazil's environmental licensing processes. SISBia integrates a user-friendly design with rigorous data standards to manage diverse taxonomic and methodological datasets. Its intuitive interface enables users to submit ecological data, manage spatial files (e.g., shapefiles), and link features (i. e. sample units) to sampling events. A key innovation is its flexible data structure, which allows users to customize data entry forms via a configurable set of user-defined attributes. The system ensures data integrity by standardizing column terms and requiring users to explicitly document sampling effort. Additionally, SISBia validates geographic coordinates against predefined spatial units. Taxonomic data is cross-checked via integration with ICMBio's taxonomic information system, Sintax, and controlled vocabularies could be used to ensure consistency. SISBia simplifies integration with GBIF by automatically mapping data to the Darwin Core standard, enabling direct export to GBIF's IPT. During this process, SISBia preserves original ecological records and spatial data that are not directly compatible with the DwC format. After validation, datasets can be published to GBIF with minimal manual intervention. As Brazil's primary database for biodiversity data related to environmental licensing, the SISBia, is in its early stages but already hosts 34,241 biodiversity records and processes a significant volume of high-quality primary data daily. Its architecture bridges national environmental monitoring with global platforms, enhancing the availability of standardized data for conservation and policy-making. By optimizing data flow from field collectors to GBIF, SISBia demonstrates how institutional tools can enhance the impact of biodiversity data infrastructures.

Session: 6803199**7020142**

23/10/25 | 16:47

Room: Ballroom B1

ORAL VIRTUAL • EN

Assessment of Brazilian biodiversity data

Presenter

Leonardo Lima Bergamini

Authors

Leonardo Lima Bergamini (Brazil)

Mariza Macedo Pinheiro (Brazil)

Angelita Coelho (Brazil)

Frederico Takahashi (Brazil)

Iona'i Moura (Brazil)

Abstract

Biodiversity is essential for the health of ecosystems. In Brazil it is not only threatened but also poorly documented, which increases the risk of underestimation and extinction of species before they are recorded and known. Here we present a study which assessed and discussed the main limitations regarding data completeness in terms of taxonomic, spatial and temporal dimensions of occurrence records for nine taxonomic groups: amphibians, arthropods, birds, fungi, mammals, mollusks, bony fish, vascular plants and reptiles, available on the SiBBR platform, the Brazilian node of GBIF. Out of a total of approximately 22 million records, 28% achieved the highest level of information completeness, presenting at least identification at the species level, valid geographic coordinates and the month and year of occurrence.

The lack of coordinates was the main limitation observed in approximately 7 million records, followed by taxonomic indeterminacy at the species level, redundant records and lack of date of records. From the most complete records, spatial patterns of quantity, sample completeness, age and record frequency were analyzed, which made it possible to highlight the locations and groups with greater data deficiencies. In addition to revealing general patterns, such as the concentration of records in more easily accessible locations, these analyses highlighted differences between the groups. While birds had more than 10 million published records with more than 40% considered complete, mollusks had less than 170 thousand records, of which less than 11% had sufficient accurate information in all dimensions. This information can help define priorities and strategies for future surveys and should be seen as an iterative process.

Reassessments may include more information to cover the multiplicity of data dimensions and incorporate environmental changes. To this end, it is essential to encourage sharing and guarantee access to biodiversity data to enhance its management and conservation.

Session: 6803199**7020189**

23/10/25 | 17:00

Room: Ballroom B1

ORAL • EN

Legal Reserves as Conservation Assets: Integrating Biodiversity Data and National Systems for 30x30

Presenter

Keila Macfadem. Juarez

Authors

Keila Macfadem. Juarez (SiBBr - RNP • Brazil)

Clara Baringo Fonseca (SiBBr - RNP • Brazil)

Karlo Gregório Guidoni Martins (SiBBr - RNP • Brazil)

Abstract

The Rural Environmental Registry (CAR) enables the spatial mapping of RLs. However, although the mapping of polygons is nearly complete across much of the country, there is still no information about the biodiversity within these areas. Currently, the conservation status of RLs is assessed primarily through satellite imagery, which shows vegetation cover but does not capture the species richness present. To effectively recognize these areas as conserved, it is essential to know which species occur within them.

Citizen science tools, such as iNaturalist and eBird, offer accessible means for recording species, allowing rural landowners and local communities to directly contribute biodiversity data. The SiBBr (Brazilian Biodiversity Information System) serves as a national platform to integrate, standardize, and publish these data, as well as to make them available through geospatial systems like the Spatial Portal.

Integrating biodiversity records with the polygons of Legal Reserves enables the assessment of species richness within these areas and their relationship to regional biodiversity. This helps to evaluate the potential of rural properties to contribute to biodiversity conservation and to determine their viability for sustainable production.

This proposal presents examples of how the articulation between CAR, citizen science applications, and SiBBr can directly contribute to validating biodiversity in rural properties, strengthening actions toward achieving the 30x30 target in Brazil.

Session: 6803199**7020176**

23/10/25 | 17:11

Room: Ballroom B1

ORAL • ES

Integridad ecológica de ecosistemas de agua dulce: aplicación de un índice multivariado en las microcuencas del Orinoco Colombiano

Presenter

Alejandra Narvaez Vallejo

Authors

Alejandra Narvaez Vallejo (IAvH • Colombia)

Luis Fernando Urbina Gonzalez (IAvH • Colombia)

Sergio Enrique Rojas Sánchez (IAvH • Colombia)

Abstract

El monitoreo efectivo de los ecosistemas de agua dulce requiere indicadores que integren tanto datos ecológicos de su estado, como de las presiones antrópicas a las que están sujetos. Proponemos un índice multivariado de integridad ecológica para la escala de microcuencas, y lo calculamos para el Orinoco colombiano, a partir de datos de coberturas de la tierra, biodiversidad, red hídrica, clima, población humana y actividades como minería, hidrocarburos y agricultura.

La integridad se define como la capacidad del ecosistema para mantener procesos ecológicos, conservar la biodiversidad y ofrecer servicios clave. Para ello, se integran cinco atributos: régimen hidrológico, calidad de agua, estructura física, conectividad longitudinal y composición biótica. Cada atributo está vinculado a amenazas específicas y se representa mediante indicadores que se combinan en un valor total de integridad.

El enfoque a escala de microcuenca y por atributo permitió una evaluación integral y detallada, útil para identificar áreas críticas y orientar acciones de manejo diferenciadas según el tipo de ecosistema y las presiones que enfrenta. La articulación del índice con tipologías de ríos y figuras de conservación, refuerza su utilidad para el seguimiento de políticas públicas, la evaluación de áreas protegidas y la planificación ambiental. Su diseño modular y basado en datos disponibles permite su actualización periódica y aplicación en otras regiones, consolidándose como una herramienta replicable para el monitoreo de la biodiversidad.

Para escalar su aplicación a nivel nacional, se requiere una mayor articulación entre entidades ambientales, académicas y territoriales que llenar vacíos fundamentales en las series de datos. Se destaca la necesidad de consolidar un mapa nacional de microcuencas, una red hídrica completa y actualizada, y registros detallados de actividades antrópicas vinculadas al recurso hídrico. La cooperación interinstitucional es clave para generar, compartir y utilizar estos insumos de manera eficiente y sostenida.

Session

6803213-2

Symposium

23/10/25 | 16:00

Room: Ballroom B2

Modern challenges of classic taxonomy, how to connect and keep catalogues up to date (Part 2)

Organizers

Olaf Bánki

Vijay Barve

Camila Plata

Description

Taxonomy, the fundamental framework of biological sciences, provides a shared understanding of every organism. Traditionally, curated taxonomic name lists were disseminated through print publications and later transitioned to online platforms. However, these resources often become rapidly outdated after publication, with limited capacity of maintenance by their original creators. Developing and maintaining taxonomic name resources is challenging, and entails innovative solutions and new ways of collaboration. These taxonomic data sources are crucial to represent biodiversity data in general, and link these to fundamental science and societal efforts. In this session we would like to bring together both providers and users of taxonomic resources to understand their challenges and how they have addressed these successfully -or not. In a collaborative environment we aim to share best practices, learn from one another's experiences, and better understand the need to connect local, national and regional taxonomic lists and derived species lists to a global effort.

Session: 6803213-2**7020880****23/10/25** | 16:00**Room:** Ballroom B2**ORAL • EN**

From Checklists to Living Catalogues: Lessons from the Catalogue of Fishes of Colombia

Presenter

Leonardo Buitrago

Authors

Leonardo Buitrago (Universidad Nacional de Colombia • Colombia)**Mariangeles Arce** (Global Biodiversity Information Facility • United States)**Henry Agudelo-Zamora** (The Academy of Natural Sciences of Drexel • Colombia)**Diego Moreno** (Universidad Nacional de Colombia • Colombia)**Lauren Raz** (Universidad Nacional de Colombia • Colombia)

Abstract

The Catalogue of Fishes of Colombia (CFC) represents a significant advancement in the management and dissemination of biodiversity information. Developed as a dynamic digital platform, the CFC integrates both freshwater and marine species while adhering to international taxonomic standards and the Darwin Core format. Through the implementation of a REST API and an intuitive user interface, it allows real-time updates and ensures interoperability with national and global platforms such as SiB Colombia, GBIF and Catalogue of Life.

This lightning talk will present the development process of the CFC as a case study, highlighting how one national initiative can evolve from static checklists into a collaborative, living catalogue. The presentation will describe how the platform supports taxonomic consistency, improves accessibility, and provides critical information for researchers, educators, conservationists, and policymakers.

The talk will also reflect on key challenges identified during the process, including the need for improved documentation of taxonomic history, the integration of genetic data, and enhanced coordination with national institutions. Additionally, it will present insights into the catalogue's governance model and the quality measures used to evaluate its structure and management.

The CFC stands as a replicable model for similar efforts targeting other biological groups, emphasizing the importance of collaboration, open data, and strategic design. It underscores the role of well-structured digital catalogues in supporting conservation and sustainable decision-making in biodiversity-rich countries.

Session: 6803213-2**7012940**

23/10/25 | 16:11

Room: Ballroom B2**ORAL • EN**

Global Taxonomic Database of Gracillariidae www.gracillariidae.net -- a machine-human teaming taxonomic service system, updatable in real time

Presenter

Jurate De Prins

Authors

Jurate De Prins (Flemish Entomological Society • Belgium)**André Heughebaert** (Belgian Federal Science Policy Office (BELSPO), Belgian Biodiversity Platform • Belgium)

Abstract

Global taxonomic catalogues are essential resources for biodiversity assessment. Even though taxonomy is probably one of the most classical disciplines for which fundamentals were set in the works of Aristotle, nevertheless, as a science, it develops rapidly together with immense biodiversity discoveries, society's need to know the living world, and the advantages of technology. In recent years, the World Catalogue of Gracillariidae (Insecta) has undergone a fascinating transformation from a human-readable book, later an online platform, to a human-machine/machine-machine teaming system updatable in real time. New technologies equipping taxonomy of insects with the modern diagnostic possibilities for visual, DNA, and behaviour data challenge the community of users with constant changes in species names and current species concepts. A species name is a fundamental global communication unit for all Life Sciences disciplines as well as for governmental legal documentation and decision making. In our presentation, we shall suggest a well-tested solution on how a small human-technology-assisted team provides human and machine-readable biodiversity data that are updatable in real time. We shall demonstrate the intelligent way we code the names of taxa and their taxonomic position, so the latest changes in synonymy and higher hierarchical position (genus, tribe, subfamily and family levels) are followed with easy adaptations. We address the user's need to present a world taxonomic database of Gracillariidae as a multi-searchable visual system with interlinked structured information on the original publication, types, their depository, type locality, distribution, host plants, DNA data accompanied with the sources of information and a huge visual gallery of verified photographs of diagnostic importance. We advocate for interlinked data with other Global initiatives such as GBIF and ChecklistBank, so our global Gracillariidae taxonomy is synchronised, up-to-date, reliable, verifiable, and resistant to specialist and public scrutiny.

Session: 6803213-2**7020497**

23/10/25 | 16:22

Room: Ballroom B2**ORAL • EN**

Integrating Consistency and Change: The Taxonomic Data Challenge in the Catalogue of Life extended Release

Presenter

Diana Hernández

Authors

Diana Hernández (Catalogue of Life • Mexico)

Camila Plata Corredor (Catalogue of Life • Colombia)

Markus Döring (GBIF • Germany)

Olaf Banki (Catalogue of Life • Netherlands)

Abstract

The Catalogue of Life eXtended Release (XR) represents a significant advancement in taxonomic data infrastructure. It enables the integration of well-established global data sources that constitutes the Catalogue of Life, with a growing range of heterogeneous and emerging taxonomic datasets by means of scalable and interoperable workflows that integrate data from each source and allow their traceability.

The XR is updated in a monthly manner through a process that ensures full version tracking and enables the inclusion of checklists available in ChecklistBank that follow different classification approaches. The outcome of integrating into COL more than 40 regional and national datasets, 30 global and over 27,000 digitized literature is an enriched and more inclusive catalogue. We will highlight the relevance of merging more than 1 million scientific names and 3 million molecular based names and how this process has helped address long-standing taxonomic gaps, particularly in underrepresented groups.

At the same time, the integration process has revealed persistent and emerging challenges, including incomplete or unresolved synonymies, gaps in higher classification, conflicting nomenclatural or taxonomic opinions across sources and the discovery of previously unnoticed homonyms. If not solved, these conflicts could undermine name resolution, data linking, and scientific communication.

To address these issues, improved workflows are being developed to detect and flag inconsistencies through upgraded Checklistbank tools ensuring better quality control, and accurate placement of names within the taxonomic tree. A key factor in the development of the XR has been the engagement of taxonomic experts in the review of the merged names, which is essential for improving the reliability of a dynamic catalogue.

This presentation will offer insights into how Catalogue of Life is evolving to remain both authoritative and adaptable, in order to support the needs of biodiversity research, conservation, and policy in an era of accelerating data growth.

Session: 6803213-2**7020662**

23/10/25 | 16:33

Room: Ballroom B2**ORAL • EN**

Integration of Catalogue of Life's taxonomic data services in GBIF

Presenter

Federico Mendez

Authors

Dave Martin (Global Biodiversity Information Facility • Denmark)**Markus Doering** (Global Biodiversity Information Facility • Denmark)**Tim Robertson** (Global Biodiversity Information Facility • Denmark)**Olaf Bánki** (Catalogue of Life • Netherlands)**Federico Mendez** (Global Biodiversity Information Facility • Spain)

Abstract

The Global Biodiversity Information Facility (GBIF) and the Catalogue of Life (COL) collaborate in developing ChecklistBank, a shared infrastructure for integrating and serving taxonomic checklists. Since December 2020, ChecklistBank has supported the monthly assembly of the Catalogue of Life releases. Recently developed data integration capabilities have led to a new version of the Catalogue of Life data product—the Catalogue of Life eXtended Release (COL XR). As of May 2025, the COL eXtended Release adds more than 420K potentially accepted species to the COL base release. It is based on 27K data sources as opposed to the 169 global data sources used in the COL base release.

With this expansion, the COL is now suitable for taxonomically organizing the more than three billion species occurrences mediated through GBIF.org. It also offers improved data quality assurance and control compared to the current GBIF Backbone Taxonomy.

To coincide with this release, GBIF has enhanced its core data processing and indexing pipelines to support multiple taxonomic backbones. The Catalogue of Life will be the first such alternative backbone, offered alongside the existing GBIF Backbone Taxonomy, which will remain available for some time.

In this presentation, we will:

- Explain the new capabilities of ChecklistBank that provide high speed lookup services
- Introduce the APIs and user interface changes that support multiple taxonomic backbones in GBIF
- Outline the data flows that enable monthly updates to Catalogue of Life that also result in more periodic taxonomic representations of the species occurrences mediated through GBIF
- Provide some insight how the GBIF and COL partnership could better address and respond to data quality issues and gaps with the wider community, and
- Summarise our roadmap for future work, including approaches to more taxonomies such as the World Register of Marine Species (WoRMS)

Session: 6803213-2

7020474

23/10/25 | 16:44

Room: Ballroom B2

ORAL • EN

Extended release of the Catalogue of Life Checklist: quantity vs. quality

Presenter

Dmitry Dmitriev

Authors

Dmitry Dmitriev (University of Illinois at Urbana-Champaign • United States)

Abstract

The *Catalogue of Life* (COL) is an international initiative that brings together a community of expert taxonomists to build a comprehensive checklist of all species living on Earth. COL is generated using ChecklistBank, a publishing platform designed to integrate numerous datasets into a single product.

Despite efforts spanning 30 years, some gaps remain unresolved in COL. There are two primary sources of these gaps: some taxonomic groups – especially megadiverse ones like beetles – lack comprehensive datasets; there is a time lag between the continuous publication of new taxon names and synonymies, and the incorporation of this new knowledge into global checklists.

An *Extended Release of COL Checklist* was developed through a collaboration between COL and the Global Biodiversity Information Facility (GBIF) to enrich the expert-based version of COL. This release includes a wider variety of taxonomic and faunistic sources (e.g., regional datasets, and parsed publications from PLAZI), aiming to add additional taxa and fill existing gaps.

The *World Auchenorrhyncha Database* (WAD) is a comprehensive resource covering the taxonomy and nomenclature of over 47,000 valid species of Hemipteran insects and their synonymies. It is one of 169 data providers for COL. In 2024, a gap analysis was conducted to identify missing data by examining an “*Extended Release*” of WAD in ChecklistBank.

As a result, out of 15,343 “extensions” incorporated into the release, 215 were added to WAD. Most of these were missing subsequent combinations and misspellings. A few recently published names had not been incorporated into the World Auchenorrhyncha Database prior to the analysis. The majority of the other “extensions” were found to be non-binomial names, chresonyms, incorrect synonymies, or misclassifications.

In conclusion, the Extended Release can be a useful tool for addressing gaps in an underrepresented taxonomic group, but can bring more chaos and damage to well curated checklists.

Session: 6803213-2**7020415**

23/10/25 | 16:55

Room: Ballroom B2**ORAL • EN**

A Collaborative Workflow to Expand Taxonomic Coverage in the Catalogue of Life eXtended Release through Plazi-Mediated Data

Presenter

Camila Plata

Authors

Camila Plata (Catalogue of Life • Netherlands)

Donat Agosti (Plazi • Switzerland)

Markus Döring (Catalogue of Life • Netherlands)

Diana Hernández-Robles (Catalogue of Life • Netherlands)

Guido Sautter (Plazi • Switzerland)

Felipe Lorenz Simões (Plazi • Switzerland)

Olaf Bánki (Catalogue of Life • Netherlands)

Abstract

The Catalogue of Life (COL) compiles species names across all taxonomic groups in collaboration with taxonomic communities. Keeping up to date with newly described taxa remains a challenge for both COL and its network. To address this and help close long-standing taxonomic gaps, an enhanced assembly process has been developed over the past two years. As a result, the recently launched Catalogue of Life eXtended Release integrates data from over 27,000 sources. Here, we detail Plazi's contribution and the collaboration between the two initiatives.

Approximately 26,000 papers processed by Plazi, originating from journals such as the EJT, Zootaxa, and PhytoKeys among other 190, are integrated. This has been critical for addressing gaps, particularly in the highly diverse insect groups, which is not fully covered by dedicated taxonomic communities. Plazi mediated data contributes around 90,000 unique names from which over 60% represent insect names, and 5% of names of species described in the last 5 years.

Plazi and COL have worked together for the past two years to create a workflow to maximize gap coverage. This collaboration includes the use of the Catalogue of Life Data Package (ColDP) standard, data quality checks, adding treatment citations, improved classification accuracy, enhanced completeness, reduced inaccuracies in treated data and ChecklistBank enhancements. Currently, checklists derived from the journals cited above are integrated into Catalogue of Life in under two weeks, significantly improving data availability for COL's usage.

As vetted catalogues continue to contribute species, Plazi's relative share decreases, and priority shifts to those authoritative sources. We are testing a feedback loop in which COL's constituent checklists evaluate Plazi's mediated data. This helps taxonomists integrate newly described species into their checklist and uncover recurring issues, which are promptly addressed to ensure higher-quality releases and better workflows.

Session: 6803213-2**7020873**

23/10/25 | 17:06

Room: Ballroom B2**ORAL • EN**

Leveraging a Catalogue of Life for the benefit of capacity enhancement, the science community, and policy impact

Presenter

Olaf Bánki

Authors

Olaf Bánki (Catalogue of Life • Netherlands)

Abstract

In recent years, Catalogue of Life has gone through many changes. Together with the Global Biodiversity Information Facility, a new data infrastructure, ChecklistBank, has been developed. Catalogue of Life's management structure has been independently reviewed, and now better accommodates the (potential) roles of Catalogue of Life. Catalogue of Life's focus is still on enabling a global consensus taxonomic reference for all known species of all living organisms on earth. At the same time, Catalogue of Life is now moving from serving a list to a more comprehensive taxonomic data service. With the launch of a new version of the Catalogue of Life, the Catalogue of Life eXtended Release, more taxonomic and nomenclatural data sources as well as other species lists are integrated than ever before. This opens up new possibilities.

In this presentation we will highlight and discuss some of the new possibilities and lessons learned Catalogue of Life could offer in collaboration with others. We will specifically address:

- How a renewed Catalogue of Life could serve as a consensus taxonomic reference service for biodiversity data infrastructures and for multilateral policy initiatives
- The importance of promoting data quality assurance and control on published taxonomic and nomenclatural data sources, and other species lists, and what role Catalogue of Life could play in this
- How we could jointly address taxonomic gaps, stimulate the development of taxonomic communities, and involve experts in taxonomic groups also where no global communities exist
- The need for capacity enhancement in using Catalogue of Life and its infrastructure ChecklistBank, and for building species lists; and
- How others can become part of the Catalogue of Life endeavour to help make it a collaboration and taxonomic data service for all.

Session

6798685

Symposium

23/10/25 | 16:00

Room: Tolima

Essential Biodiversity Variables: From concept to operationalization

Organizers

Yvan Le Bras

Jean-Michel Lord

Petteri Vihervaara

Nestor Fernandez

Alice Hughes

Description

Essential Biodiversity Variables (EBVs) is a concept introduced to advance the collection, sharing and use of biodiversity information (Pereira et al. 2013; Navarro et al. 2017). If the concept is now quite well known, “EBV operationalization” remains a challenge we need to face to answer assessment needs in all areas (marine, terrestrial, and freshwater). The goal of the session is to showcase operational solutions to facilitate the way to go from collection of systematic biodiversity observations to open and interoperable databases and thus better guide conservation and sustainable development strategies.

The session proposes to mix presentations of GEO BON “internal” “EBV operationalization pilots” and related “EBV data cube”, “Galaxy-Ecology” and “Bon-in-a-box pipelines” solutions and “external” EBV operationalization initiatives who can be submit to session organizers.

Session: 6798685**7015555**

23/10/25 | 16:05

Room: Tolima

ORAL • EN

Community-Driven, Reproducible, and Scalable EBV Workflows with BON in a Box

Presenter

Jory Griffith

Authors

Jory Griffith (GEO BON, McGill University • Canada)**Jean-Michel Lord** (GEO BON, McGill University • Canada)**Guillaume Larocque** (McGill University, Quebec Centre for Biodiversity Science • Canada)

Abstract

The Essential Biodiversity Variable (EBV) framework was created to standardize the measurement of biodiversity and enable comparison across time and space. While the EBV concept has gained traction within the biodiversity monitoring community, there has not been widespread use of EBVs in practice. This is due, in part, to a lack of consensus about how to turn raw data into EBVs in a standard way that is also flexible enough to translate between spatial scales and biological systems. BON in a Box is a free, open access, and community contributed biodiversity analysis platform that can help address this problem by allowing users to share and run code to calculate EBVs in a standardized and reproducible way. BON in a box automates biodiversity analyses by connecting individual scripts into pipelines that can be parameterized by a user form. Because it is an open and community contributed platform, users can customize and build upon existing analyses. The inherent transparency and proposed review process increase the scientific rigor of the EBV workflows. In sum, BON in a Box provides a comprehensive and accessible tool for scientists and policymakers around the world to operationalize their EBV workflows, and helps standardize and harmonize the way biodiversity data is transformed. This presentation will show how BON in a Box can help increase reusability and accessibility of EBV workflows.

Session: 6798685**7019963**

23/10/25 | 16:20

Room: Tolima

ORAL • EN

French BON EBV operationalization pilot: Reusing existing informatics solutions and open-source communities to connect existing data ecosystem and high-performance computing

Presenter

Yvan Le Bras

Authors

Coline Royaux (France)

Pauline Segumineau (France)

Arthur Barreau (Université Rennes 1 MNHN UMR ISYEB • France)

Olivier Norvez (MNHN Data Terra THEIA and PNDB Land Surface and Biodiversity Data Hubs • France)

Marie Jossé (CNRS IFREMER Data Terra • France)

Jean-Baptiste Mihoub (Sorbonne Université • France)

Björn Grüning (Germany)

Dominique Pelletier (IFREMER • France)

Marc Eléaume (France)

Yvan Le Bras (MNHN Data Terra PNDB Biodiversity Data Hub UAR 2047 DoHNÉE • France)

Abstract

Thanks to the Data Terra (French digital research infrastructure for Earth system and environment), at the PNDB (French Biodiversity data hub), we started in 2018 the use of existing informatics solutions to propose operational ways to manage, share and analyze biodiversity and auxiliary data and metadata. Starting from a combination of a computational workflow oriented open-source solution, the Galaxy platform, and a pivotal metadata standard, Ecological Metadata Language (EML), we designed an iterative model to propose an operational Biodiversity information system allowing scaling from local, where Biodiversity is, to global, in an accessible, transparent and reusable manner.

We propose here to present actual state of the pilot showcasing the relevance of 1/ the “atomization-generalization framework” designed for Galaxy Ecology initiative <https://doi.org/10.1093/gigascience/giae122> to allow reusing biodiversity indicators computational workflows in different taxonomic, spatial and temporal extents and 2/ the use of EML metadata standard as a pivotal and common language to allow reaching required high FAIRness in biodiversity monitoring.

Session: 6798685**7013825**

23/10/25 | 16:35

Room: Tolima

ORAL • EN

Advancing Biodiversity Monitoring through the EBV Framework in Asia: Insights and Challenges of APBON

Presenter

Yayoi Takeuchi

Authors

Yayoi Takeuchi (Japan)

Jamie Kass (Tohoku University, Japan • Japan)

Takehisa Yamakita (Japan Agency for Marine–Earth Science and Technology, Japan • Japan)

Masahiro Nakaoka (Hokkaido University, Japan • Japan)

Alice Hughes (University of Melbourne, Australia • Australia)

Yongyut Trisurat (Japan)

Hiroyuki Muraoka (The University of Tokyo, Japan • Japan)

Abstract

The Asia–Pacific Biodiversity Observation Network (APBON), established in 2009, promotes biodiversity monitoring, open-data sharing, and capacity building across the Asia–Pacific region. By fostering collaboration among research institutions, NGOs, and policy-makers, APBON enables science-based decision-making for biodiversity conservation. In 2021, APBON published a strategic plan highlighting key priority areas: addressing biodiversity data gaps, promoting interdisciplinary research on biodiversity and ecosystem services, and facilitating science-policy dialogues aligned with global goals and National Biodiversity Strategies and Action Plans (NBSAPs).

In recent years, global initiatives such as the Kunming–Montreal Global Biodiversity Framework (KMGBF), IPBES’s monitoring assessment, and GEO BON’s GBiOS concept have significantly increased the awareness of the need of, and demand for robust biodiversity data and monitoring systems. In response, we are now exploring how the AP region can effectively meet these emerging demands. Key issues under consideration include: data gaps and accessibility, sociopolitical constraints on data sharing, and the need for regional collaboration for the development of Essential Biodiversity Variables (EBVs), and contributions to the implementation of updated NBSAPs under the KMGBF. In particular, the EBV framework, initially developed under GEO BON, offers a promising approach to standardize data across different dimensions of biodiversity and harmonize biodiversity observation. However, contextual interpretation and adaptation are necessary to ensure its relevance and applicability in the AP region. In this presentation, we will discuss the challenges and opportunities of applying the EBV framework from an Asian perspective, and how building a regional biodiversity observation system

Session: 6798685**7021022**

23/10/25 | 16:30

Room: Tolima

LIGHTNING TALK • EN

Optimizing the use of participatory monitoring data to calculate Essential Biodiversity Variables at local scales

Presenter

Andres Felipe Suarez Castro

Authors

Andres Felipe Suarez Castro (Australia)

Juan Pablo Lopez Ordoñez (Conservación Internacional Colombia • Colombia)

Andrés Paez (Conservación Internacional Colombia • Colombia)

Abstract

Participatory biodiversity monitoring is a key tool for territorial environmental management and the development of biodiversity indicators. It enables the involvement of local communities, environmental authorities, and citizen scientists in data collection and analysis. However, implementation in the development of biodiversity indicators faces challenges such as variability in data quality and a lack of methodological standardization, which complicate integration with conventional monitoring systems. As a result, the use of participatory monitoring to produce a wide range of robust indicators remains limited—particularly in highly biodiverse regions where data access and management are difficult. This study proposes a protocol for integrating participatory monitoring data to generate biodiversity indicators in an Andean–Amazonian transition corridor of Colombia. We examine how globally proposed indicators can be applied at local scales and demonstrate the utility of participatory data when compared with established biodiversity databases. Based on a review of 37 metrics from the Essential Biodiversity Variables (EBVs) conceptual framework, we selected six feasible indicators for protocol implementation. These indicators include metrics related to threat mitigation and species restoration, absolute and relative abundance of indicator species, a biodiversity integrity index, and species diversity measures. Indicators were calculated using more than 12,000 records obtained from local monitoring groups. Our findings show that while databases such as the Global Biodiversity Information Facility (GBIF) and eBird are valuable for identifying temporal trends, participatory monitoring significantly is key to enhance spatial representativeness. Participatory monitoring also reduced the uncertainty in the selection of indicator species that are tailored to monitor management actions at local scales. This study represents a concrete step toward operationalizing EBVs in agricultural and protected landscapes, and it will help to strengthen conservation efforts by aligning global goals with local priorities.

Session: **6798685****7020433**

23/10/25 | 16:55

Room: Tolima

LIGHTNING TALK VIRTUAL • EN

Linking Essential Biodiversity Variables to GBF Indicators Through Remote Sensing for Enhanced Biodiversity Monitoring and Reporting

Presenter

Elnaz Neinavaz

Authors

Elnaz Neinavaz (University of Twente| ITC • Netherlands)

Andrew K Skidmore (University of Twente|ITC • Netherlands)

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Susanne Thulin (Brockmann Geomatics • Sweden)

Petra Philipson (Brockmann Geomatics • Sweden)

Maria Hallfors (SYKE • Finland)

Abstract

Essential Biodiversity Variables (EBVs) have been developed as a framework to standardize and streamline the observation, integration, and dissemination of biodiversity data across temporal and spatial scales. EBVs are derived from various data sources, from *in situ* observations to Earth observation technologies data. In parallel, the Kunming-Montreal Global Biodiversity Framework (GBF) has introduced a suite of indicators to guide and evaluate progress toward biodiversity targets. To this end, EBVs provide a scientifically robust foundation for tracking and reporting on biodiversity changes over time and across regions, typically visualized through change detection localized time-series data or spatially aggregated maps. Remote sensing plays a pivotal role in this process by offering consistent, repeatable, and scalable data to produce information on biodiversity, making it a key enabler for both EBV generation and GBF indicator reporting. Given the complementary nature of these two frameworks, establishing a coherent linkage between EBVs and GBF indicators is not only logical but essential for effective policy development, implementation, assessment, and adaptation. In this study, we strive to systematically map the connections between EBVs and the GBF indicator framework. We explore the alignment of EBVs with current remote sensing biodiversity products to assess their potential for operational integration into regional and national biodiversity strategies and action plans. By elucidating these linkages, our work supports harmonizing scientific monitoring efforts with policy-oriented monitoring and reporting needs, ultimately enhancing the global capacity to assess and conserve biodiversity in line with international commitments.

Session: 6798685**7019770**

23/10/25 | 17:00

Room: Tolima

LIGHTNING TALK VIRTUAL • EN

Towards an Integrated Coastal Observation System in France for Monitoring Essential Biodiversity Variables

Presenter

Clémence Cotten

Authors

Clémence Cotten (IFREMER • France)

Alain Lefebvre (IFREMER • France)

Annaig Le Guen (CNRS • France)

Erwann Quimbert (IFREMER • France)

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Laëtitia Campistron (IUEM • France)

Mark Hoebeke (Station Biologique de Roscoff • France)

Mylene Lorre-Guidt (DATA TERRA • France)

Cédric Chauvel (IUEM • France)

Abstract

France's National Research Infrastructure for Coastal Ocean and Littoral Observation (ILICO) is dedicated to the long-term observation of coastal and littoral systems at the interface of continent, ocean, and atmosphere, in both mainland and overseas territories. Through its nine certified National Observation Services (SNOs), ILICO monitors key environmental parameters across biodiversity (e.g., phytoplankton, benthic macroinvertebrates), coastal dynamics (e.g., shoreline change, sea level), and physico-chemical conditions. These multidisciplinary observations are crucial for tracking changes in Essential Biodiversity Variables (EBVs) and informing ecosystem-based management strategies.

To address the challenge of integrating multi-platform, multi-scale, and multi-variable data, ILICO collaborates with the ODATIS ocean data cluster—part of the French DATA TERRA research e-infrastructure—to improve data management and ensure compliance with the FAIR principles. This collaboration led to the development of a dedicated data portal that allows users to access, visualize, and cross-analyze the diverse datasets produced by ILICO's SNOs.

A core challenge of the project was the harmonization of data, for which the OGC SensorThings API standard was selected, enabling interoperability across originally heterogeneous formats. Particular attention was paid to biodiversity datasets, which are often complex and not natively aligned with SensorThings. Common vocabularies, such as those provided by WoRMS and SeaDataNet, were used to group data by EBVs and facilitate thematic exploration across observation services.

The portal, designed with UX expertise, offers a user-friendly interface that supports both expert and non-expert users. It enables integrated access to time series and spatial datasets related to coastal biodiversity, enhancing the visibility and reusability of long-term observation data. Ultimately, this infrastructure contributes to enable the scientific community and decision-makers to characterize biodiversity trends and pressures across France's coastal environments. Other themes will also be explored via this portal, such as eutrophication, extreme events, and cold and heat waves.

Session: 6798685**7014867**

23/10/25 | 17:05

Room: Tolima

LIGHTNING TALK • EN

Addressing bottlenecks in EBV generation in Europe: Which monitoring programs are ready to generate EBVs for policy?

Presenter

Maria Blasi

Authors

Maria Blasi (Spain)

Alejandra Morán-Ordóñez (University of Bern • Switzerland)

David Martí (CREAF • Spain)

Dani Villero (CREAF • Spain)

Lluís Brotons (CREAF • Spain)

— EuropaBON network (Spain)

Abstract

Essential Biodiversity Variables (EBVs) are defined as a set of indicators that can effectively evaluate the success of conservation and restoration measures and are able to monitor progress towards the achievement of conservation goals. Here, we present an analysis of the major limitations in the capacity to derive functional EBVs at the European level. In this study, we evaluated existing biodiversity monitoring programs of in situ data collection, coordinated at the European scale, that could support the generation of EBVs. The list of EBVs was defined in EuropaBON project to allow for measuring spatiotemporal patterns of biodiversity across Europe's freshwater, marine, and terrestrial realms, encompassing a wide range of taxonomic groups and ecosystems. We evaluated 16 monitoring programs that could potentially produce 36 EBVs. Each EBV was evaluated according to 16 criteria (grouped in three main categories: 1) data collection and sampling; 2) models, interoperability, and IT infrastructure; and 3) data integration) to assess where bottlenecks for the generation of that EBV lie. The results show us where these obstacles are shared among EBVs and monitoring initiatives, and indicate ways to collectively tackle data flow bottlenecks. This study is a collaborative work managed with the EuropaBON network and a wide range of stakeholders.

Session **6803025**

Symposium

23/10/25 | 16:00

Room: Caldas

The Power and Pitfalls of Civic Science

Organizers

Dan Lear
Ely Wallis
Ruben Perez

Description

We invite submissions exploring the role of participatory and civic science in biodiversity research and in their contribution to regional and international policy development. Engaging non-professional volunteers in data collection offers exciting opportunities to expand spatial and temporal coverage, enhance public engagement, and foster inclusive scientific collaboration. However, this approach also presents challenges, including data quality assurance, standardization, participant training, and long-term project sustainability.

We welcome contributions on innovative methodologies, case studies, and frameworks that address these challenges while leveraging the strengths of citizen science. Topics may include data validation techniques, ethical considerations, effective partnerships between researchers and communities, and the integration of citizen science data into decision-making processes.

Session: 6803025**7018648**

23/10/25 | 16:00

Room: Caldas

ORAL • EN

The Power of Validated Participatory Science Data: Using eBird Status and Trends to Inform Policy and Management

Presenter

Matt Strimas-Mackey

Authors

Matt Strimas-Mackey (Cornell Lab of Ornithology • United States)

Abstract

Effective biodiversity conservation relies on robust monitoring data to inform strategic policy and management decisions. Traditional structured surveys conducted by professional observers, while valuable, are often limited in spatial, temporal, and taxonomic coverage due to high costs and logistical constraints. Participatory science programs, which engage volunteer data collectors, offer a promising solution to expand data collection. However, such programs often facilitate the collection of large quantities of data by having relatively unstructured protocols, and so validation of information from participatory science programs is important for wide acceptance.

Little structure in the data-collection process requires that analyses of the resulting data account for noise due to variability in the sampling process and bias introduced by potentially non-representative sampling. In the case of the participatory science program eBird, machine learning techniques are used by the eBird Status and Trends project to mitigate sampling noise and bias when estimating species distributions, relative abundances and inter-annual trends for bird species globally. In addition to analytical approaches, rigorous validation using independent datasets is crucial before integrating these data products into decision-making frameworks.

This presentation will highlight two case studies demonstrating successful collaborations with the United States Fish and Wildlife Service (USFWS) to validate eBird Status and Trends data products. The USFWS conducts systematic aerial surveys for waterfowl and eagle populations across the United States, providing an invaluable independent benchmark. We found strong agreement between eBird-based relative abundance estimates and these professional aerial surveys for most species. Furthermore, we show that models combining structured professional surveys with validated participatory science data can achieve superior predictive power and broader spatial and temporal coverage than either data source alone. Finally, we highlight how the USFWS.

Session: 6803025**7018540**

23/10/25 | 16:12

Room: Caldas

ORAL • EN

From Shore to Server: Connecting Marine Civic Science to Global Biodiversity Data through DASSH and OBIS-UK

Presenter

Chloe Figueroa Ashforth

Authors

Chloe Figueroa Ashforth (Marine Biological Association • United Kingdom)

Julie Bunt (Marine Biological Association • United Kingdom)

Dan Lear (Marine Biological Association • United Kingdom)

Abstract

DASSH (the UK Archive for Marine Species and Habitats Data and UK Node of OBIS) provides tools, services and expertise to support the archiving, management and publication of marine biodiversity data in standardised formats, and its integration into national and global data systems. This presentation will focus on the range of civic-science activities that DASSH supports, from individual civic-scientists and national initiatives to European projects tackling the challenges that accompany civic science data.

With civic science generating large volumes of valuable biodiversity data, there is a need to support civic scientists in producing FAIR, high quality data. DASSH, in partnership with Natural England and supported by the UK Governments marine Natural Capital and Ecosystem Assessment Programme, have produced an online Citizen Science Best Practice Data Guidance tool. The tool summarises over 60 sources of existing recommendations into a resource that provides data-focused guidance at each stage of the data lifecycle, from planning a civic science project to sharing and reusing the data produced, with initiatives including The UK Rock Pool Project and iNaturalist used as case studies to demonstrate how FAIR data practices can be applied regardless of scale.

DASSH has worked closely with The UK Rock Pool Project to establish data flows to OBIS-UK for the data collected as part of The Big Rock Pool Challenge, engaging communities in exploring the UK's marine biodiversity, using iNaturalist. DASSH has developed an automated reporting method for detections of invasive non-native and horizon species at an early stage, informing changes to the invasive non-native species list and improving invasive species management and mitigation.

Session: **6803025****7017830**

23/10/25 | 16:23

Room: Caldas

ORAL • EN

Geographic redistributions are insufficient to mitigate exposure to climate change in North American birds

Presenter

Jeremy Cohen

Authors

Jeremy Cohen (United States)

Walter Jetz (Yale University • United States)

Abstract

As climate change accelerates, many species must move poleward or upslope to conserve their environmental niches and limit their exposure. While such geographic redistributions have been extensively reported, an assessment of species' success in limiting their exposure to novel conditions is missing. Here, we develop a method to account for biases in tens of millions of citizen science observations and evaluate how 406 bird species native to the US and Canada have mitigated their environmental niche loss using geographical redistributions. We find that most redistributions were only partially effective at mitigating exposure to climate change. Over 20 years, species on average redistributed their summertime ranges $\sim 0.64^\circ$ north, averting their expected exposure to warming by $\sim 1.28^\circ\text{C}$, roughly half of the warming they would have experienced if they remained stationary. Meanwhile, species only mitigated $\sim 0.47^\circ\text{C}$ (11% of expected warming) in winter, and nearly all experienced warming of $>2^\circ\text{C}$. Species moving the furthest north and possessing traits associated with dispersal succeeded most in limiting their niche loss. Species' historical niches are becoming increasingly mismatched with contemporary climates even in a highly mobile taxon, raising concerns about the ability of other wildlife to persist in a warmer world.

Session: 6803025**7020870**

23/10/25 | 16:36

Room: Caldas

ORAL VIRTUAL • EN

Adaptive citizen science: Spatially targeting recording effort by volunteers to improve biodiversity monitoring

Presenter

Michael Pocock

Authors

Michael Pocock (UK Centre for Ecology & Hydrology • United Kingdom)

Abstract

Volunteer-collected ('citizen science') data are a vital source of information for biodiversity monitoring from local to international scales. Vast numbers of 'unstructured' records are collected by people from when and where they choose. This flexibility supports a high uptake of citizen science but it means that the records are not equally valuable: for effective biodiversity monitoring, we don't need simply *more* records, we need *more informative* records. We present two tools from the UK to support people who want to choose to make records from the places that we need them most. First, in the DECIDE Tool we identified targets for future recording as the areas of highest uncertainty from spatial distribution models of butterfly and moth data, so that new data would optimally improve the distribution models. Second, the Targeting Revisits Maps we highlighted locations for insect groups that had either been visited in only one year in the past, or squares that had previously been well-recorded but had not been recently visited, so that new data would optimally improve trend models. Both tools were co-designed with potential users to be relevant, actionable and appealing, and we assessed their acceptability via user feedback.

Here we focused on biodiversity recording in the UK, which is a relatively data-rich country, but this vision for 'precision citizen science' (gaining information we need from the places we need it most) would be even more valuable in data-sparse regions of the world – for the mutual benefit of participants and data users.

Session: **6803025****7020583**

23/10/25 | 16:47

Room: Caldas

ORAL • EN

A new platform to build and support citizen science projects in biodiversity

Presenter

Andrea Tarallo

Authors

Andrea Tarallo (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Alberto Basset** (University of Salento, Department of Biological and Environmental Sciences and Technologies • Italy)**Francesco Cozzoli** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Francesco De Leo** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Davide Raho** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Ilaria Rosati** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)

Abstract

Citizen science has emerged as a powerful approach to engage the public in scientific research, particularly in biodiversity and ecosystem monitoring. In this field, the active participation of citizens in scientific research is becoming increasingly important, contributing to data collection. However, creating, maintaining and managing applications for the collection of research data by non-professionals present several difficulties and critical issues. These include the need for IT skills for developing and maintaining the whole system, the high infrastructural costs related with the collection and management of high volumes of data produced, together with the growing need to generate structured data, enriched with metadata and described using controlled vocabularies to ensure reusability and machine actionability. In this context, LifeWatch Italy, the Italian distributed centre of LifeWatch ERIC, has developed a Citizen Science Platform to facilitate knowledge sharing, project development, and data management in citizen science initiatives. The Platform offers various functionalities, including a) a section dedicated to fundamental knowledge about citizen science, including its history, methodologies, and key principles; b) a practical guide for developing and managing citizen science projects supporting users through the essential steps of project formulation, community engagement, data management, and communication; c) a searchable repository of training materials to support skills uptake in citizen science methodologies and management; d) a comprehensive directory of citizen science projects, visualised on an interactive map; e) a feature allowing users to create customised web applications for the collection of a diverse set of data types. To illustrate the practical impact of the Citizen Science Platform, we present the Hic Sunt Lupi project, a citizen science initiative focused on monitoring wolf populations in Apulia region (Italy). Utilising the platform's resources, the project successfully engaged the public in data collection, facilitated by the web application functionalities.

Session: **6803025****7013587**

23/10/25 | 17:00

Room: Caldas

ORAL • EN

Citizen Science to the Grassroots: Taking Biodiversity Data Collection to the Grassroots in Ekiti State, Nigeria Using the iNaturalist Application

Presenter

Babajide Agboola

Authors

Babajide Agboola (Agbo-Veterinary and Environmental Consult Limited • Nigeria)

Olly Owen (Ekiti State Government • Nigeria)

Akinyemi Akinyugha (Ekiti State Government • Nigeria)

Taiye Adeyanju (University of Ibadan • Nigeria)

Abubakar Ringim (Federal University Dutse • Nigeria)

Venmak Agboola (Federal University of Technology, Akure • Nigeria)

Oluwaseyi Ebenezer (Triple Green Environmental Development Foundation • Nigeria)

Chloe Strevens (Oxford University • United Kingdom)

Abstract

Biodiversity conservation efforts in Nigeria are often hindered by limited data, centralized research structures, and resource constraints. To address these challenges, the Ekiti Biodiversity Survey Project (EBSP) launched an innovative citizen science initiative in Ekiti State, leveraging the iNaturalist application to engage local communities in biodiversity monitoring. This grassroots approach empowers residents including youth, students, traditional custodians, and conservation enthusiasts to document flora and fauna using a simple mobile app. Through workshops, seminars, and outreach programs, EBSP builds capacity and fosters environmental stewardship while generating high-quality, geo-tagged biodiversity data. Since its inception, the project has facilitated over 7,000 observations and identified more than 1000 species, including rare and endangered taxa such as the Ibadan Malimbe (*Malimbus ibadanensis*) and the tick spider (*Ricinoides*). In addition to digital engagement, EBSP collaborates with community leaders to assess sacred forests and groves, recommending their legal protection under Ekiti State Forestry Law as Community Protected Areas (CPA). These culturally significant sites like Oke-Abanijorin and Igbo-Ogun serve as biodiversity hotspots and community conserved ecosystems. The project not only enhances biodiversity documentation but also promotes conservation ethics rooted in local traditions.

Furthermore, EBSP is championing the effort to restore some of the identified community protected forest, by donation and monitoring the replanting of Indigenous tree seedlings as well raising awareness and fostering dialogue among stakeholders to address broader conservation challenges in southwest Nigeria. By combining citizen science, traditional knowledge, and technology, the Ekiti Biodiversity Survey Project exemplifies an inclusive, participatory model of environmental conservation. It underscores the value of community engagement in achieving long-term ecological sustainability and represents a replicable framework for biodiversity initiatives across Africa and beyond.

Session

6799160

Symposium

23/10/25 | 16:00

Room: Valle

Enhancing the FAIRness of biological survey data with Darwin Core and the Humboldt extension

Organizers

Kate Ingenloff

Anahita Kazem

Yanina V. Sica

Description

Broad availability of FAIR and open biodiversity survey and monitoring data (for example, data resulting from long-term ecological research efforts or camera trap surveys) is critical to addressing ecological research questions regarding changes in biodiversity status and subsequently informing relevant policy decisions. The contextual information about a survey that is necessary to assess the appropriateness of data for re-use in such applications, however, is often reported as unstructured metadata. The Darwin Core (<https://dwc.tdwg.org/>) standard and the recently ratified Humboldt extension (<https://eco.tdwg.org/>) provide a mechanism by which to capture the sampling context of biological survey data (e.g., sampling protocol, scope, and effort) in a structured way, thereby enhancing data discovery, ensuring machine readability of dataset metadata, and improving interoperability of data from heterogeneous sources. Implementation of the standard, however, may feel daunting to data holders. This session provides a forum for field researchers, data managers, or data stewards who hold biodiversity datasets and would like to standardize the data implementing DwC and Humboldt extension vocabulary to share experiences and discuss challenges for those interested in sharing and effective reuse of biodiversity survey data.

Session: 6799160**7021027**

23/10/25 | 16:05

Room: Valle

ORAL • EN

From methods and protocols to event hierarchy: a primer on using the Humboldt Extension to Darwin Core

Presenter

Kate Ingenloff

Authors

Kate Ingenloff (Global Biodiversity Information Facility Secretariat • Denmark)**Anahita J.N. Kazem** (German Centre for Integrative Biodiversity Research (iDiv) & Friedrich Schiller University Jena • Germany)**Yanina V. Sica** (Senckenberg Biodiversity & Climate Research Centre • Germany)

Abstract

In the face of the global biodiversity crisis, provision of biodiversity data that is maximally effective for downstream use in science, conservation, and policy is essential. The Darwin Core (DwC) standard has played a central role in providing a standardized structure and vocabulary for these data. However, early iterations of the standard were not optimized to capture the full context of ecological surveys, such as sampling design and effort, scope, and the absence of detections. This information is therefore often shared as metadata in an unstructured manner, limiting the correct interpretation and potential reuse of the data. The Humboldt Extension to DwC was introduced to address these issues, enriching the vocabulary with 55 additional terms. Practical implementation of the standard, however, may feel daunting to data holders. For example, there are often multiple ways of representing a complex hierarchical sampling design, particularly in the case of compilations. Once the Event hierarchy has been established, decisions remain regarding the most appropriate level at which to populate a given term initially, and whether values should be propagated at other levels; answers may differ depending upon the term in question. Here we provide a primer and conceptual guide for users of the new extension, outlining ways to approach the problem and pitfalls to avoid. The presentation is aimed at both newcomers to DwC and experienced users seeking to supplement existing Darwin Core Archives with the Humboldt Extension.

Session: 6799160**7013731**

23/10/25 | 16:20

Room: Valle

ORAL • EN

Structuring biological survey metadata for reuse: Implementing the Humboldt Extension in Flemish bird monitoring datasets on GBIF

Presenter

Stijn Cooleman

Authors

Stijn Cooleman (Belgian Biodiversity Platform (BBPF) & Research Institute for Nature and Forest (INBO) • Belgium)**André Heughebaert** (Belgian Biodiversity Platform (BBPF) • Belgium)**Dimitri Brosens** (Research Institute for Nature and Forest (INBO) • Belgium)

Abstract

The effective reuse of biodiversity data is essential for informing science-based policy. As the Global Biodiversity Information Facility (GBIF) increasingly aggregates data from diverse biological surveys, machine-readable metadata becomes progressively crucial. Structuring survey metadata from textual descriptions into standardized format improves their comparability and alignment with the FAIR (Findable, Accessible, Interoperable, Reusable) principles. The Humboldt Extension provides a controlled vocabulary to capture key methodological details of ecological inventories (eco), enabling more robust analyses of biodiversity indices across spatial and temporal scales.

At the Belgian Biodiversity Platform, we apply the Humboldt Extension guidelines to enhance two bird monitoring datasets on GBIF. Although both represent counts of observed birds in Flemish areas, they differ in spatial scope and methodology: the Common Breeding bird monitoring in Flanders, published by INBO, uses point counts across 1x1 km squares throughout the region, while the Bird census counts at the Zwin Nature Park, published by BBPF, combine point and transect counts within one location.

In this presentation, we review our practices for selecting and mapping eco terms in both sampling-event datasets. We thereby highlight our findings on how to structure their events' metadata hierarchically to reflect spatial nesting, sampling effort, and taxonomic scope. We propose a schematization that facilitates the detection protocol-specific nuances, such as the exclusion of certain species, and supports the more accurate derivation of species densities, abundances, and absences.

Implementing the Humboldt Extension in these real-world cases demonstrates the practical value of structured metadata for enhancing biodiversity data interoperability and reusability. This standardization generally contributes to meeting targets of the Global Biodiversity Framework.

Session: 6799160**7020027**

23/10/25 | 16:33

Room: Valle

ORAL VIRTUAL • EN

Application of Darwin Core on biodiversity monitoring data: nested occurrences, measurements and graphical metadata

Presenter

Guillaume Body

Authors

Guillaume Body (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Chloé Vinet (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Sophie Pamerlon (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Anne-Sophie Archambeau (Patrinat (OFB-MNHN-CNRS-IRD) • France)

Francesca Jaroszynska (French Biodiversity Agency (OFB) • France)

Sarah Valentin (CIRAD • France)

Abstract

The use of Darwin Core for biodiversity monitoring data is essential, and increasingly popular. Through two different consortia in Europe, Enetwild and Biodiversa+, we experimented its use on various biodiversity data: hunting bags, species density estimations, epidemiological records, electrofishing protocols, common bird point count records, aerial monitoring of marine megafauna, eDNA surveys, acoustic monitoring of bats and soil monitoring protocols. We intensively used the ‘Event Core’, the ‘Occurrence’ and ‘Measurement or Fact’ extensions, and we applied a nested structure of occurrences and measurements to properly standardise our records. We developed a RShiny tool to facilitate data handling. Visualization of the data structure became essential and we strongly suggest to find a place for that in the metadata information.

Session: 6799160**7010151**

23/10/25 | 16:47

Room: Valle

ORAL • EN

Mapping nested vegetation plot data to Darwin Core and the Humboldt Extension: challenges and open questions

Presenter

Salza Palpurina

Authors

Salza Palpurina (GBIF ECA support team | National Museum of Natural History, Bulgarian Academy of Sciences • Bulgaria)**Kate Ingenloff** (GBIFS • Denmark)

Abstract

Vegetation plot data, particularly those based on nested sampling designs, pose unique challenges when aligning with biodiversity data standards such as Darwin Core and the Humboldt Extension. In this presentation, I will share my ongoing experience working to publish such a dataset using the Sampling event data model. Rather than presenting a complete solution, I aim to highlight specific implementation questions that emerged during the process—for example, how best to represent plot hierarchy, define sampling effort across spatial scales, and structure abiotic and biotic data in a way that remains interoperable and faithful to the original design. My goal is to invite discussion with other vegetation scientists and data managers on possible approaches, and to identify where further community guidance or refinement of best practices might be needed. I hope this case will resonate with others working on complex ecological data and help inform the broader adoption of FAIR and standardized vegetation datasets.

Session: 6799160**7020705**

23/10/25 | 17:02

Room: Valle

ORAL • EN

Lessons from Census and Trawl-Based Marine Datasets

Presenter

Yi-Ming Gan

Authors

Yi-Ming Gan (Royal Belgian Institute of Natural Sciences • Belgium)

Pablo Deschepper (Royal Belgian Institute of Natural Sciences • Belgium)

Charlie Plasman (Royal Belgian Institute of Natural Sciences • Belgium)

Anton P. Van de Putte (Royal Belgian Institute of Natural Sciences • Belgium)

Abstract

The Humboldt Extension enables the structured representation of survey design, scope, and sampling effort of biodiversity surveys. In this session, we explore its application across two contrasting marine use cases and reflect on its value for enhancing data interpretation.

Our first case study involves a marine census dataset targeting a fixed species list across predefined stations. The Humboldt Extension provided a clear framework to define target taxa, survey scopes, and effort, making it easier to interpret non-detections.

In contrast, the BROKE-West fish dataset is a subset of the catch from a trawl survey in the Southern Ocean. It highlights the challenges of applying the Humboldt Extension to more complex datasets. Not everything caught in a trawl net is necessarily published in a single dataset, as the catch is often sorted by taxonomic group and distributed to different researchers, resulting in separate datasets. This makes it difficult to specify the overall target scope of the survey. The sampling gears used in marine surveys are often not the standard gear or optimised for detecting all target species, further complicating the specification of target scope and interpretation of data.

We discuss lessons learned, considerations for publishing and interpreting the data of Humboldt Extension datasets, and potential improvements to better support more complex or less structured surveys.

Session: 6799160**7020774**

23/10/25 | 17:15

Room: Valle

ORAL • EN

BiodivBank: a streamlined solution facilitating FAIR and open sharing of structured species abundance and assemblage data

Presenter

Anahita J.N. Kazem

Authors

Anahita J.N. Kazem (German Centre for Integrative Biodiversity Research (iDiv) & Friedrich Schiller University Jena • Germany)**Birgitta König-Ries** (Friedrich Schiller University Jena • Germany)**Henrique M. Pereira** (German Centre for Integrative Biodiversity Research (iDiv) & Martin Luther University Halle-Wittenberg • Germany)**Jonathan M. Chase** (German Centre for Integrative Biodiversity Research (iDiv) & Martin Luther University Halle-Wittenberg • Germany)

Abstract

Understanding biodiversity and applying this knowledge for positive impact relies on access to reliable data with broad geographic and taxonomic coverage. Data on species abundances are particularly valuable for documenting trends over time or community effects, and whilst a wealth of such information exists, much is neither interoperable nor readily usable. We have recently implemented a prototype for a dedicated global and public data repository, with the goal of gathering and harmonizing the heterogeneous datasets currently scattered among generalist repositories, smaller subject-specific databases and the academic literature. The platform features a dynamic metadata entry form, to facilitate more rapid, intuitive and accurate entry of the extensive contextual information required to underpin greater search functionality and make data genuinely reusable. Data upload options are flexible, and when structured data is imported following pre-defined templates, Darwin Core Archives can be created and registered with GBIF or OBIS at the press of a button. Variables can additionally be mapped to alternative community-accepted data standards, ontologies or external services. The product therefore combines the advantages of a fully-fledged data repository with the additional visibility offered by mobilization to GBIF. Our repository was designed with the Humboldt Extension in mind, and we are currently conducting user tests to understand how we can best support data providers in representing their event-based data using this extension, as well as ensuring that the portal meets the needs of a diverse range of potential stakeholders.

Session

6798023

Symposium

23/10/25 | 16:00

Room: Cauca

Challenges and solutions for high-throughput biodiversity monitoring

Organizers

Niels Raes

Elaine van Ommen-Kloeke

Lain E. Pardo

Nastassia Patin

Kathleen Pitz

Diego Lizcano

Mauricio Vela

Angélica Diaz-Pulido

Description

New tools and technologies for high-throughput biodiversity monitoring—including camera traps, insect cameras, audio devices, eDNA sampling, drones, and remotely sensed data—are rapidly developing. When combined with AI species identification and wireless networks, these tools enable near real-time monitoring but present significant challenges around data management, standardization, and ethical considerations.

This session will address critical questions facing researchers in the field: data storage requirements, compression considerations, AI algorithm consistency, machine attribution in observation records, absence data documentation, privacy concerns with human subjects, and DNA sequence data management. We'll explore the unique qualities of sequence data for biodiversity research beyond species identification, including indexing, searching capabilities, taxonomic interpretation, and taxon-independent biodiversity measurements.

We invite presenters to share solutions, experiences, and collaborative opportunities that address these global and regional challenges, with an emphasis on integrating and democratizing biodiversity monitoring data to improve management decisions worldwide. We will also examine how, although monitoring has advanced using new technologies such as by using camera traps and community participatory methods, data remains dispersed across platforms.

In particular, we would welcome abstracts that demonstrate initiatives in South America using platforms like Wildlife Insights, SIB Colombia, Bon in a Box, and the Otus Network.

Session: 6798023**7010127**

23/10/25 | 16:00

Room: Cauca

ORAL • EN

SIREN - Advancing Real-time Biodiversity Monitoring through Emerging Technological Convergence

Presenter

Robert Lewis

Authors

Robert Lewis (Norwegian Institute for Nature Research • Norway)

Benjamin Cretois (Norwegian Institute for Nature Research • Norway)

Baard Nossu (SINTEF • Norway)

Luis Caetano (SINTEF • Norway)

Abstract

The SIREN (Sensor-Integrated Real-time Ecological Network) initiative pioneers AI-driven biodiversity monitoring by leveraging low-power edge devices and large language models (LLMs) to generate near real-time ecological alerts. Biodiversity and environmental sensors (e.g., bioacoustic recorders, microclimate loggers, and camera traps) generate vast, high-volume data streams, while in remote, off-grid deployments, limited energy availability and the need for efficient transmission pipelines make mobilizing near real-time streams autonomously and over prolonged periods unsustainable.

SIREN explores three core technological pillars to overcome these challenges: (1) modular sensor units with energy-optimized microcontrollers for on-chip TinyML preprocessing of high-bandwidth data (e.g., bioacoustics) prior to transmission; (2) federated learning frameworks that continuously refine locally trained models across distributed nodes, eliminating the need for raw data exchange; and (3) server-side large language model processing and neural graph architectures that synthesize metadata streams that reveal network-wide patterns and processes, and communicate near real-time ecological/environmental alerts.

Through these converging technological advances, we demonstrate a scalable, low-energy, and decentralized pipeline for democratized biodiversity monitoring and actionable conservation insights. We conclude with a forward-looking perspective on how decentralized sensor contributions align with equitable, data-driven ecosystem stewardship, incentivized via emerging biodiversity finance models and regenerative finance instruments.

Session: 6798023**7015406**

23/10/25 | 16:12

Room: Cauca

ORAL • EN

Smart nature reserves

Presenter

Laurens Hogeweg

Authors

Laurens Hogeweg (Naturalis Biodiversity Center • Netherlands)

Vincent Kalkman (Netherlands)

Marten Schoonman (Naturalis Biodiversity Center • Netherlands)

Elaine van Ommen Kloeke (Netherlands)

Niels Raes (Naturalis Biodiversity Center • Netherlands)

Abstract

The introduction of affordable high-quality sensors (cameras, microphones, DNA samplers) has led to the possibility of setting up continuous monitoring schemes for biodiversity with the potential for near-real time biodiversity monitoring, to better understand drivers of long-term change, and also effects of short-term interventions. The large digital data streams being generated require novel ways of analysing them, including an integrated way of combining AI-generated results and ecological analysis.

In the first part we will discuss our experiences with setting up digital sensor networks and biodiversity research infrastructures (BRI) for addressing these challenges. The ARISE platform is a Dutch platform for collecting and analysing sensor data using AI models and since September 2025 in production. Since March 2025 the Biodiversity Meets Data (BMD) project is developing a Single Access Point (SAP) for high-throughput biodiversity monitoring, biodiversity data, and biodiversity analyses with a focus on Europe's Natura 2000 areas and builds on a.o. ARISE. The MAMBO project (since 2023) is providing AI models for image and sound identification to our BRIs.

Bringing the results of these projects together allows us to set up the smartest nature reserves in the world. Monitoring nature reserves is paramount in driving (European) nature policy. Generating insight into its ecology poses some unique challenges in terms of a sufficiently dense network of portable and non-disturbing sensors. These dense networks generate even larger data streams and require novel AI workflows to analyse and annotate them. To ensure that our AI-generated results meet the expectations of the ecologists (and ultimately policy makers) we introduce the concept of meta AI models (MAM) that provide quality checks on large (billion scale) AI-identified datasets. The quality-checked AI-identified datasets subsequently allows our end-users to go from data to knowledge through intuitive virtual lab environments and dashboards.

Session: 6798023**7020643**

23/10/25 | 16:25

Room: Cauca

ORAL • ES

Red OTUS: monitoreo multiactor para un país megadiverso

Presenter

Angélica Díaz-Pulido

Authors

Angélica Díaz-Pulido (Instituto Humboldt • Colombia)**Jose Manuel Ochoa** (Instituto Humboldt • Colombia)**Sonia Rodriguez** (Instituto Humboldt • Colombia)**Juan Pablo Lopez Ordoñez** (Conservación Internacional - Colombia • Colombia)**Francisco Cruz** (Conservación Internacional - Colombia • Colombia)**Fabio Arjona** (Conservación Internacional - Colombia • Colombia)**Jorge Ahumada** (Wildlife Insights • Colombia)

Abstract

Frente a los desafíos actuales para la conservación de la biodiversidad, especialmente en países megadiversos como Colombia, es fundamental fomentar una colaboración efectiva entre autoridades ambientales, institutos de investigación, comunidades locales, ONG's y academia, así como del sector privado. Solo así podremos afianzar estrategias para construir un enfoque integral y sostenible para el conocimiento y la protección de la fauna silvestre.

Colombia ha asumido el compromiso de la meta 30x30, buscando conservar su biodiversidad en áreas protegidas a nivel nacional y regional. No obstante, muchas de estas áreas carecen aún de sistemas robustos de monitoreo de fauna. En respuesta a esta necesidad, surge la red OTUS, como una iniciativa de ciencia participativa que impulsa el reconocimiento de la biodiversidad mediante el uso de tecnologías, gestión colaborativa de datos.

A través del uso de cámaras trampa, OTUS genera imágenes que son procesadas con algoritmos de inteligencia artificial en la plataforma Wildlife Insights, y convertidas en registros biológicos públicos dentro del Sistema de Información sobre Biodiversidad de Colombia, nodo regional de GBIF. Este flujo de datos vivos permite convertir observaciones puntuales en conocimiento abierto, útil para la toma de decisiones de conservación y manejo.

La red OTUS enfrenta retos logísticos y ecológicos para la implementación de los esquemas de monitoreo; proponiendo una estructura colaborativa, en la que cada actor aporta conocimiento, capacidades, equipos y recursos. En su primera etapa (2024-2026), más de 700 cámaras trampa han sido vinculadas en todo el país, con la participación de diversos sectores, para lograr una gran fotografía nacional de la biodiversidad en campañas sincronizadas de fototrampeo, durante los meses de octubre y marzo. Este esfuerzo coordinado permitirá generar indicadores comparables en el tiempo, tanto a nivel de comunidades como de las poblaciones silvestres insumos, que fortalecen la toma de decisiones a escala local, regional y nacional.

Session: 6798023**7018812**

23/10/25 | 16:36

Room: Cauca

ORAL • EN

Enabling Plant Monitoring Through eDNA Metabarcoding: The Crucial Role of Biodiversity Data Infrastructures

Presenter

Birgit Gemeinholzer

Authors**BIRGIT GEMEINHOLZER** (UNIVERSITÄT KASSEL • Germany)**Abstract**

Plants, as autotrophs, are the foundation of terrestrial ecosystems and play crucial roles in food webs. They are directly impacted by climate change, which is expected to have profound effects on ecosystems, primary production, and agriculture. Currently, around two out of five plant species are threatened with extinction, which will also likely have severe consequences for other organisms. However, our understanding of the functional interdependencies of plants and their associated networks (e.g. food webs, pollination, dispersal) is limited. Plant metabarcoding offers a standardized, rapid method for identifying organisms across space and time, supporting the monitoring of these interdependencies. However, there is an urgent need to provide easy access and clear guidance to routine sampling, laboratory and data analysis, by also considering the respective documentation of data and metadata to streamline monitoring activities within and across countries and regions. Workflows and recommendations provided by national biodiversity data infrastructures (e.g. NFDI4Biodiversity in Germany and others), based on scientific recommendations from a consortium of researchers (e.g. METAPLANTCODE, funded by Biodiversa+ and co-funded by the EU, and others) to provide FAIR data in accordance to GBIF recommendations and exchange formats and linked to international networks, allow data accessibility on a global scale. This not only enables the tracking of endangered species and modelling of informative indicator species, but also supports monitoring ecosystem health, food webs, invasive alien species, and shifts in distribution ranges.

Session: **6798023****7020719**

23/10/25 | 16:48

Room: Cauca

ORAL • EN

Developing a Strategy for Incorporating Innovations into Brazil's Biodiversity Monitoring Program

Presenter

Rodrigo Jorge

Authors

RODRIGO JORGE (Instituto Chico Mendes de Conservação da Biodiversidade • Brazil)

CECILIA CRONEMBERGER (Instituto Chico Mendes de Conservação da Biodiversidade • Brazil)

Abstract

Currently, Brazil has the Biodiversity Monitoring Program, known as the Monitora Program, which is either being implemented or is already operational in 129 federal protected areas managed by ICMBio. These units cover all of the country's biomes and a wide variety of environments. To structure this program, biodiversity targets that reflect the conservation status of different taxonomic groups present in these areas were selected. The sampling protocols developed are low-cost and easy to implement, allowing them to be carried out without the need for specialists.

With the rapid advancement of technology, new opportunities have emerged to address the sampling challenges of the current protocols and to include targets that are not yet covered by Monitora. Some innovations are already being tested, such as data collection on mammals using camera traps, acoustic landscape monitoring, and the use of environmental DNA to detect the presence of species of interest. However, it became clear that it was necessary to establish criteria to evaluate and select new innovation proposals.

Therefore, after ten years of data collection, a seminar was held to present innovations potentially applicable to Monitora. ICMBio and its partners began identifying and discussing criteria for evaluating innovation proposals, including assessing their necessity in addressing program challenges, compatibility with its guidelines and principles, costs and funding sources, existing or potential partnerships, technological infrastructure needs, operational feasibility, autonomy for implementation and maintenance, potential for community participation, and scalability.

In addition, we identified and discussed the current challenges in implementing the Monitora Program at various stages (data collection and management, analysis, interpretation, and dissemination of results) that can be overcome through innovation—referred to as “inspirations for inventors.” These elements, along with others, make up the proposal for the Strategy for Incorporating Innovations into the Monitora Program, which is in the final stages of development.



DATOS
VIVOS
2025

Day 4 - Friday, October 24

Día 4 - Viernes 24 de octubre

Symposia & Panel Sessions

*Sesiones de
Simposios y Paneles*

Session

6796507-1

Symposium

24/10/25 | 10:45

Room: Ballroom A

Unlocking Biodiversity data Potential in Latin America: Tools and Practices of Data Integration (Part 1)

Organizers

Marius Bottin

Ricardo Segovia

Juan Manuel Saez Hidalgo

Description

Biodiversity data holds immense potential for addressing critical environmental challenges, but its true power lies in integration. Combining disparate datasets across various sources enables us to uncover complex ecological patterns, monitor species distributions, and inform conservation strategies. Networking among specialists developing biodiversity data integration strategies is therefore essential to harness regionally diverse ecosystems through common and innovative data management approaches.

This session invites Latin American researchers, data managers, and developers to showcase their work on biodiversity data integration, facilitating the sharing of experiences and advancements for establishing concrete regional collaboration agendas. We aim to foster a dynamic exchange of perspectives on current approaches, best practices, open-source application development, and remaining challenges. Presentations are encouraged to address:

- Developments of open source tools applications and tools for the integration of data, which facilitate data sharing and interoperability
- Dataflows using existing tools to integrate or promote the use of large datasets
- Research studies using various data types or various datasets

Session: 6796507-1**6999627****24/10/25** | 10:50**Room:** Ballroom A**ORAL • ES**

Portales Symbiota para la Integración de Información de Biodiversidad en Latinoamérica

Presenter

K. Samanta Orellana

Authors

K. Samanta Orellana (University of Kansas • United States)**Edward Gilbert** (University of Kansas • United States)**Katelin Pearson** (University of Kansas • United States)**Gregory Post** (University of Kansas • United States)**Mark Fisher** (University of Kansas • United States)**Nico Franz** (University of Kansas • United States)

Abstract

Symbiota es un software de código abierto para el manejo y movilización de datos de biodiversidad. Los portales Symbiota (<https://symbiota.org/symbiota-portals/>), generalmente con enfoque taxonómico o regional, son utilizados por más de 1,200 colecciones de historia natural para digitalizar y manejar sus datos, incluyendo elementos del espécimen extendido. Los portales Symbiota también pueden incorporar datos de colecciones y proyectos externos, expandiendo la disponibilidad de información para las comunidades de usuarios. La integración de datos y las herramientas especializadas disponibles en portales Symbiota, también permiten la generación de recursos interactivos para agilizar la documentación e investigación de la biodiversidad (p.e. listados de especies y claves taxonómicas). Además, al seguir estándares (p.e. Darwin Core, Audiovisual Core) y principios (p.e. FAIR) internacionales, las colecciones digitalizadas en Symbiota pueden ser movilizadas directamente a agregadores regionales y globales (p.e. iDigBio, GBIF), incrementando el alcance de los datos. La mayoría de portales Symbiota han sido financiados por proyectos en Estados Unidos y son mantenidos por comunidades de ese país en conjunto con el equipo Symbiota de iDigBio, en la Universidad de Kansas. Sin embargo, el fácil acceso a portales existentes ha motivado su uso por colecciones alrededor del mundo. Traducciones al español de portales y documentación relevantes, han sido especialmente beneficiosas para incrementar la participación de usuarios de Latinoamérica. Portales como Flora Neotropical (<https://serv.biokic.asu.edu/neotrop/plantae/>), la Red de Herbarios Mexicanos (<https://herbanwmex.net>), y el portal de Biodiversidad de Guatemala (<https://biodiversidad.gt>) son utilizados activamente por colecciones latinoamericanas, contribuyendo con más de 500,000 especímenes digitalizados. Perspectivas acerca del uso de portales Symbiota en Latinoamérica, así como su potencial para la integración de información de biodiversidad, serán compartidos durante la presentación.

Session: 6796507-1**7020629**

24/10/25 | 11:02

Room: Ballroom A

ORAL • EN

Integrating Colombian Biodiversity Data: Information Systems, Platforms and Projects in the Humboldt Institute

Presenter

Marius Bottin

Authors

Marius Bottin (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Maria Helena Olaya Rodríguez** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Lina María Sánchez Clavijo** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Erika Suarez Valencia** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Johan Manuel Calderón** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Carolina Castro-Moreno** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)**Diego Randolph Pérez Rincón** (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)

Abstract

Over its 30 years of existence, the Alexander von Humboldt Biological Resources Research Institute has produced and compiled a great quantity of data on Colombian biodiversity, through its own research projects or in collaboration with other institutions. A strong commitment to open data and the scientific dissemination requirements from our institutional missions have led us to implement and manage various information systems and web platforms to make this data (<https://datos.humboldt.org.co/>) and related information (e.g. <https://biotablero.humboldt.org.co/>) publicly accessible. Behind these publications our goal is to provide inputs for transformative processes addressing the current biodiversity crisis and to support decision-making at different scales. This requires providing useful content for a variety of audiences, including the scientific community, public and private stakeholders. It also involves integrating different specialized systems and data sources into meaningful and precise information, which is not without challenges. Moreover, the need for a better inclusion of social, economical and cultural aspects of biodiversity has highlighted this necessity of data integration. The Scientific Information Office (GIC) is constantly reforming, enhancing and updating the institutional platforms and information systems to tackle these complex tasks. Through the presentation of our current data workflows and our projects for improvement, we will offer a comprehensive view of institutional solutions, explore current challenges and difficulties and foster a discussion on the implementation of future tools.

Session: 6796507-1**7023575**

24/10/25 | 11:15

Room: Ballroom A

ORAL VIRTUAL • EN

Digital strategies for preserving zoological collections data at the Museu Nacional|UFRJ: challenges and approaches

Presenter

Mariane Targino

Authors

Mariane Targino (Museu Nacional|UFRJ • Brazil)

Julianna Freires Barbosa (Museu Nacional|UFRJ • Brazil)

Gabriela A. Jardim (Museu Nacional|UFRJ • Brazil)

Durval Santos (Museu Nacional|UFRJ • Brazil)

Eduardo Dalcin (Instituto de Pesquisa Jardim Botânico do Rio de Janeiro • Brazil)

Cristiana Serejo (Museu Nacional|UFRJ • Brazil)

Abstract

The Museu Nacional, Brazil's oldest scientific institution, suffered a devastating fire in 2018 that destroyed much of its historic building and physical collections. Less visible, but equally critical, was the loss of associated data: catalogues, spreadsheets, and digital files that were never backed up or had been stored only locally. Many collections had data recorded in physical ledgers that were not digitised; others kept spreadsheets or files on hard drives that were also consumed by the fire. This tragedy exposed the vulnerability of decentralised data management and highlighted the urgent need for institutional-level data governance. In response, a FAPERJ-funded project (2022–2025) is enabling the migration of the museum's zoological collections into Specify 7, a web-based collections management system hosted on institutional servers with automated backup protocols. A Collection Management Policy was also approved, requiring all curatorial teams to adopt digital systems. The zoological collections are divided into three departments—Entomology (17 subcollections), Invertebrates (17), and Vertebrates (5)—comprising 39 datasets and over 640,000 records. The migration process involved: (1) mapping and comparing existing data structures across collections; (2) analysing Specify's data model and import requirements; and (3) cleaning and standardising data with collection managers. So far, all Entomology subcollections and the Cnidaria collection have been successfully migrated. This initiative represents not just a technical upgrade, but a shift towards sustainable, shared, and recoverable biodiversity data infrastructure. It also offers a cautionary tale for institutions globally: data loss is not a hypothetical risk, and preservation strategies must extend beyond physical specimens.

Session: 6796507-1

7015728

24/10/25 | 11:29

Room: Ballroom A

ORAL • ES

Gestión de colecciones con Specify: aprendizajes desde la práctica institucional

Presenter

Kevin G. Borja Acosta

Authors

Kevin G. Borja Acosta (Instituto de Investigación de Recursos Biológicos Alexander von Humboldt • Colombia)

Abstract

La gestión eficiente de datos es fundamental para el funcionamiento y la proyección científica de los museos de historia natural. En este contexto, el software Specify se ha consolidado como una herramienta robusta para la administración de colecciones biológicas, facilitando procesos clave como la catalogación, trazabilidad, análisis y generación de reportes. No obstante, su implementación también enfrenta desafíos importantes, entre ellos la necesidad de integrar datos con otros sistemas institucionales, la estandarización terminológica, y la capacitación del personal en el uso técnico de la plataforma.

Este trabajo explora los principales retos y soluciones asociados al uso de Specify en museos de historia natural, a partir de experiencias prácticas en contextos institucionales. Se destacan sus fortalezas como la personalización de campos, la gestión de registros jerárquicos y la posibilidad de mantener integridad y trazabilidad de los datos a largo plazo. Asimismo, se identifican oportunidades de mejora relacionadas con la interoperabilidad, la automatización de flujos de trabajo y el fortalecimiento de capacidades técnicas del equipo humano.

El análisis evidencia que, pese a las barreras iniciales, el uso de Specify puede contribuir significativamente a la optimización de procesos y a la visibilidad científica de las colecciones, especialmente si se acompaña de una estrategia institucional clara de gestión de datos y fortalecimiento tecnológico.

Session: 6796507-1**7019935**

24/10/25 | 11:41

Room: Ballroom A

ORAL • EN

Fewer Errors, Better Science: The Role of ECODATA in Ecological Data Management

Presenter

Clara Baringo Fonseca

Authors

Clara Baringo Fonseca (Rede Nacional de Ensino e Pesquisa • Brazil)

Karlo Gregório Guidoni Martins (SiBBr - RNP • Brazil)

Yohana Pereira Ditzel (SiBBr - RNP • Brazil)

Abstract

On November 5, 2015, the Fundão Dam, owned by Samarco Mineração S.A., suffered a catastrophic failure, releasing approximately 55 to 62 million cubic meters of mining tailings into the Doce River. The disaster caused severe impacts, as the river is a critical source of water and food for numerous communities. As part of the environmental compensation efforts, funding was allocated to support aquatic and terrestrial monitoring programs, as well as periodic assessments of the Doce River's water quality.

Within this context, the Brazilian Biodiversity Information System (SiBBr) was commissioned to coordinate the mobilization and quality control of all biodiversity and environmental data related to the recovery projects. During the partnership, the SiBBr team also contributed to the development of a data entry and quality tool featuring user access controls, aimed at facilitating data standardization, the integration of environmental variables and measurements, and the validation of both measurements and overall data quality.

The tool automatically links spreadsheets, assigns unique IDs, generates detailed inconsistency reports, and enables data publishers to correct certain errors directly on-screen. To support data quality assurance, it integrates principles and recommendations from the TDWG Data Quality Interest Group, aligning with international biodiversity data standards. The tool is now publicly available, streamlining the structured entry of ecological data and metadata, enhancing both data quality and the publisher's workflow.

This presentation aims to introduce the tool, highlighting how it facilitates data entry and improves data quality, thereby easing the workload for data publishers and mobilizing more biodiversity data. Such improvements are crucial to support informed decision-making for the conservation and management of natural resources.

Session: 6796507-1

7020930

24/10/25 | 11:55

Room: Ballroom A

ORAL • EN

Rasgos-CL: enhancing plant trait completeness in a data-poor region

Presenter

Dylan Craven

Authors

Dylan Craven (Universidad Mayor • Chile)

Elias Encina Alfaro (Universidad Mayor • Chile)

Laura Renderos (Universidad Mayor • Chile)

Abstract

Research purpose: Global initiatives to compile trait data frequently fail to integrate data from regions where English is not the primary language and due to a lack of connections with local professional networks. Using Rasgos-CL (<https://rasgos.cl/>), a database of trait data for the woody flora of Chile, we illustrate the potential for regional databases to fill gaps in trait data.

Methods: We compiled trait information by searching published literature in Spanish and English and requesting data from national research institutes for 716 native woody species that occur in continental Chile. The 24 traits in the database capture key plant morphological, physiological, and reproductive characteristics. We then compared trait coverage in Rasgos-CL to global plant trait databases, and examined geographical biases in missing trait values.

Results: Overall, we mobilized 26,081 trait records for 716 native woody species. Rasgos-CL has 647 species with data for at least five traits. Trait completeness, i.e., the percentage of species with trait data, exceeded 80% for fruit type, mycorrhizal type, leaf habit, leaf organization, and maximum plant height. Trait completeness was lower for traits associated with reproduction than other trait groups. We found a limited number of trait records in global plant trait databases for species in Rasgos-CL. By combining data from global databases with that of Rasgos-CL, we significantly increased trait completeness for five traits, from ~ 1-25% to ~ 14 - 92%. We identified a consistent geographical bias in trait completeness for individual traits and trait groups, with trait completeness being higher in central and southern Chile than in northern Chile. This geographical bias was even stronger for traits with lower overall trait completeness, such as pollination syndromes.

Conclusions: With Rasgos-CL, we show that a regional-based approach to building a trait database addresses key barriers that contribute to persistent gaps in biodiversity data.

Session: 6796507-1**7015899**

24/10/25 | 12:07

Room: Ballroom A

ORAL • EN

Assessing Species Habitat Changes Using the Species Habitat Index: A Case Study in Colombia's Tropical Dry Forest

Presenter

Maria Isabel Arce Plata

Authors

Maria Isabel Arce Plata (Université de Montréal • Colombia)

Abstract

We assessed the Species Habitat Index (SHI) for 755 plant, bird, and mammal species inhabiting the tropical dry forest (TDF) in Colombia. The SHI, proposed as a component indicator in the monitoring framework of the Kunming-Montreal Global Biodiversity Framework (KM-GBF), supports the assessment of Goal A by quantifying changes in habitat extent and connectivity relative to a baseline. To compute the index, we integrated species habitat preferences and range maps from the International Union for Conservation of Nature (IUCN), species distribution models from BioModelos, and the human footprint both data produced by the Alexander von Humboldt Institute in Colombia, and land cover maps from the Institute of Hydrology, Meteorology and Environmental Studies (IDEAM). We focused on the TDF, a critically endangered ecosystem that has been reduced to around 2% of its original extent. Our analysis reveals that Colombia's TDF lost nearly one-third of its forest cover since 1990, with only modest gains observed between 2010 and 2018. Most of the loss was due to conversion to pastures. We used two approaches to assess connectivity, GISFrag and Omniscape. Overall, we found a decline of approximately 20% in both habitat extent and connectivity between 2000 and 2020, leaving only ~800,000 ha of remaining habitat, where only 13% lies within some figure of protected area. However, over 1 million hectares of successional forest within the potential TDF range offer significant opportunities for ecological restoration. To facilitate broader use, we published the workflow for the SHI assessment using global data through the BON in a Box platform, developed by the Group on Earth Observations Biodiversity Observation Network (GEO BON).

Session: 6796507-1**7020926**

24/10/25 | 12:20

Room: Ballroom A

LIGHTNING TALK • ES

FREDPlanet: Integración de Datos Forestales mediante Gamificación, IoT y Ciencia Ciudadana en Latinoamérica

Presenter

Jenny Rodriguez Garcia

Authors

Jenny Rodriguez Garcia (Corporación Red Forestal • Colombia)

Abstract

FREDPlanet representa una innovadora y patentada plataforma de integración de datos forestales que combina ciencia ciudadana, gamificación y tecnología IoT para generar el primer catálogo vivo de diversidad arbórea de Latinoamérica y del mundo. Esta red forestal digital integra múltiples flujos de datos para crear productos científicos que conectan observaciones de campo con necesidades de investigación y política forestal.

La plataforma integra tres componentes principales de datos: (1) avistamientos forestales georeferenciados capturados por usuarios a través de una aplicación gamificada, incluyendo registros fenológicos detallados de flores y frutos; (2) datos ambientales en tiempo real generados por dispositivos IoT conectados directamente a árboles, midiendo cuatro variables clave; y (3) metadatos de usuarios certificados que garantizan la calidad de las observaciones.

El geovisor (redforestal.com/es/fredplanet) permite la visualización y descarga de datos geoespaciales, mientras que el gestor de información IoT (fredplanet.com) procesa datos de sensores arbóreos. La gamificación incentiva la participación ciudadana mediante rankings mundiales de avistadores y certificaciones profesionales, creando una comunidad activa de observadores forestales.

Esta integración tecnológica genera productos únicos: un catálogo dinámico de especies arbóreas con registros fenológicos inéditos, mapas de distribución actualizados continuamente, y datos ambientales de alta resolución temporal. Los usuarios técnicos pueden acceder a datasets certificados, mientras que investigadores y tomadores de decisiones obtienen información actualizada sobre biodiversidad forestal.

FREDPlanet demuestra cómo la integración de datos heterogéneos (ciudadanos, IoT, geoespaciales) puede crear productos científicos valiosos que acortan la brecha entre observaciones de campo, investigación académica y políticas de conservación. La plataforma establece un nuevo paradigma para el monitoreo forestal participativo en Latinoamérica, combinando innovación tecnológica con engagement ciudadano para generar conocimiento científico de alta calidad.

Session: 6796507-1**7016823**

24/10/25 | 12:28

Room: Ballroom A

LIGHTNING TALK VIRTUAL • EN

Taxonomy OWLizer: A Web Tool for Converting Taxonomic Data into OWL Ontologies

Presenter

Filipi Miranda Soares

Authors

Filipi Miranda Soares (University of Sao Paulo • Brazil)

Luís Ferreira Pires (University of Twente • Netherlands)

Debora Pignatari Drucker (University of Twente • Brazil)

Luiz Olavo Bonino da Silva Santos (Embrapa Agricultura Digital • Netherlands)

Fernando Elias Corrêa (University of Twente • Brazil)

Dilvan de Abreu Moreira (University of Sao Paulo • Brazil)

Kelly Rosa Braghetto (University of Sao Paulo • Brazil)

Alexandre Cláudio Botazzo Delbem (University of Sao Paulo • Brazil)

Antonio Mauro Saraiva (University of Sao Paulo • Brazil)

Abstract

The growing demand for high-quality, interoperable biodiversity data exposes the current challenges of standardizing taxonomic information across platforms. While the GBIF Backbone Taxonomy (GBIF-BT) offers a valuable reference for species names, translating this information into formal ontology structures for semantic integration remains a complex task. A key challenge lies in the dynamic nature of taxonomic knowledge: as GBIF-BT is continuously updated, ontologies built manually from its data risk becoming outdated or misaligned. Without automated mechanisms for synchronizing with these updates, such ontologies may fail to reflect current taxonomic consensus, limiting their interoperability and long-term utility in biodiversity informatics.

To address this problem, we developed the Taxonomy OWLizer, a lightweight web application that allows users to convert species names into OWL ontologies based on taxonomic data retrieved directly from the GBIF-BT API. Users input one or multiple scientific names, and the application fetches, organizes, and outputs a structured OWL file, facilitating taxonomic integration into semantic web projects. OWLizer automates synonym handling and taxonomic hierarchy generation, and reuses GBIF URIs in the code, following the Linked Data principles. It aims to lower the technical barriers for researchers working in biodiversity informatics who need machine-actionable taxonomies but may lack programming expertise.

The Taxonomy OWLizer was implemented using HTML, JavaScript, Bootstrap, and a Flask backend, with support from ChatGPT for code drafting and debugging. This AI-assisted development approach accelerated prototyping and helped streamline the implementation process.

The Taxonomy OWLizer is available at <https://filipi-soares.github.io/TaxonOWLConverter/>, with the backend hosted on GitHub. It was described in detail in Soares et al. (2025), and a backup is maintained on Zenodo (Soares, 2025). OWLizer is a prototype developed using free-tier services, and as such, it may experience performance or availability limitations. Despite these constraints, it provides a useful starting point for automating taxonomic ontological modeling.

Session

6798998-1

Symposium

24/10/25 | 10:45

Room: Ballroom B1

Sampling with intention: optimizing strategies for monitoring biodiversity (Part 1)

Organizers

Laura Pollock

Katherine Hebert

David Rolnick

Tanya Berger-Wolf

Description

Biodiversity is changing, but the nature and cause of these changes remains an open question for the majority of taxa on the planet. Knowing how biodiversity is changing, how species are responding to threats, and how we monitor requires data. The core of the Global Biodiversity Framework is a monitoring framework that converts a variety of datastreams into indicators of progress towards biodiversity targets. The ideal version of this—intentionally designed, well-funded structured surveys and frequent optimised monitoring—is rarely possible. But the vast streams of incoming data from satellites, UAVs, camera traps, acoustic records, eDNA, telemetry, and community science are already building a dynamic evidence base. The question is how to make these datastreams maximally effective to capture biodiversity and its changes. In this session, we will bring together scientists and conservation practitioners to showcase the cutting-edge science on AI and adaptive sample optimization, examples of successful approaches in management and practice, and perspectives on how to incentivise users to collect biodiversity data where we need it most. We will mix theory and practice to highlight actionable ways to build effective biodiversity data streams in different ecosystems, to ensure we are well-equipped to bend the curve of biodiversity loss.

Session: 6798998-1**7020096****24/10/25** | 10:45**Room:** Ballroom B1**ORAL • EN**

Reimagining biodiversity monitoring: Integrating diverse data streams to fill global shortfalls

Presenter

Isaac Eckert

Authors

Isaac Eckert (McGill University • Canada)**Laura J. Pollock** (McGill University • Canada)

Abstract

Rapid increases in data collection have ushered in an era of unprecedented data availability. However, large data gaps persist, hindering our ability to monitor ongoing biodiversity change. Moving forward we need to develop a monitoring framework that integrates data from diverse data streams to provide the evidence needed by practitioners to make informed policy decisions. Luckily, advances in artificial intelligence (AI) have unlocked novel ways of collecting, analyzing, and interpreting biodiversity data – potentially supercharging our ability to achieve a seamless monitoring framework. Here, I address remaining biodiversity data shortfalls and discuss how different streams of biodiversity can be leveraged alongside novel AI powered tools to fill persistent gaps. Specifically, I focus on how the rise of community science and recent renewed increase in natural history collections is benefiting the field of biodiversity science and discuss how these largely disparate data streams complement one another in their ability to capture Earth's biodiversity. I show that, accompanying rapid increases in data availability, AI is allowing researchers to quickly glean and extract complex ecological information and patterns from the now overwhelming amount of available biodiversity data. Looking ahead, designing new ways of combining diverse data streams and harnessing the power of AI to generate meaningful ecological information could transform our understanding of the natural world and our ability to protect it.

Session: 6798998-1**7003623**

24/10/25 | 10:55

Room: Ballroom B1

ORAL • EN

Global gaps in plant biodiversity data and their implications for conservation and modelling

Presenter

Brian Maitner

Authors

Brian Maitner (University of South Florida • United States)

Rachael Gallagher (Macquarie University • Australia)

Jens-Christian Svenning (Aarhus University • Denmark)

Melanie Tietje (Aarhus University • Denmark)

Elizabeth Wenk (UNSW Sydney • Australia)

Wolf Eiserhardt (Aarhus University • Denmark)

Abstract

There is an increasingly urgent need to understand the global distribution of biodiversity in order to understand how biodiversity is changing, how those changes will impact people, and how best to conserve it. At a minimum, this requires geographic information about species (e.g., occurrence records). However, if we wish to go further and focus on aspects of biodiversity that are more strongly tied to ecosystem functioning and nature's contributions to people, we need additional data, particularly phylogenetic data and trait data. Where this information is incomplete, it may lead to erroneous conclusions. Thus, we need to understand spatial completeness of data, drivers of geographic biases, and identify solutions for filling gaps.

To address this need, we assessed geographic, phylogenetic, and trait data availability relative to a comprehensive set of regional species checklists for vascular plants. We focus on plants, as they represent the overwhelming majority of biomass on Earth and are the primary drivers of terrestrial ecosystem functioning and nature's contributions to people. We compared the Raunkiærian (trait) shortfall with the Wallacean (distributional) and the Darwinian (phylogenetic) shortfalls and tested whether data completeness correlates with emerging anthropogenic changes. We found that trait completeness is associated with socioeconomic and biological factors influencing sampling likelihood: completeness was positively associated with mean species range size, research expenditure, and human population density and negatively associated with endemism and richness. Trait completeness was significantly correlated with climate change, human footprint, and phylogenetic completeness, but was not significantly correlated with biodiversity intactness or distributional completeness. Integration of a second, regional trait database (AusTraits) more than doubled completeness in Australia, indicating that the creation and integration of regional databases can rapidly expand trait completeness.

Session: 6798998-1**7014706**

24/10/25 | 11:05

Room: Ballroom B1**LIGHTNING TALK • EN**

Where to explore? Identifying distribution gaps on range-restricted birds in the Northern Tropical Andes

Presenter

Wilderson Medina

Authors**Wilderson Medina** (Tropical Mountains Research Foundation • Colombia)**Stuart Pimm** (Duke University • United States)**Natalia Ocampo-Peñuela** (University of California • United States)**Ryan Huang** (University of Pretoria • United States)**Abstract**

The lack of reliable data and human-induced threats are the main drivers of the current biodiversity data crisis. Further knowledge of species distribution gaps in megadiverse and high-endemism regions is critical to developing accurate monitoring assessments. Here, we provide insights on where to precisely allocate additional sampling efforts by mapping priority exploration areas for range-restricted birds in the Northern Andes. We mapped the Area of Habitat (AOH) for 281 range-restricted forest-dependent birds to identify uncertain regions.

Each AOH is comprised of probably occupied (closer to presence points) and uncertain areas. Uncertain areas are those concentrating a high number (>25 in a 5×5 sq km) of eBird checklists where a single species has not been detected. We prioritized species with uncertain areas covering more than 50% of their distribution. Likewise, we estimated cumulative uncertainty by stacking all uncertain regions. We combined this map with a richness map (cumulative AOH) to identify priority exploration areas: high uncertainty (>0.5) and high species richness (>10 spp.). Finally, we analyzed human impact in priority exploration regions. Based on knowledge gaps within the Area of Habitat (AOH) of 281 range-restricted birds in the Northern Andes, we identified 75 priority species whose ranges require urgent exploration.

Priority exploration areas cover only 10% (74,196 sq km) of the entire exploration map and are particularly concentrated towards the Western Andes. The human impact analysis reveals the Western Andes as the region with the most influence of human activities. Despite its importance, many birders continue accessing the same spots. Birders, who are not always scientifically driven, usually target unique yet accessible species, leaving little room for research and monitoring. Our findings suggest that the chances of discovering new distribution expansions or retractions increase when further and adequately planned sampling efforts across priority areas and on priority species are carefully considered.

Session: 6798998-1**7020739**

24/10/25 | 11:10

Room: Ballroom B1

LIGHTNING TALK • EN

Developing monitoring strategies for aquatic fungal biodiversity

Presenter

Andreas Bruder

Authors**Andreas Bruder** (Institute of Microbiology, University of Applied Sciences and Arts of Southern Switzerland (SUPSI) • Switzerland)**Isabel Fernandes** (Institute of Microbiology, University of Applied Sciences and Arts of Southern Switzerland (SUPSI) • Switzerland)**Abstract**

The biodiversity of aquatic fungi is still largely unknown, including the taxonomy and biogeography of species and their sensitivity to environmental changes. Despite increasing recognition of the importance of aquatic fungi for ecosystems and societies, they are largely overlooked in biodiversity monitoring programs, unlike other key aquatic organism groups, such as fish and invertebrates. These gaps in knowledge and policy impede effective management and conservation of aquatic fungi and the crucial ecosystem processes and services they provide. Through MOSTFUN, a Biodiversa+ project, we aim to develop the conceptual steps and experience needed to include aquatic fungi in routine biodiversity monitoring programs. We leverage and add value to existing biodiversity monitoring programs and networks designed for other organism groups by reanalyzing their data, or samples either from publicly available archives or previous sampling efforts. Additionally, we are evaluating the procedures and experiences of existing biodiversity monitoring programs to determine how aquatic fungal biodiversity could be added to them. This approach is possible thanks to increasingly efficient, and accessible molecular tools and public databases that contain rapidly growing volumes of molecular data of different types. While the project develops and focuses on examples on the European scale, we will generate scalable knowledge and recommendations, potentially transferable to other regions. This knowledge transfer is ensured through close collaboration with relevant stakeholder groups and will be developed into a Knowledge-to-Action Hub for aquatic fungi. This will also allow for collaboration with other ongoing initiatives on the conservation of aquatic fungi and ensure the continuation of our efforts after the project's lifetime.

Session: 6798998-1

7014558

24/10/25 | 11:15

Room: Ballroom B1

LIGHTNING TALK • ES

Gestión de datos de monitoreo e investigación en Parques Nacionales Naturales de Colombia

Presenter

Elizabeth Cristina Sánchez Toro

Authors

Elizabeth Cristina Sánchez Toro (Parques Nacionales Naturales de Colombia • Colombia)

Betsy Viviana Rodríguez Cabeza (Parques Nacionales Naturales de Colombia • Colombia)

Marta Cecilia Díaz Leguizamón (Parques Nacionales Naturales de Colombia • Colombia)

Jorge Parra (WCS • Colombia)

Manuel Rodríguez (WCS • Colombia)

Lina María Caro (WCS • Colombia)

Abstract

Un aspecto relevante para la toma informada de decisiones en las áreas protegidas de Parques Nacionales Naturales de Colombia (PNNC), es el monitoreo y la investigación, a través del monitoreo entendemos las dinámicas e impactos sobre los objetos de conservación, las presiones y los servicios ecosistémicos en respuesta a las decisiones de manejo priorizadas en el instrumento de planeación de cada área protegida, y a través de la investigación se abordan los vacíos de conocimiento de la biodiversidad, cultura y servicios ecosistémicos inmersos en las áreas protegidas y territorios colindantes. Lo anterior como insumo clave para evaluar el cumplimiento de los objetivos de conservación. Retomando los aprendizajes institucionales, se avanzó en el fortalecimiento de la planificación del monitoreo y la investigación; así como en el diseño e implementación del flujo de datos resultantes de su implementación, el cual presenta pautas para el registro de datos y validaciones técnicas que garantizan su calidad para su uso dentro y fuera de la Entidad. El proceso, presenta un componente tecnológico que le apunta a la consolidación de un sistema de información de monitoreo e investigación, que conjuga herramientas libres como SMART (Spatial monitoring and reporting tool) para la captura, espacialización, almacenamiento y reporte de la información; y licenciadas como ArcGis Online que funciona como herramienta de visualización y publicación de los datos y resultados. Este avance de PNNC y WCS ha significado grandes esfuerzos de capacitación para el uso de herramientas tecnológicas, adquisición de equipos y la estructuración y generación de modelos de datos que permiten el flujo e interoperabilidad con otras herramientas. En el contexto del manejo de áreas protegidas esta iniciativa facilita la disposición y uso de la información para evaluar y mejorar la efectividad de manejo, así como el uso y apropiación por aliados estratégicos y el público en general.

Session: 6798998-1**7009675**

24/10/25 | 11:20

Room: Ballroom B1**ORAL • EN**

An adaptive sampling framework for targeted biodiversity monitoring in participatory citizen science

Presenter

Corey Callaghan

Authors

Corey Callaghan (University of Florida • United States)

Abstract

With ongoing biodiversity declines, the demand for spatially explicit biodiversity data has outpaced the capacity of professional monitoring networks. Participatory citizen science has emerged as a powerful complementary approach, but data quality and utility are often limited by unstructured sampling. In this talk, I present a framework for *adaptive sampling* in participatory science, an approach where the value of a new observation is informed by existing data and specific ecological or conservation objectives. Drawing on case studies ranging from theoretical explorations to empirical demonstration, I show how adaptive sampling can enhance biodiversity monitoring by promoting data collection at times and locations where new observations are expected to be most informative. Together, these case studies illustrate the potential for adaptive sampling to guide participatory biodiversity monitoring efforts toward greater scientific impact. I conclude by discussing future directions and practical considerations for implementing adaptive sampling protocols, including infrastructure, participant engagement, and integration with conservation decision-making.

Session: 6798998-1**7019990**

24/10/25 | 11:30

Room: Ballroom B1

ORAL • EN

Co-creating a tool to incentivize data collection in high priority areas for monitoring bird populations

Presenter

Lauren Oldham

Authors

Lauren Oldham (Cornell Lab of Ornithology • United States)

Abstract

Monitoring biodiversity through structured surveys is often challenging due to financial and logistical constraints, but participatory science data can fill monitoring gaps by providing cost-effective data collection. Cornell Lab of Ornithology utilizes participatory science data to develop its data products of global, high resolution ranges and abundances for 2900 bird species. These products combine eBird user- submitted checklists, which provide counts of birds at specific locations and dates, with remotely-sensed environmental data to generate standardized ecological information, even in areas that don't have eBird checklist contributions. While previous external validation efforts have shown these products to be reliable, many areas would benefit from having more eBird checklist data to improve the accuracy of the data products.

To visualize and understand areas with unique habitat configurations lacking data, we created a series of modeled data products describing areas that would benefit the most from additional eBird contributions. However, data products rarely stand alone, and effort is needed to describe, display, and provide guidance for how to incentivize birders and partner organizations to contribute data from these undersampled locations. To address this challenge, we have collaborated with regional bird conservation coalitions, which include local and federal representatives, to develop a web application to help strategically direct sampling activities to undersampled regions and submit eBird checklists from high priority areas.

In this presentation, we will describe the process of developing this application with partner organizations, examining the friction of different goals for different audiences. We will also discuss how user feedback sessions with both internal outreach teams and partners influenced changes in the data representation, how the final product may be used to incentivize users to collect bird data in the highest priority areas, and offer lessons learned about the process that could be applied for the purposes of guiding biodiversity data sampling.

Session: 6798998-1**7020782**

24/10/25 | 11:40

Room: Ballroom B1

ORAL • EN

New approaches for data deficient species on iNaturalist

Presenter

Carrie Seltzer

Authors

Carrie Seltzer (iNaturalist • United States)

Scott Loarie (iNaturalist • United States)

Abstract

Of the world's ~2 million described species, iNaturalist has at least one observation for about 500,000 unique taxa. Over 100,000 of those species have enough data points to begin modeling their geographic ranges. The resulting maps are available under the iNaturalist Open Range Maps dataset. However, 400,000 species are "data deficient" on iNaturalist with fewer than 100 observations (but at least one).

The ability on iNaturalist to separate the act of observing from the expertise of identifying through the community identification process has allowed for much broader participation in biodiversity recording. In 2025, we are piloting new functionality on iNaturalist to draw attention to these data deficient species and fill the gaps for both observing and identifying them. The functionality will target both people who may be able to observe data deficient species and people who may be able to identify them, since these can be different people. Identifiers are iNaturalist community members who have provided identifications to observation of these data deficient species in the past. The feature will surface observations with tentative IDs of these species that require additional review. Observers are iNaturalist community members who have recently made observations at the same season and place as existing observations of data deficient species. They will see these observations as examples of species at specific seasons and places where they can potentially create new observations of these species. Both groups will see new panels on their dashboard when logged into the iNaturalist website.

This presentation will share the preliminary results of this new functionality, including how many formerly data deficient species were able to move out of that category. We'll also explore its potential in other parts of the world beyond Canada.

Session: 6798998-1**7006148**

24/10/25 | 11:50

Room: Ballroom B1

ORAL • EN

Blitz the Gap: guiding citizen science toward specific research and conservation needs

Presenter

Laura Pollock

Authors

Laura Pollock (McGill University • Canada)

Katherine Hebert (Canada)

Diane Srivastava (University of British Columbia • Canada)

Abstract

Tracking the state of nature is impossible without good data. We lack detailed data at a relevant scale to track biodiversity change by 2030 for most taxa in most areas of the world. We can't solve this without citizen science—a growing data-collecting force untethered from constraints of structured monitoring programs. But, we also can't solve this with citizen science data as-is.

In this talk, we introduce the Blitz the Gap initiative to rapidly fill critical data gaps in Canada using iNaturalist. Canada hosts a substantial portion of the world's intact ecosystems, but is also experiencing rapid climate change and lacks data in the places where we need it most. Blitz the Gap is a series of sampling 'challenges' and bioblitzes that address a breadth of science needs including: better representation of target species (at-risk, endemic, invasive), under-represented taxon groups, under-sampled regions, key habitats, stressors (climate change impacts), and linking community science with conservation applications (designation of Key Biodiversity Areas) and educational outreach (libraries in under-sampled regions). Challenges were designed and built for iNaturalist users by scientists, conservationists, avid naturalists, and avid coders in working groups across Canada from the Living Data Project.

We discuss results from our first summer of sampling, lessons learned, and future directions. In particular, we found: 1) existing adaptive sampling algorithms are too narrow and not practical without realistic constraints, 2) communication of the challenges is as important as creating them in the first place, 3) data gaps are huge, but filling them is feasible even in sparsely populated areas, and 4) we lack a platform to design such challenges. We believe this work can be a starting point for re-thinking the field of adaptive sampling, catalyzing research on more realistic algorithms and a dedicated platform, and more seamlessly integrating citizen science and biodiversity science.

Session: 6798998-1**7019743****24/10/25** | 12:00**Room:** Ballroom B1**ORAL • EN**

Integrating long-term and intra-annual data for better understanding of biodiversity change through time

Presenter

Marta Jarzyna

Authors

Marta Jarzyna (The Ohio State University • United States)

Abstract

Understanding long-term biodiversity trends is crucial for assessing the impacts of biodiversity change on ecosystems and human well-being, as well as for forecasting future dynamics. However, reliably capturing these trends requires more than annual snapshots—it demands high-resolution, intra-annual (seasonal) data to capture the full complexity and variability of biodiversity. Single annual snapshots often miss critical seasonal events, such as migration or breeding, which are experiencing significant temporal shifts and are crucial for interpreting long-term changes. Despite the importance of this finer temporal resolution, regions with both long-term and seasonal-scale monitoring remain exceedingly rare. Using birds as a focal example, I illustrate why integrating long-term and intra-annual data is essential for understanding biodiversity patterns across time. I then highlight the global gaps in such data and propose potential methodological frameworks to address these deficiencies—bridging spatial and temporal gaps to enhance our ability to track and predict biodiversity change.

Session: 6798998-1**7013624**

24/10/25 | 12:10

Room: Ballroom B1

ORAL • EN

Continental-scale mammal monitoring enabled by integrating camera trap networks and citizen science

Presenter

Roland Kays

Authors

Roland Kays (NC Museum of Natural Sciences & NC State University • United States)**Benjamin Golstein** (NC State University • United States)**Alex Jensen** (NC Museum of Natural Sciences • United States)**Michael Cove** (NC Museum of Natural Sciences • United States)**Brigit Rooney** (Smithsonian Conservation Biology Institute • United States)**Fabiola Iannarilli** (Max Planck Institute for Animal Behavior • Germany)**Leticia Moretto** (São Paulo State University (UNESP),, Brazil • Brazil)**Rita Bianchi** (São Paulo State University (UNESP),, Brazil • Brazil)**Eduardo Silva-Rodríguez** (Universidad Austral de Chile • Chile)**Keita Fukasawa** (National Institute for Environmental Studies • Japan)

Abstract

Monitoring populations of wild animals is a critical conservation need but collecting robust, standardized data at appropriate scales is challenging. Here we describe how we combine structured camera trap data with unstructured citizen science observations to model the abundance of mammals at large scales. First, we are scaling up the use of camera traps through the Snapshot megacollaboration model that brings together the efforts of hundreds of professional camera trappers each year. The data management and computer vision tools of Wildlife Insights have been critical for organizing and cataloging these large datasets from distributed field teams. We have used this approach for annual surveys of the United States since 2019, recording >1M wildlife records from >12K locations. This collaborative model has also now expanded to new Snapshot monitoring networks in Europe, Japan, Brazil and Chile. We complement these camera data with citizen science observations from iNaturalist. With over 5 million observations of non-domesticated mammals, the size of this photo- vouchered collection has nearly surpassed the world's natural history mammal collections, and continues to grow at 18% per year, with over 1 million mammal observations in 2024. However, caution is needed since some species are difficult to identify in a photograph. We aggregate these observations in 50km grid cells, use the total number of mammal observations as a measure of effort, and combine them with the camera trap data via an integrated abundance model for 36 North American species. We find a strong agreement between the two datasets, with support for joint analysis for 92% of species models. These models allow us to map species abundance over continental scales and reveal environmental associations that can include nonstationary effects. Future work should continue to expand camera sampling, improve the quality of iNaturalist records, and use this approach to monitor population trends for mammals.

Session: 6798998-1**7014330**

24/10/25 | 12:20

Room: Ballroom B1

ORAL • EN

Isolating and integrating multiple data streams within heterogeneous monitoring data

Presenter

Diana Bowler

Authors

Diana Bowler (UK Centre for Ecology and Hydrology • United Kingdom)**James Pearce-Higgins** (British Trust for Ornithology • United Kingdom)**Michael Pocock** (UK Centre for Ecology and Hydrology • United Kingdom)

Abstract

Data aggregators of species occurrence records, such as GBIF, have revolutionized biodiversity research, enabling analyses at spatial and temporal scales that were formerly not possible. One of the challenges with these data sets is that they are heterogeneous – comprising diverse data streams collected in different ways. Currently, in most ecological analyses, these data are pooled together, ignoring their inherent variability and focusing on the simplest information provided by all. However, better documentation of metadata associated with each species observation offers the potential to isolate different monitoring data streams that were collected in different ways (e.g., complete checklists and abundance data) and make full use of their respective information contents. Here, we use dragonfly species occurrence records from GBIF to assess the value of isolating and integrating multiple data streams for different ecological questions. We describe trends in the metadata typically reported with dragonfly observations that highlight changes in collection and reporting practices. We then show the findings from a series of ecological models that vary in integration approaches for understanding spatio-temporal trends in species distributions. We conclude with suggestions on how metadata documentation could help progress towards semi-structured monitoring for insects, improving data quality and information value, and filling urgent knowledge gaps about insect trends.

Session: 6798998-1**7020504****24/10/25** | 12:30**Room:** Ballroom B1**ORAL • EN**

Opportunities for AI to Help Guide Sampling

Presenter

David Rolnick

Authors

David Rolnick (McGill University • Canada)

Abstract

Machine learning and AI techniques are increasingly used in biodiversity monitoring for applications such as identification of species from sensor data. In this talk, we will consider how AI tools can also be used in ways that guide strategies for sampling and data collection.

Uncertainty quantification techniques can inform where new observations have the most value. Systems for flagging potentially novel species can provide insights on priority taxa for study. And sampling protocols can also be designed with downstream AI use cases in mind

- e.g. the collection of datapoints that maximally improve the performance of identification algorithms. We will discuss the potential of such AI-integrated monitoring methods, and what challenges may arise as they are further developed.

Session

6799115

Symposium

24/10/25 | 10:45

Room: Ballroom B2

Invasive alien species data: state of the art, challenges and a way forward

Organizers

Lien Reyserhove

Quentin Groom

Andrew Rodrigues

Description

Invasive alien species (IAS) pose a significant threat to biodiversity. Efforts to observe and manage IAS have expanded significantly. Understanding where they occur, how they spread, and how best to manage them requires high-quality, accessible, and interoperable data. The number of IAS records and papers using GBIF-mediated data for biological invasion research is increasing every year. However, challenges remain in terms of data accessibility, standards and use. To help address these issues, two new task groups were launched in 2024:

- GBIF's IAS Task Group, focused on mobilizing and improving biodiversity data for IAS research and policy.
- TDWG's IAS Task Group, working to enhance the standardized exchange of IAS data.

In this session, we will explore ways to improve data accessibility, standards and use to support IAS research and management. We welcome contributions on:

- the mobilization and sharing of IAS data following FAIR principles, including data standards for monitoring and managing IAS
- case studies on using GBIF-mediated IAS data for research and policy
- identifying and addressing key knowledge gaps in IAS data
- and many more

If you are working with IAS data, whether as a researcher, practitioner, or policymaker, we encourage you to participate!

Session: 6799115**7020786**

24/10/25 | 10:45

Room: Ballroom B2**ORAL • EN**

Improving data interoperability for invasive alien species: progress from the TDWG task group

Presenter

Lien Reyserhove

Authors

Lien Reyserhove (Research Institute for Nature and Forest (INBO) • Belgium)

Abstract

Data interoperability is a persistent challenge in biodiversity informatics, limiting our ability to share existing knowledge. This challenge equally applies to the field of invasion biology, where the absence of standardized terms, vocabularies and clear definitions limits the sharing and aggregation of data. These data range from field observations, impact assessments, the recording of management actions, species lists and more. Given the transboundary nature of biological invasions, sharing such information is paramount for a proper understanding and management of invasive alien species (IAS). To address these issues, a new TDWG task group kicked-off in 2024. Its objective is to further improve the Darwin Core standard to better support the exchange of IAS-related information. One of the first tasks of the task group was to develop a series of use cases that capture real-world scenarios across research, management, and policy domains. These use cases are the foundation of the group's work. They were used as a starting point for an online interactive workshop held in September to identify the existing limitations (gap analysis) of the Darwin Core standard with respect to invasive alien species.

This presentation will offer a comprehensive update on the Task Group's activities, focusing on the entire process from the initial collection of use cases to the results of the gap analysis. The ultimate goal of this presentation is to start a dialogue on the group's methodology and to establish a clear foundation for the next stages of the work.

Session: 6799115**7019867**

24/10/25 | 10:55

Room: Ballroom B2**ORAL • EN**

From local to continental: upscaling reproducible, open workflows for invasive species checklists

Presenter

Quentin Groom

Authors

Lien Reyserhove (Research Institute for Nature and Forest (INBO) • Belgium)**Tim Adriaens** (Research Institute for Nature and Forest (INBO) • Belgium)**Quentin Groom** (Meise Botanic Garden • Belgium)**Jakovos Demetriou** (The Cyprus Institute • Cyprus)**Piero Genovesi** (Institute for Environmental Protection and Research • Italy)**João Gonçalves** (CIBIO • Portugal)**Sanne Govaert** (Research Institute for Nature and Forest (INBO) • Belgium)**Kelly Martinou** (The Cyprus Institute • Cyprus)**Daniyar Memedemin** (Ovidius University • Romania)**Shyama Pagad** (University of Auckland • New Zealand)

Abstract

The compilation and maintenance of national species lists of introduced and invasive species (IIS) involves a wide range of tasks, including expert consultation, coordination, data aggregation and standardization. This process demands considerable time and resources. Given the highly dynamic nature of biological invasions, this often means a portion of the data may already be outdated by the time it's made public. Additionally, once published, there's no guarantee of regular updates over time. To ensure sustained and timely updates, automated workflows built on open science and FAIR principles offer a powerful solution. As an example, the Global Register for Introduced and Invasive Species - Belgium (GRIIS Belgium) was produced by integrating local checklists into a national IIS checklist using (semi)- automated, reproducible workflows.

The strength of these open source, documented workflows lies in their reproducibility and scalability. Building on the experience of GRIIS Belgium, the recently launched project OneSTOP aims to extend these automated pipelines to create national IIS checklists for Cyprus, Portugal and Romania. To foster local ownership and support from local expert communities, the project aims to empower local experts with the skills to manage and maintain these workflows. More ambitiously, it seeks to scale these workflows to compile a unified IIS checklist for Europe. Such a continent-wide list is critical for implementing measures to prevent and mitigate the impact of invasive alien species on biodiversity and ecosystem services in Europe.

This presentation will highlight the tools, data pipelines, communication approaches and training strategies that underlie the production of both national and continental IIS species lists. We will demonstrate how the OneSTOP approach builds upon and contributes to existing initiatives such as GRIIS and the European Alien Species Information Network (EASIN) by providing scalable, reproducible products, built on open science.

Session: 6799115**7020580**

24/10/25 | 11:05

Room: Ballroom B2**ORAL • EN**

DASCO: A workflow to integrate checklists and coordinate-based occurrence records to assess alien species distributions at high resolution

Presenter

Hanno Seebens

Authors

Hanno Seebens (University of Giessen • Germany)**Ekin Kaplan** (University of Vienna • Austria)

Abstract

Governments and researchers worldwide have invested much effort to gather information about alien species occurrences in certain regions. This has resulted in a distinct increase in available data of alien species occurrences worldwide. However, alien species occurrences are usually provided as regional checklists, which is too coarse to track changes of species distributions and to implement management measures. Biodiversity data platforms like GBIF and OBIS provide detailed information about species occurrences in general, but records often lack information about the invasion status of the recorded population. To close this gap, we have developed a workflow called DASCO to integrate regional checklists of alien species and site-specific occurrence records. The workflow has been tested using a comprehensive dataset of standardised regional checklists of >37.000 alien species worldwide. For each species and region, where the species is listed as being alien, occurrence records are obtained from OBIS and GBIF, which generates a dataset of >40 million records of alien populations worldwide. This information can then be used to assess the distribution of alien species at high resolution. The workflow also allows assigning occurrence information to other geographic units. For example, checklists of marine alien species, which is often available only at the national scale, can be divided by marine ecoregions. Thus, by integrating coordinate-based occurrence records and checklists, it is possible to develop checklists at sub-national scale for often over-looked geographic units such as ecoregions or habitats. The output of DASCO can provide a basis for species distribution models and to assess the status and trends of alien species at high spatial resolution. The workflow is implemented in R and in full compliance with the FAIR data principles of open science.

Session: 6799115**7020798**

24/10/25 | 11:15

Room: Ballroom B2

ORAL VIRTUAL • EN

Co-developing a unified framework for reporting invasive alien species removal projects

Presenter

Nigel Taylor

Authors

Nigel Taylor (University of Cambridge • United Kingdom)**Katie Costello** (International Union for Conservation of Nature • United Kingdom)**Tamryn Venter** (International Union for Conservation of Nature • United Kingdom)**Sam Reynolds** (University of Cambridge • United Kingdom)**Thomas Worthington** (University of Cambridge • United Kingdom)**Alec Christie** (Imperial College London • United Kingdom)**William Sutherland** (University of Cambridge • United Kingdom)**David Aldridge** (University of Cambridge • United Kingdom)**Kevin Smith** (International Union for Conservation of Nature • United Kingdom)**Ana Nunes** (International Union for Conservation of Nature • United Kingdom)

Abstract

Coordinated, effective and efficient management of invasive alien species (IAS) critically depends on access to standardised data on past and ongoing control efforts. Current data are often fragmented and difficult to find, inconsistently formatted, or remain unpublished – particularly for less successful management attempts. This severely hinders our ability to synthesise information and use evidence to design effective, and cost-effective, future management.

A centralised knowledge sharing platform on IAS removal projects would help address these problems. As a first step towards this, we have co-created a unified data framework to capture information from all such projects – whatever their target IAS, objective (e.g. eradication or containment), IAS removal method, location, spatial scale, ecological level and degree of success.

We reviewed existing frameworks, standards and databases to generate a first draft of the framework. This first iteration was refined through a series of workshops, engaging >70 participants with expertise in IAS management from >30 countries.

The framework records project details, target IAS, goals, actions taken, economic costs and benefits, monitoring, reflections on implementation, and linked resources. FAIR data principles were considered at all stages of framework design. For example, as far as possible, data are entered using preset options based on existing data standards (e.g. Darwin Core) to ensure interoperability. A key challenge in developing the framework was balancing the need to capture sufficient detail about projects to fully understand their context, without it being too onerous to complete.

Future work will include: (a) using the framework to populate a database of IAS removal projects, (b) converting the framework and database into an online platform, where users can interact with existing data and submit their own, (c) creating artificial intelligence tools to aid data extraction and entry, and (d) developing crosswalks with terminology in other platforms, to maximise interoperability.

Session: 6799115**7020620**

24/10/25 | 11:30

Room: Ballroom B2**ORAL • EN**

Mobilization of Biodiversity Data for Invasive Species Management in Romania

Presenter

Cristina Preda

Authors**Cristina Preda** (Ovidius University of Constanta • Romania)**Laurentiu Rozylowicz** (University of Bucharest • Romania)**Dan Cogalniceanu** (Ovidius University of Constanta • Romania)**Nicolae Manta** (Ministry of Environment, Water and Forests • Romania)**Daniyar Memedemin** (Ovidius University of Constanta • Romania)**Florina Stanescu** (Ovidius University of Constanta • Romania)**Marian Tudor** (Ovidius University of Constanta • Romania)**Marius Skolka** (Ovidius University of Constanta • Romania)**Abstract**

Effective management of invasive alien species (IAS) is crucial to biodiversity conservation, ecosystem health, and compliance with legislation, notably Regulation 1143/2014 in the European Union (EU). According to the latest national IAS inventory, Romania's diverse landscapes host about 800 alien species, including 22 IAS of EU concern. Presently, the distribution data for alien species comes from national and regional surveys (about 220,000 records) and peer-reviewed articles. For example, the national survey coordinated by the Ministry of Environment between 2019 and 2022 generated 210,000 geo-referenced occurrence records. Part of the data (i.e., data for plants and fish) have been published in GBIF as high-quality, accessible, and interoperable data, as supplementary information attached to research papers, rather than as independent datasets. The remaining data is openly available in a Zenodo repository (https://zenodo.org/communities/ias_romania/), but not as a structured database. A growing number of occurrence records is also available from citizen science platforms such as iNaturalist, i.e., about 17,000 records for 504 species up to May 2024.

Despite intensive surveys carried out in the last decade, most alien species distribution data from Romania are still fragmented and inconsistent, hindering invasive species management. A way forward to facilitating timely and informed management actions is the mobilization of IAS data and integration of these data streams through an existing platform such as GBIF, following the FAIR principles. Romania can benefit even more from this unique infrastructure by joining the GBIF network and establishing a national node. The data will require standardising taxonomic nomenclature, proper metadata formats, and geospatial tagging across all sources thus generating interoperable datasets. Improved data quality and accessibility would enhance early warning systems, risk assessments, management planning and policy reporting. This integrated approach would facilitate the implementation of EU Regulation 1143/2014 in Romania, support collaboration across sectors, and foster transparency and public involvement.

Session: 6799115**7020679**

24/10/25 | 11:45

Room: Ballroom B2**ORAL • EN**

Challenges of Marine Alien Species Data

Presenter

Eduardo Arlé

Authors

Eduardo Arlé (Tel Aviv University • Israel)**Jonathan Belmaker** (Tel Aviv University • Israel)**Gil Rilov** (Israel Oceanographic & Limnological Institute • Israel)**Anton Kovalev** (Israel Oceanographic & Limnological Institute • Israel)**Iris Preiss** (Israel Oceanographic & Limnological Institute • Israel)

Abstract

The availability, quality, and usability of data on invasive alien species (IAS) in marine environments remain far behind those for terrestrial systems. While data mobilisation efforts have advanced substantially on land, marine IAS data face unique and underappreciated challenges. The marine environment is inherently more complex – its three-dimensional nature requires incorporating depth in addition to latitude and longitude. Furthermore, biological processes often vary strongly with seasonality. Ocean warming and oceanic currents can drive rapid and large-scale spread of invasions, and marine systems are warming faster than terrestrial ones. These phenomena make marine distributional shifts especially pressing. Despite these challenges, marine data collection and interpretation approaches remain heavily shaped by terrestrial paradigms. This tendency leads to mismatches between data structure, ecological reality, and analytical methods. As a result, marine IAS studies are frequently limited by inadequate or inappropriately treated occurrence data. This contribution highlights the urgent need to recognise the complexity and specificities of marine environments when working with IAS data. We argue that methodological approaches must be adapted – or newly developed – specifically for marine contexts, considering the structure, resolution, and availability of occurrence records. To move forward, we propose a collaborative effort involving data collectors, data providers, modellers, and developers of analytical tools such as R packages. This joint approach is essential to develop a dedicated marine IAS data toolbox that can support accurate collation, interpretation, modelling, and application of marine records in both research and management. By drawing attention to these issues and outlining a path toward concrete, field-wide collaboration, we aim to foster discussion on how to close the marine–terrestrial data gap and enhance the FAIRness and fitness-for-use of marine IAS data.

Session: 6799115**7013319****24/10/25** | 12:00**Room:** Ballroom B2**ORAL • EN**

Modelling trends in biological invasion for policy reporting

Presenter**MELODIE MCGEOCH****Authors****MELODIE MCGEOCH** (MONASH UNIVERSITY • Australia)**Abstract**

A change in the number of invasive alien species (IAS) arriving or establishing over time is an intuitive indicator of the threat that IAS pose to biodiversity and of the success, or otherwise, of biosecurity measures. This indicator has been adopted by international policy multiple times, including the current Target 6 of the Kunming-Montreal Global Biodiversity Framework (GBF). Although intuitive as an indicator, its calculation requires careful consideration of different forms of bias, including inherent lags in the invasion process. Significant advances in data standards for IAS, data integration, open data and modelling approaches are now coming together to overcome what has been a long-standing constraint to quantifying and using invasion trends as an indicator. This is clearly exemplified by recent estimates of invasion trends across localities in the Antarctic. The challenges that remain for Target 6 of the GBF include the gap between the science and the many agencies responsible for using and reporting on the indicator, as well as the asynchronous timelines for progress across science and policy.

Session: 6799115**7019818****24/10/25** | 12:15**Room:** Ballroom B2**ORAL • EN**

Standardizing and Integrating Alien Species distribution data, a workflow and dataset for exploring alien species' biogeographic trajectories

Presenter

Manuela Gómez-Suárez

Authors

Manuela Gómez-Suárez (Justus-Liebig-University • Germany)**Philipp Laeseke** (Justus-Liebig-University • Germany)**Hanno Seebens** (Justus-Liebig-University • Germany)

Abstract

Over the past decade, significant efforts have been made to map the distribution of alien species globally to assess the status of biological invasions. Although multiple studies have compiled records and datasets of where alien species have been introduced, limited data are available for their regions of origin. However, knowledge about the origins of alien species is essential information to understand and predict biological invasions and to prepare for the future. To address this gap, we have extended an existing workflow to standardize and integrate information for alien species distributions, including characteristics related to the alien status of a species in a location (e.g. first introduction record, degree of establishment, among others), as well as their native regions, obtained from checklists and range maps. We applied the workflow to multiple sources to build SInAS, a standardized dataset that provides information on the non-native regions for ca. 36,000 alien species, and the native regions for over 18,000 of these species. It allows analyzing patterns of source regions, flows of alien species distributions and spread globally and across continents. In an initial analysis, we found that wealthy regions, like Northern America and Europe, are significant donor regions for the introduction of alien vertebrates (birds, mammals, amphibians, reptiles and fishes) and vascular plants. Remarkably, more than 80% of mammals native to Europe have been introduced elsewhere. Conversely, biodiverse regions, such as South America and Southern Asia, show a lower ratio of donated alien species relative to their species richness. By incorporating both native and alien distributions, our dataset offers a robust foundation for future research, enabling comprehensive insights into the biogeographic histories of alien species and facilitating analysis of factors driving species introductions in new environments.

Session: 6799115**7017470****24/10/25** | 12:30**Room:** Ballroom B2**ORAL • EN**

Adapting a globally-trained single-species plant identification model for multi-species detection of invasive alien plants in roadside imagery

Presenter

Hervé Goëau

Authors

Hervé Goëau (Cirad • France)

Vincent Espitalier (France)

Jean-Christophe Lombardo (France)

Christophe Botella (France)

Toke Thomas Høye (Denmark)

Mads Dyrmann (Denmark)

Pierre Bonnet (France)

Alexis Joly (France)

Abstract

Most automated species identification models are trained on close-up images of individual organisms, often contributed by citizen scientists. While effective in controlled conditions, these models face severe limitations when deployed in real-world biodiversity monitoring tasks, especially for Invasive Alien Species (IAS), which often occur in complex, cluttered environments such as roadsides. In this study, we explore how to adapt an existing large-scale plant identification model, originally trained on single-species images from platforms like Pl@ntNet, to the task of detecting multiple IAS simultaneously in high-resolution roadside imagery.

We propose and evaluate two strategies: (1) Tiling, which segments the image into overlapping tiles that are individually processed by the pretrained model, with their outputs subsequently aggregated to produce predictions at the full-image level; and (2) VaMIS, which adapts the model's transformer architecture to larger input resolutions via spatial encoding interpolation. Both methods are tested with and without fine-tuning on a dedicated IAS dataset from Denmark, covering six invasive plant taxa. Our results show that tiling without any fine-tuning achieves competitive performance (AUC > 91%), making it a practical solution when labeled training data is scarce or unavailable.

By reusing existing citizen science-trained models and extending them to realistic, high-resolution imagery, our work contributes to making the automated detection of invasive alien plants more scalable and transferable, and facilitates the integration of model outputs into interoperable biodiversity data workflows. It demonstrates a viable path for leveraging pretrained biodiversity models beyond their original scope, enabling large-scale, low-cost monitoring aligned with FAIR data principles. This contribution exemplifies how computational adaptation strategies can bridge the gap between species identification models and the heterogeneous data realities of IAS research and policy.

Session

6821915

Symposium

24/10/25 | 10:45

Room: Tolima

Business sector and biodiversity data: towards a nature-positive future

Organizers

Dairo Escobar**Ricardo Ortiz Gallego**

Description

Data is essential for biodiversity conservation, and the business sector generates a substantial amount of this data annually through environmental impact assessments and national monitoring programs. While this data has traditionally been limited to reports and inaccessible to the wider community, the landscape is evolving as more companies publish open biodiversity data through platforms like GBIF.

This symposium aims to foster scientific and technical exchange while cultivating communities of practice around the publication, access, and use of data by the business sector. Its objectives include:

- Sharing national, regional, and global experiences where businesses actively contribute to open biodiversity data mobilization.
- Showcasing the uses and applications of open biodiversity data in the corporate sector, including AI and data science applications in public policy.
- Identifying existing challenges and opportunities for leveraging data in business decision-making to manage nature-related risks and opportunities.

Session: 6821915**7020677**

24/10/25 | 10:50

Room: Tolima

ORAL • EN

The business case for investing in biodiversity data

Presenter

Fevziye Hasan

Authors

Fevziye Hasan (Museum of Evolution, Uppsala University • Sweden)

Tobias Andermann (Uppsala University • Sweden)

Jakob Nyström (Uppsala University • Sweden)

André da Silva (Sweden)

Emma Granqvist (Sweden)

Robert Goodsell (Sweden)

Fabian Roger (DNAIR • Switzerland)

Fredrik Ronquist (Sweden)

Veronika Johansson (GBIF Sweden • Sweden)

Tomas Roslin (Sweden)

Abstract

The business sector's growing awareness of its reliance on biodiversity and related financial risks has driven strong demand for nature- positive investments. A critical foundation for such investments are biodiversity data. Without these data, and the tools built from it, no actors can assess their impacts and dependencies on the ecosystems they rely on. Although the "biodiversity data gap" is becoming widely acknowledged, there is still limited knowledge of the origins of open biodiversity data, and few science-based innovative financing solutions to incentivise the private sector to invest in large-scale data collection and mobilisation.

In this talk, I will present an end-to-end framework that maps the path from raw biodiversity data to data products and business use cases, intended to establish a shared language between business and biodiversity research. I will demonstrate that specimen-based primary data form the basis of observation-based data, such as those generated by environmental DNA, computer vision and acoustic monitoring.

These, in turn, makeup the large-scale datasets hosted by platforms like the Global Biodiversity Information Facility (GBIF), which are known to deliver a strong economic return on investment for both science, society and by extension, business.

I will then argue the business case for investing in open biodiversity data, with examples from the business and finance sectors. Finally, I will showcase an innovative financing mechanism to incentivise and reward direct investment in biodiversity data, including data from untapped natural history collections and ground-truthed data generated by new technologies. I hope to conclude the talk by emphasising the significant potential of private sector interest in biodiversity data, highlighting the value of information and the role of biodiversity data certification as incentives for businesses to invest financially in data collection and mobilisation. Such investment is essential for creating better data products and accelerating solutions to the biodiversity crisis.

Session: 6821915**7020324**

24/10/25 | 11:00

Room: Tolima

ORAL VIRTUAL • EN

Unlocking Access: Findings from the Piloting of a Nature Data Public Facility

Presenter

Sean Donnelly

Authors

Sean Donnelly (Taskforce on Nature-related Financial Disclosures (TNFD) • United Kingdom)

Abstract

The Taskforce on Nature-related Financial Disclosures (TNFD) is currently piloting the Nature Data Public Facility (NDPF), a global initiative to make nature-related data more accessible, usable, and decision-ready for corporate and financial actors. In partnership with data providers and end users around the world, the NDPF is testing a set of shared metadata standards, data quality principles, and licensing models to address core frictions in the biodiversity data landscape.

This presentation will share early findings from the NDPF pilot programme, conducted throughout 2025 across Brazil, Japan, South Africa, and Australia. We will present insights on what makes biodiversity data more discoverable, trustworthy, and actionable for businesses— particularly in the context of TNFD and science-based frameworks such as the SBTN and NPI. We will highlight challenges around data licensing, sustainability, and metadata interoperability, as well as the perspectives of upstream data providers on incentives and barriers to wider data sharing.

Our session will preview some of the emerging recommendations and infrastructure options being explored in advance of the full TNFD release at COP30. We aim to engage the audience in a discussion about how public-private collaboration can unlock more equitable access to nature data while ensuring providers can sustain and scale their operations. With increasing pressure on companies to understand and disclose their nature-related impacts and dependencies, the time is right to explore shared infrastructure models that could better serve both data originators and users.

This presentation will offer a first look at whether and how a facility like the NDPF might support a more inclusive, efficient, and trustworthy nature data ecosystem—contributing to nature-positive outcomes.

Session: 6821915**7020976**

24/10/25 | 11:10

Room: Tolima

ORAL VIRTUAL • EN

Assessing the direct impacts of businesses on biodiversity

Presenter

Karel Mokany

Authors

Karel Mokany (CSIRO • Australia)

Abstract

There is a rapidly growing need for efficient but rigorous methods for businesses to regularly assess and disclose their biodiversity impacts. Here we present a habitat-based analytical approach for estimating the direct impacts of a business on biodiversity. Our broad approach considers the time series of a businesses spatial footprint, with the biodiversity position derived as the accumulated positive and negative impacts over space and time. This approach has been formalised and made available via a web-served digital tool, which we demonstrate for an organisation with 50 operational sites across Australia (>460,000 ha). Three complementary habitat-based biodiversity indicators are implemented, which all use as their basis a fine resolution annual (1987, to 2024) time series of ecosystem condition. For the case-study organisation assessed, we show how the biodiversity position has changed over time, past to present, and link these changes to historic management decisions. We also demonstrate how this biodiversity monitoring assessment can be directly linked to future-looking scenario analyses, to help businesses make decisions that improve their current biodiversity position into the future.

Session: 6821915**7020248**

24/10/25 | 11:20

Room: Tolima

ORAL • EN

Data-driven nature-based solutions: a case study to evaluate the impact of large-scale agroforestry initiatives in the coffee sector in Cauca

Presenter

Viviana Ruiz-Gutierrez

Authors

Viviana Ruiz-Gutierrez (Cornell Lab of Ornithology • United States)

Abstract

The escalating impacts of climate change are posing a growing threat to biodiversity worldwide. In response, policymakers and stakeholders have invested in nature-positive solutions, including agroforestry and reforestation, to help mitigate these threats. However, the effectiveness of current solutions are often limited as projects are frequently designed and implemented in isolation of critical outcomes for biodiversity. A key driver of this misalignment is the lack of a data-driven framework to help the private sector design, implement, and assess the impact of nature-based solutions on biodiversity.

In this presentation, we will showcase our experience working with industry leaders to develop a data-driven, cost-effective, and globally scalable framework for evaluating impacts and dependencies on nature. . More specifically, we will present how we have worked alongside Nespresso's AAA Sustainable Quality Program to develop a data driven approach to measure the state of nature called the Biodiversity Progress Index (BPI). The BPI leverages AI technology with local knowledge found in Cornell's eBird project, which has amassed over 1.9 billion bird species observations worldwide. We will share insights from our collaboration with Nespresso to use the BPI to evaluate the state of nature on 84,000 coffee farms worldwide. Furthermore, we will present a case study of how we used the BPI to evaluate the biodiversity impact of the planting of over 3 million trees in >12,000 coffee farms in the Cauca region of Colombia, impacting over 152,000 hectares. Our results provide a roadmap for data-driven nature-based solutions, by showing how investments in agroforestry have resulted in nature-positive outcomes- in less than 10yrs, tree cover on AAA farms doubled, and the contribution of AAA coffee farms to biodiversity increased by 10%.

Session: 6821915**7019852**

24/10/25 | 11:30

Room: Tolima

LIGHTNING TALK VIRTUAL • EN

Bringing data from the North Sea back to life: Ecosystem-based analytics to assess the changes in biodiversity of an ecosystem.

Presenter

Verena Schrameyer

Authors

Verena Schrameyer (DHI A S • Denmark)

Lars O. Mortensen (DHI A S • Denmark)

Ole Bjørn Brodnicke (DHI A S • Denmark)

Jesper Goodley Dannisoe (DHI A S • Denmark)

Jonas Brandi Mortensen (DHI A S • Denmark)

Abstract

For 30+ years, large areas around Oil & Gas infrastructures in the North Sea has been monitored regularly. This data is now being made available to the public through a new portal, initiated by TotalEnergies. Concurrently, concerns for marine biodiversity have increased, due to the alarming decline of species. This has led to an emphasis on biodiversity protection, as seen in initiatives like the EU Marine Strategy Framework Directive. It has also sparked interest in net-positive contributions to biodiversity from the private sector. However, the current metrics of biodiversity often concentrates solely on taxonomic diversity, while neglecting the multi-facets that make up the diversity of an ecosystem. Consequently, there is a need for a framework that considers multiple dimensions of biodiversity within an ecosystem context.

This study reconciles various data sources on biodiversity measures and indicators with ecosystem structure and functioning, enabling marine operators, stakeholders, and managers to assess the broader effects of their biodiversity efforts. Additionally, the study shows how working across decades of seabed data can provide new knowledge to year-to-year changes in the composition of species and their ecological role.

Session: 6821915**7015143**

24/10/25 | 11:35

Room: Tolima

LIGHTNING TALK • ES

Datos abiertos para la gestión de impactos en peces en embalses de generación de energía de EPM

Presenter

Andres Felipe Galeano Moreno

Authors

Andres Felipe Galeano Moreno (Empresas Públicas de Medellín • Colombia)

Abstract

La formación de un embalse con fines de generación de energía genera cambios en el sistema fluvial, ocasionando impactos que afectan la ictiofauna tanto por los cambios en la fragmentación longitudinal como por la conformación de un nuevo hábitat. La identificación y cuantificación de los mismos, y las interacciones que se suscitan a partir de dicho cambio, exigen una mirada holística e integrativa con estudios adelantados por la academia que soporten de manera acertada la toma de decisiones y contribuyan de manera efectiva en la protección y conservación de los peces.

Es así como, bajo el marco de actuación Gestión Integral del Recurso Hídrico y la Biodiversidad, desde el año 2017 y a través de una alianza con la Universidad de Antioquia, Empresas Públicas de Medellín desarrollo una agenda de investigaciones que buscaron establecer la respuesta de la ictiofauna a la formación de embalses mediante un enfoque integrativo determinando los cambios temporales y espaciales de las poblaciones de peces en los diferentes sistemas hídricos, con enfoques que incluyeron: ADN ambiental, ictioplancton, genética, taxonomía, prevalencia parasitaria, conservación, etc.

Fruto de este ejercicio, a través de diversas estrategias se han hecho disponibles al público datos que incluyen el registro de 56 especies que representan cerca del 24% de las especies reportadas para la cuenca Magdalena-Cuenca, el fortalecimiento de la colección de ictiología de la Universidad de Antioquia (CIUA), la divulgación de las secuencias COX de 42 especies y 12S de 52 especies, la construcción de una fototeca con 138 especies (de las que 67 son topotipos) en CavFish, y el aporte a la publicación de un libro y de 16 artículos de investigación.

Session: 6821915**7020072**

24/10/25 | 11:40

Room: Tolima

LIGHTNING TALK • ES

Del dato al impacto: visualizando oportunidades económicas en la conservación de los ecosistemas

Presenter

Henry Alterio

Authors

Henry Alterio (Colombia)

Valentina Amador (Ecosimple • Colombia)

German Rivera (Ecosimple • Colombia)

Abstract

En Ecosimple generamos soluciones innovadoras que integran principios económicos con estrategias de conservación, con el objetivo de fomentar el uso sostenible de los recursos naturales. Por eso desarrollamos la herramienta “*Economic Benefits of natural capital Investments (EBI)*”, diseñada para apoyar a instituciones, empresas, inversionistas y comunidad en general a entender el impacto económico en la biodiversidad y cómo su conservación puede aportar beneficios a la sociedad.

EBI se compone de tres componentes interrelacionados. El primero permite visualizar el estado de conservación de los ecosistemas, la identificación de áreas para destinar acciones de conservación y el valor económico de los servicios ecosistémicos que estos prestan. El segundo facilita la identificación de zonas con potencial para el desarrollo de mercados ambientales, como pagos por servicios ambientales (PSA), créditos de carbono. El tercero ofrece una mirada comparativa sobre los países que han desarrollado cuentas ambientales de recursos naturales, lo que permite entender avances y oportunidades a escala regional.

A través de estudios de caso, análisis multiescalares, instrumentos de geoprocésamiento y análisis económico, la herramienta visibiliza el aporte de diversos actores, desde comunidades locales hasta el sector privado, en la conservación del capital natural y la sostenibilidad de los territorios. Nuestra propuesta se alinea directamente con los objetivos del simposio y de la conferencia de datos vivos, al demostrar cómo los datos, particularmente aquellos generados por el sector empresarial y territorial, pueden transformarse en conocimiento accesible y útil para orientar inversiones y fomentar la acción colectiva en torno a la biodiversidad. En este sentido, EBI contribuye activamente a la movilización, uso y aplicación de datos abiertos sobre naturaleza, promoviendo una visión compartida entre economía, empresa y territorio.

Session: 6821915**7020987**

24/10/25 | 11:45

Room: Tolima

ORAL • EN

Empowering the businesses sector to share biodiversity data: the Colombian experience

Presenter

Dairo Escobar

Authors

Dairo Escobar (ANDI • Colombia)

Dora María Moncada Rasmussen (ANDI • Colombia)

Diana Suárez Ortiz (ANDI • Colombia)

María Cecilia Londoño Murcia (Instituto Humboldt - SiB Colombia • Colombia)

Ricardo Ortiz-Gallego (Instituto Humboldt - SiB Colombia • Colombia)

Esteban Marentes Herrera (Instituto Humboldt - SiB Colombia • Colombia)

Camila Andrea Plata Corredor (Catalogue of Life • Colombia)

Abstract

Biodiversity data are essential for planning, implementing and monitoring conservation and sustainable use strategies. Conversely, a significant amount of these data are systematically collected by the business sector through environmental impact assessments and monitoring programs. However, accessing these data can present challenges, as they are not always readily available. This can hinder the ability to identify patterns and make informed assessments of changes over time and space.

Consequently, SiB Colombia and the National Business Association of Colombia (ANDI) have established a collaborative initiative. This initiative, initiated in 2020, aims to enhance the involvement of the business sector in promoting biodiversity knowledge. It seeks to achieve this by facilitating the participation of the business sector as a key contributor of data to biodiversity research and decision-making.

In order to accomplish this objective of establishing a business community focused on data sharing, it was imperative that the alliance first identify the obstacles that impeded the voluntary sharing of biodiversity data by the business sector. This understanding enabled us to identify the communication style of business entities, how they manage biodiversity information, and their interests and needs. This informed our identification of the significance of business associations in terms of their engagement, as well as the necessity to develop sector-specific instruments that enhance the value of the data management they already perform for other purposes.

Here we will tell the story of how this alliance has successfully managed to consolidate a community of more than 60 companies and 5 million biodiversity data records over the past 5 years. This community is considered one of the most important sources of open data in the country, after citizen science.

Session: 6821915**7022382**

24/10/25 | 11:55

Room: Tolima

ORAL • ES

Datos abiertos sobre biodiversidad en EPM: una experiencia empresarial estratégica para la sostenibilidad y toma de decisiones basada en evidencia

Presenter

Yesenia García Morera

Authors

Yesenia García Morera (Empresas Públicas de Medellín EPM • Colombia)

Abstract

En el marco de la alianza entre SiB Colombia y ANDI “Datos abiertos sobre biodiversidad desde el sector empresarial”, EPM ha liderado la publicación de datos sobre biodiversidad como parte de su compromiso con la sostenibilidad, la transparencia y la toma de decisiones basada en evidencia. A la fecha, ha publicado 59 conjuntos de datos con más de 2,3 millones de registros biológicos, que representan más de 4.200 especies del país. Esta información ha sido citada 379 veces en publicaciones científicas indexadas de alto impacto

como *Biological Conservation*, *Scientific Report* y *Journal of Biogeography*, así como en plataformas como la Lista Roja de Especies Amenazadas de la UICN, demostrando su calidad, utilidad científica y relevancia para la conservación.

La participación en esta alianza y en la Red de Datos Biodiversidad y Desarrollo Colombia ha sido clave para consolidar esta estrategia, aportando además al Elemento Estratégico 3 – Entorno Facilitador de la Hoja de Ruta Biodiversidad y Empresa 2030 de ANDI, con el fortalecimiento de alianzas entre empresas y universidades, ONGs y entidades gubernamentales para generar capacidades internas, promover una cultura organizacional basada en evidencia y facilitar la visibilidad pública de un repositorio corporativo de biodiversidad revisado por expertos internacionales.

La presente ponencia por tanto, compartirá aprendizajes, resultados y retos en la gestión de datos abiertos de biodiversidad, resaltando la contribución a un futuro positivo para la naturaleza y al posicionamiento de EPM como una empresa comprometida con la sostenibilidad y la gestión de la biodiversidad basada en datos de calidad e interoperables. Compartirá como ha sido la gestión, publicación y aplicación de estos datos para apoyar procesos de seguimiento ambiental, caracterizaciones, evaluación de impactos, monitoreo, cumplimiento normativo y reporte en informes empresariales, destacando metodologías para analítica de datos y el desarrollo de tableros corporativos para facilitar la toma de decisiones empresariales.

Session: 6821915**7019971**

24/10/25 | 12:05

Room: Tolima

ORAL • EN

The use and publication of open biodiversity data in the business sector -- the consultant's perspective

Presenter

Cédric Elleboode

Authors

Cédric Elleboode (Biotope • France)

Nicolas Roques (Biotope • France)

Abstract

In the business sector, biodiversity assessments are most commonly conducted by specialist consultancies. These studies are typically carried out within the framework of environmental impact assessments for development projects, subsequent biodiversity monitoring, or as part of voluntary actions under a company's Environmental, Social and Governance (ESG) policy.

A key component of these consultancy-led studies is the initial baseline analysis, during which consultants compile and analyze existing biodiversity data to characterize the study site and determine the need for additional field surveys. In case of field surveys, project developers increasingly require consultants to publish newly acquired primary biodiversity data.

As a result, biodiversity consultancies play a pivotal role at the interface between data reuse and data generation – both leveraging existing biodiversity datasets and ensuring the dissemination of new data acquired through business sector activities.

In this session, we will present how an international consultancy such as Biotope integrates open biodiversity data into its baseline studies. We will also describe how Biotope shares newly collected primary biodiversity data, notably via the French Depobio platform and the Global Biodiversity Information Facility (GBIF). This presentation will also highlight the main challenges encountered when accessing and reusing existing data, as well as those related to data publication and standardization.

Session: 6821915

7022380

24/10/25 | 12:15

Room: Tolima

LIGHTNING TALK • ES

Movilización de datos abiertos sobre biodiversidad desde el sector empresarial: la experiencia de Smurfit Westrock Colombia

Presenter

Wilmar López Oviedo

Authors

Wilmar López Oviedo (Smurfit Westrock Colombia • Colombia)

Abstract

El acceso a datos abiertos es fundamental para la toma de decisiones informadas que promuevan la conservación de la biodiversidad. El sector empresarial, a través de evaluaciones de impacto ambiental, monitoreo ecológico y cumplimiento normativo, genera cada año grandes volúmenes de información ambiental. Sin embargo, gran parte de estos datos permanecen subutilizados o inaccesibles fuera del ámbito corporativo. En este contexto, se ha evidenciado un cambio progresivo con la participación creciente de empresas en iniciativas de datos abiertos sobre biodiversidad. Smurfit Westrock Colombia, como miembro activo del grupo de publicadores del Sistema de Información sobre Biodiversidad de Colombia (SiB Colombia), nodo nacional del GBIF, ha iniciado un proceso sistemático de publicación de datos provenientes de sus áreas naturales en conservación. Esta ponencia presenta una experiencia concreta de movilización de datos abiertos por parte del sector forestal privado. Se exponen las motivaciones institucionales, el diseño de los procesos de publicación, los principales retos enfrentados y las lecciones aprendidas. Asimismo, se describen aplicaciones específicas de los datos publicados en evaluaciones internas y reportes de sostenibilidad corporativa. Finalmente, se analiza cómo la articulación con plataformas e instituciones nacionales ha contribuido al fortalecimiento de iniciativas internas de investigación y monitoreo, permitiendo una planificación más informada y estratégica de la gestión de la biodiversidad. Se concluye con una reflexión sobre la necesidad de fomentar sinergias entre los sectores público, privado y académico para potenciar el uso y valor de los datos abiertos en la respuesta a los retos ambientales contemporáneos.

Session: 6821915**7020020**

24/10/25 | 12:20

Room: Tolima

LIGHTNING TALK • ES

El Sueño de Chocolate: Monitoreo Comunitario para Proteger la Biodiversidad

Presenter

Andrea Camacho

Authors

Diego Bernal (CasaLuker - Luker Chocolate • Colombia)

Andrea Camacho (Colombia)

Abstract

En Luker Chocolate compramos alrededor de 20.000 toneladas de cacao al año en diferentes regiones de Colombia a más de 15.000 pequeños agricultores. Como pilar de nuestra estrategia de sostenibilidad, contamos con un plan colaborativo llamado *El Sueño de Chocolate*, a través del cual buscamos generar valor compartido con las comunidades y el medio ambiente en ciertos territorios de nuestra cadena de valor.

Como parte de este plan, desarrollamos el proyecto Guardianes Ambientales, que promueve la educación ambiental y el fortalecimiento de capacidades comunitarias para la protección de la biodiversidad. Este proyecto sensibiliza y forma a las familias productoras de cacao en temas como el valor de los ecosistemas, el rol de la biodiversidad y su protección mediante prácticas agrícolas cotidianas.

En alianza con Animal Bank, creamos la aplicación *Avista*, una herramienta de monitoreo comunitario de fauna que permite a las comunidades registrar observaciones de especies mediante fotografías. Estos datos son clasificados junto a biólogos y se integran en nuestros sistemas de información geográfica.

Combinando esta información con datos propios de nuestros cultivos, datos públicos del IDEAM y plataformas como SiB Colombia y GBIF, fortalecemos el conocimiento sobre los ecosistemas y la fauna local, lo cual nos permite estructurar y robustecer planes de acción basados en datos para la conservación de la biodiversidad en territorios.

Este enfoque demuestra cómo las comunidades rurales, con acompañamiento técnico, pueden ser agentes clave en la generación de datos para la toma de decisiones ambientales.

Session: 6821915**7020981**

24/10/25 | 12:25

Room: Tolima

LIGHTNING TALK • ES

El sector financiero y privado como motores para la Conservación de la Biodiversidad - Observaciones desde los datos abiertos

Presenter

Juliana Acuña

Authors

Juliana Acuña (ERM • Colombia)

César Burgos (ERM • Colombia)

Nicols Reina (ERM • Colombia)

Catherine Sahley (ERM • Perú)

Abstract

El sector financiero y privado son fundamentales para la conservación de la naturaleza. Se ha estimado que, para revertir la crisis ambiental, son necesarios al menos 20 billones de dólares al año. Esto, es sólo posible con la transformación de la relación con la naturaleza de estos sectores, tal como lo presenta la Meta 19 del MGB.

Por ello, es necesario que el sector financiero realice inversiones seguras en asuntos A&S y que las Compañías desarrollen ejercicios de TNFD y rutas de naturaleza positiva, como parte de la gestión corporativa de biodiversidad. En ambos casos, los datos abiertos lo hacen posible.

Las Normas de Desempeño para el sector financiero, habilitan los impactos positivos sobre la biodiversidad, a través de la evaluación de hábitats críticos, una mejor gestión corporativa de la biodiversidad, y planes de acción que incluyan acciones voluntarias de conservación, para los proyectos financiados. En Colombia, las inversiones del sector financiero en proyectos superan los billones de dólares, esto demuestra la importancia de los datos abiertos para asegurar una adecuada gestión de la biodiversidad en las inversiones.

Por otro lado, la alineación con el marco de divulgación TNFD requiere de la evaluación de impactos, dependencias, riesgos y oportunidades de naturaleza, que parte, también, del conocimiento de la biodiversidad, y permiten una gestión eficaz de los riesgos.

Esta presentación muestra cómo, a través de las debidas diligencias y la implementación de marcos como el TNFD y Nature Positive, posibles gracias a los datos abiertos, ERM ayuda a las Compañías y entidades financieras a minimizar sus riesgos de naturaleza, a la vez que generan impactos positivos en la biodiversidad.

A pesar de la utilidad de los datos disponibles, la brecha de información es inmensa, lo que lleva a un aletargamiento en las acciones de conservación desde el sector financiero y privado.

Session: 6821915**7021017**

24/10/25 | 12:30

Room: Tolima

LIGHTNING TALK • ES

Lecciones sobre datos abiertos de biodiversidad a partir del estudio ictiológico en ecosistemas estratégicos de Campo Arauca, Saravena, Arauca

Presenter

Laura Lozano

Authors

Laura Lozano (Parex Resources • Colombia)

Edna Penagos (Fundación Orinoquia Biodiversa • Colombia)

Abstract

La publicación de datos abiertos de biodiversidad por parte del sector empresarial en el Sistema de Información sobre Biodiversidad de Colombia (SiB Colombia) es una práctica estratégica que promueve la sostenibilidad y la generación de conocimiento colectivo, los estudios ambientales realizados por empresas representan una fuente valiosa de información que, al compartirse, fortalece la gestión ambiental del país.

Arauca se encuentra entre los departamentos con menor cantidad de registros biológicos georreferenciados, actualmente, el SiB Colombiano cuenta con un total de 107.069 registros para el departamento, correspondientes a 4.187 especies documentadas, lo que representa cerca del 5,2 % de las especies reportadas a nivel nacional, lo cual revela una fuerte subrepresentación en el sistema. Estos datos se concentran principalmente en ciertos grupos biológicos, como las aves, mientras que otros, como peces, insectos y plantas, están subrepresentados, dificultando una comprensión integral de la biodiversidad regional.

En el 2023, en colaboración con la Fundación Orinoquia Biodiversa, Parex inició un estudio para evaluar la composición, la estructura y la importancia socioeconómica y cultural de la ictiofauna presente en el Campo Arauca, localizado en el municipio de Saravena, Arauca, una región poco estudiada dentro de la cuenca del Orinoco. La investigación se basó en la recolección de datos biológicos, revisión de fuentes secundarias y trabajo comunitario.

Publicar esta información en el SiB Colombia permitiría integrar datos actualizados sobre una región históricamente submuestreada. Además, es una muestra del rol de las empresas en la generación de conocimiento y en el cumplimiento de compromisos como el Convenio de Diversidad Biológica y los objetivos de desarrollo sostenible. La colaboración entre instituciones, el sector empresarial y comunidades locales es esencial para cerrar las brechas de información y promover una gestión sostenible de los recursos naturales en el departamento.

Session: 6821915**7020221**

24/10/25 | 12:35

Room: Tolima

LIGHTNING TALK • EN

20 years of The Camisea Biodiversity Monitoring Program in the Peruvian Amazon

Data collection for conservation in a changing landscape

Presenter

Catherine Sahley

Authors

Catherine Sahley (Environmental Resource Management • United States)

Sheila Romero (Environmental Resource Management • Perú)

Abstract

We present an overview of the Camisea Biodiversity Monitoring Program in Peru to demonstrate how data availability in a highly biodiverse landscape, in combination with changing data needs over the Camisea Project lifecycle, shaped the understanding, collection and utilization of biodiversity data and conservation efforts in the Peruvian Amazon. The Camisea Gas Project extracts and transports natural gas originating near the Urubamba River in Megantoni District in the Cusco Region of Peru. It has been in operation since 2004 and has continuously implemented a Biodiversity Monitoring Program (BMP) to facilitate adaptive management in this remote and biodiversity rich area.

During the first decade of the Camisea BMP, the focus was on collecting field data for multiple taxonomic groups to measure direct Project impacts. However, due to the remoteness of the area and lack of roads, field surveys, while effective, were both logistically intensive and expensive. Over time, as biodiversity and Project impacts were better understood, efforts focused on implementing newer technologies to improve monitoring efficiency as well better understand biodiversity throughout the landscape. We provide an overview of i) biodiversity and ecosystems services concerns, international standards, data needs and availability at the outset of the project; ii) how the Project collected and managed data during its first decade and how data collection has evolved over time iii) how biodiversity impacts, risks and opportunities have changed over time and iv) what data collection and management looks like 20 years after the BMP began.

We also discuss learned lessons and review challenges with data and its management including i) contribution of the private sector for generating robust baselines, museum collections and species inventories ii) benefits and challenges of using online databases and most importantly iii) challenges of translating biodiversity data into information that serves as a tool for sustainable development and conservation.

Session

6960773-6

Symposium

24/10/25 | 10:45

Room: Caldas

Data Integration & Platform Development (Contributed Oral presentations)

Organizers

Jory Griffith

Sam Leeflang

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-6**7020857**

24/10/25 | 10:45

Room: Caldas

ORAL • EN

BioMap - Integration Platform for Polish Biodiversity Data

Presenter

Piotr Tykarski

Authors

Piotr Tykarski (University of Warsaw • Poland)**Robert Meronka** (University of Warsaw • Poland)

Abstract

The Biodiversity Map, a long-term initiative of the Polish Biodiversity Information Network (KSIB), integrates, presents, and manages comprehensive scientific data on species to support biodiversity research. The initial prototype, developed using a PHP framework, amassed 1.4 million occurrence records, primarily focusing on Poland's insects (Coleoptera, Hemiptera, Lepidoptera), later expanding to include other arthropod groups. This early system linked taxonomy, occurrences, bibliography, collections, and author data, connecting data categories in scientific documentation, essential for scientific communities.

The new BioMap portal (portal.biomap.pl) follows the same paradigm, integrating diverse data sources and enabling users to browse and filter content. The system organizes data into views called "perspectives": taxa, occurrences, collections, datasets, publications, authors, locations, and checklists, each offering a unique view of the data's dimensions and relationships. For instance, users can explore publications linked to areas near a selected map locality or collections tied to species in a publication.

BioMap now has no taxonomic limits, with its taxonomy tree (based on ITIS Data Model v.2.3) anchoring all occurrence records. Particular attention was given to standardizing and harmonizing author names, including authors of taxa. The database has been enriched with data from the digitization of resources from 18 Polish scientific institutions, comprising 9.5 million records, including over 2 million specimens, and the Digital Catalogue of Biodiversity of Poland, providing a comprehensive checklist of eukaryotic and cyanobacteria species.

The application uses PostgreSQL/PostGIS, the PHP Laravel framework, Vue.js as the primary front-end layer, and OpenLayers to serve spatial data from a GIS server. A five-level privilege system allows users to edit data (CRUD), control access, and manage record visibility, protecting sensitive data while encouraging public sharing post-publication. All occurrence records are linked to at least one dataset, and datasets with "fixed" status are permanent and publishable on GBIF.

Session: 6960773-6**7020841**

24/10/25 | 13:12

Room: Caldas**ORAL • EN**

Wiring Biodiversity: Laying the Foundations for Biological Data Integration in SAEON's Open Data Platform

Presenter

Daniëlle Seymour

Authors

Daniëlle Seymour (South African Environmental Observation Network • South Africa)

Abstract

The South African Environmental Observation Network (SAEON) Open Data Platform (ODP) is a FAIR-aligned, CoreTrustSeal-certified infrastructure that supports the long-term stewardship, discovery, and reuse of environmental observation data in South Africa. Designed primarily to manage and share abiotic data—such as climate, oceanographic, and terrestrial measurements, the SAEON ODP has matured through the adoption of global metadata standards, including ISO 19115 and DataCite. However, as national and international scientific and policy agendas increasingly call for integrated, cross-domain environmental information, the need to support biodiversity data within SAEON's infrastructure has become a strategic priority.

This presentation showcases the foundational work underway to enable the inclusion of biodiversity data within the existing SAEON data ecosystem. We focus on the development of a biological metadata schema mapping, aligning the Ecological Metadata Language (EML) with existing standards already in use. This early-stage effort sets the stage for implementing enhanced workflows and data pipelines capable of handling biological complexity, from taxonomic hierarchies to sampling events and trait data.

By aligning this work with FAIR principles and the broader goals of interoperability, this initiative aims to improve the accessibility of biodiversity data for scientific research, national assessments (e.g. the South African Risk and Vulnerability Atlas), and contributing to global aggregators. While integration into the system is still in progress, this talk outlines the conceptual architecture, technical considerations, and design choices shaping the path forward. Through this, we aim to contribute to the broader discourse on how environmental data infrastructures can evolve to represent life in all its forms and support biodiversity-related decision-making.

Session: 6960773-6**7016119**

24/10/25 | 11:05

Room: Caldas

ORAL • EN

Biodiversidades: a data-driven platform for updating Mexico's Ecosystem Assessment

Presenter

Patricia Koleff

Authors

Patricia Koleff (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO) • Mexico)**Tania Urquiza-Haas** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)**Sylvia Patricia Ruiz González** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)**Angélica Eliabeth Martínez Bauer** (Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO • Mexico)**Oscar Godínez Gómez** (School of Natural Resources and Environment, Department of Wildlife Ecology and Conservation, University of Florida • United States)**Jonathan Vidal Solórzano Villegas** (Centro de investigaciones en geografía ambiental, UNAM • Mexico)**Diana Lucero Ramírez Mejía** (Vrije Universiteit Amsterdam • Netherlands)**Roberto Rangel Heras** (Centro de investigaciones en geografía ambiental, UNAM • Mexico)**Miguel Angel Blanco Calderón** (Consultor independiente • Nicaragua)

Abstract

In 2008, Mexico launched a comprehensive national ecosystem assessment involving hundreds of researchers across the country. This resulted in the publication of 'Capital Natural de México' (CNM) in 2008, which contains four volumes and three SPM documents. ; it was coordinated by the National Commission for the Knowledge and Use of Biodiversity (CONABIO). CNM synthesizes the available knowledge on the components, structure, and functioning of the biodiversity of Mexico; the threats and trajectories of anthropogenic impact, together with its conservation status; it also assesses the policies, institutions, and instruments that have been created for its sustainable management. Nearly two decades later, the demand for updated and accessible biodiversity information has grown, driven by accelerating environmental change and the need for informed public policies.

To address this, we present Biodiversidades, a new open-access digital platform designed to update and extend Mexico's ecosystem assessment in a dynamic and interactive format. The platform integrates geospatial, statistical and synthesized data from official monitoring systems, scientific research, and national biodiversity databases. It enables users to explore key indicators on species distribution, ecosystem extent and condition, conservation gaps, and policy responses

By providing updated interactive visualizations, downloadable datasets and descriptions on key elements of Mexico's ecosystem assessment, Biodiversidades reinforces Mexico's forefront capacity to contribute towards biodiversity monitoring frameworks and aligns with global commitments such as the Kunming Montreal Global Biodiversity Framework. This presentation will showcase the platform's structure, indicator framework, data sources, along with its role and potential to inform conservation priorities and environmental challenges, among other relevant issues for effective biodiversity governance.

Session: **6960773-6****7020033**

24/10/25 | 11:15

Room: Caldas

ORAL • EN

LifeWatch Italy infrastructure: a national asset for Open and FAIR Biodiversity Data

Presenter

Andrea Tarallo

Authors

Andrea Tarallo (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Alberto Basset** (University of Salento, Department of Biological and Environmental Sciences and Technologies • Italy)**Francesco De Leo** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Cristina Di Muri** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Mariantonietta La Marra** (University of Salento, Department of Biological and Environmental Sciences and Technologies • Italy)**Martina Pulieri** (University of Salento, Department of Biological and Environmental Sciences and Technologies • Italy)**Davide Raho** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)**Ilaria Rosati** (National Research Council of Italy (CNR), Institute of Research on Terrestrial Ecosystems (IRET) • Italy)

Abstract

LifeWatch Italy is the Italian Distributed Centre of LifeWatch ERIC, the distributed e-Science Infrastructure for biodiversity and ecosystem research. Its primary aim is to develop and maintain digital solutions for the FAIR and open management of digital research products. Such products come from our scientific community in various forms, ranging from research data to scripts, training materials, and more. In recent years, LifeWatch Italy has significantly enhanced its infrastructure to effectively manage this diverse set of products by developing different platforms to support scientists throughout the entire research cycle. Among those, the LifeWatch Italy Data Portal share and manage (meta)data through a curation workflow which include a taxonomic validation against curated national and international taxonomic backbones (e.g. CoL, WoRMs, and GBIF), and the use of standard and semantic artefacts to annotate metadata attributes, including dataset variables (i.e. ontologies, controlled vocabularies, Darwin Core). Curated and standardised data can be automatically retrieved by DataLabs, a service which supports collaborative data analysis and modelling. Data, algorithms and services produced by DataLabs can be published, along with their associated metadata, in the Data Portal and Metadata Catalogue. Finally, the helpdesk and an e-training platform support user in using the LifeWatch Italy's digital services. The development of such an infrastructure is not a process with a defined start and end, but rather a continuous endeavour. Indeed, efforts are already underway to keep the infrastructure aligned with emerging technologies and initiatives to facilitate the data mobilisation of our scientific community.

Session: 6960773-6**7007354****24/10/25** | 11:25**Room:** Caldas**ORAL • EN**

Frictionless Data 101: how to document and validate datasets or create community standards with the Data Package standard

Presenter

Peter Desmet

Authors

Peter Desmet (Research Institute for Nature and Forest (INBO) • Belgium)

Abstract

Data Package is an open, generic, lightweight, and extensible standard for describing datasets, files and tabular data. First released in 2007 by the Open Knowledge Foundation (OKFN) to address challenges in open government data, it is now used in multiple domains to document datasets, improve data quality, facilitate reproducible workflows, and develop community standards. The standard is supported by comprehensive open source software tools (including in Python, R and Javascript) and an active maintenance group. In this talk I will cover:

- The Data Package standard, covering its specifications for describing datasets, files, file formats and tabular data.
- How to document a dataset as a data package, increasing its Findability, Accessibility, Interoperability, and Reuse (FAIR).
- How to use software to read, describe, validate and create data packages, either in a graphical user interface or as part of a reproducible workflow.
- How to leverage the Data Package standard to address domain-specific needs or develop community standards—as has been done for Darwin Core Data Package and Camtrap DP.
- What new features are introduced in Data Package version 2 (released in 2024), development plans, and how to contribute.

Session: 6960773-6**7020792**

24/10/25 | 11:35

Room: Caldas

ORAL • EN

From Friction to Flow: UX-Driven Improvements to Biodiversity Data Access

Presenter

Chandra Earl

Authors

Chandra Earl (NEON (National Ecological Observatory Network) • United States)

Abstract

Biodiversity data platforms are often built by researchers for researchers, resulting in dense, complex interfaces that often assume familiarity with the underlying biological data structures. While these tools support expert use, they risk excluding broader audiences—such as early-career scientists, interdisciplinary researchers, or anyone unfamiliar with specialized terminology. Improving usability is essential to ensure biodiversity data is discoverable, understandable, and usable across a wider community. A redesign of the platform supporting access to ecological samples from the NEON (National Ecological Observatory Network) project focused on lowering the barrier to discovery by aligning the interface with user needs and expectations.

The process was grounded in developing a comprehensive website brief that defined platform goals, identified target audiences, and informed decisions throughout the redesign. This included developing user personas, mapping current and future site structures, wireframing key pages, reviewing similar platforms through a UI/UX lens, and refining the visual design to align more clearly with NEON's broader branding and identity. Lightweight user testing informed interface decisions, and analytics tracking was implemented to evaluate engagement. The resulting redesign introduced clearer navigation, tighter integration within the parent brand, and modern layouts that better support both exploratory and task-focused users in searching for, understanding, and accessing sample data—while also surfacing broader needs across the platform, including outdated tools and missing features that have shaped priorities for future development. This work demonstrates how structured, user-centered design can make biodiversity tools more approachable, helping platforms serve a wider range of users while amplifying the accessibility and impact of the data they provide.

Session: 6960773-6**7013608**

24/10/25 | 11:45

Room: Caldas

LIGHTNING TALK • EN

Data Management in the Biodiversity Domain: The GFBio Data Submission & Brokerage Service

Presenter

Jimena Linares

Authors**Jimena Linares** (German Federation for Biological Data GFBio e.V. • Germany)**Abstract**

The NFDI4Biodiversity[1] is a German consortium under the umbrella of the National Research Data Infrastructure (NFDI) dedicated to mobilising biodiversity and environmental data for collective use.

The consortium offers support in research data management through different services provided by the partners. The GFBio's Submission and Brokering service[2], is a single drop-off point for heterogeneous data produced during a research project. The data is distributed to the partner data centers[3], in there they will be processed and interlinked.

You get individual expert support for metadata standardization for commonly used schemas and standards to achieve FAIRness, obtain a persistent identifier, and can choose when do you want your data to be public by setting an embargo date.

Meet us to discuss your project and how make your data available!

1. <https://www.nfdi4biodiversity.org/en/>

2. <https://submissions.gfbio.org>

3. <https://www.nfdi4biodiversity.org/en/datenzentren/>

Session: 6960773-6**7021035**

24/10/25 | 11:50

Room: Caldas

LIGHTNING TALK • EN

Cultivating Symbiosis - Open Source Platform Cooperativism, Cyclical Data & Ancestral Wisdom for Regenerative Futures.

Presenter

David A. Divas

Authors

David A. Divas (SINTROP.IA • Guatemala)

Abstract

The escalating climate crisis and biodiversity loss in Mesoamerica demand novel technological paradigms that empower, rather than indebt, smallholder farming communities. SINTROP.IA addresses this by developing an integrated, open-source platform that weaves community knowledge with advanced data ecosystems and open technology for next-generation agroecology.

Our innovation centers on four interoperable pillars:

- 1) BioPulso: user-reparable, affordable bioambiental sensor arrays (bioclimatic, soil, water, bioacoustic) designed for high-fidelity, spatio-temporal data generation on agroecosystem health and biodiversity metrics.
- 2) MAR.IA: an Infrastructure-as-Code (IaaS) platform utilizing fine-tuned open-source LLMs for AI-driven precision agroecology, a cooperative data/algorithm marketplace (Ocean Protocol/Celo based), and integration of Traditional Ecological Knowledge (TEK)
- 3) EcoBloom: modular, climate-smart greenhouses manufactured from local bamboo and upcycled plastics, designed for optimal resource use and resilience.
- 4) EcoForge: containerized bioeconomy workshops enabling local communities to transform plastic and organic waste into bioplastics and valuable resources, fostering circularity.

Through this vertically integrated system, significantly more cost-effective than existing solutions, facilitates a shift from extractive models to community-owned productive infrastructure. SINTROP.IA uniquely combines open-hardware accessibility with sophisticated AI and a cooperative framework, creating a novel pathway for scaling regenerative agriculture and democratizing access to vital next generation tools for a resilient and biodiverse future.

We hope that by sharing our experiences from our journey, our insights on advancing progress in a grassroots way, and forging a path forward for collaboration despite the existing monolith of technology and society may be helpful, or even inspiring to others across the world. We aim to prove it's possible, and would enjoy the privilege of launching publically (we're in "stealth" mode) at Living Data 2025.

Session: 6960773-6**7020978**

24/10/25 | 11:55

Room: Caldas

ORAL • EN

The Atlas of Living Australia's services to environmental decision-making

Presenter

Peggy Newman

Authors

Peggy Newman (CSIRO • Australia)

Cameron Slatyer (CSIRO • Australia)

Abstract

With three tiers of government, environmental decision-making in Australia faces challenges around the segregated nature of data and accountability. Local and state/territory levels of government are responsible for environmental decision-making at local and regional scales, while the Commonwealth is responsible for matters of national environmental significance. There have been many calls to improve this. A 2021 meeting of all Environment Ministers called for “one-touch environmental approvals”, effectively reducing “green-tape”.

The Atlas of Living Australia, hosted by CSIRO, was established via funding from the Australian government. It makes an aggregated national dataset publicly available and develops and maintains software and data flows that underpin critical biodiversity data services to researchers, government and industry.

The ALA adds to this valuable dataset by delivering a nationally consistent taxonomic backbone. It offers services that benefit government, including biosecurity alerts (an email alerting a subscriber to new records of invasive species), management of sensitive or restricted species data (generalisation of records regarded as sensitive by government), and environmental reporting (providing data for the five- yearly national State of Environment Report).

To better understand its role in dealing with these issues, we undertook a review of government usage from 2016 to 2022, finding that there were 3,198 government users within 179 agencies, with 62% of agencies being local councils.

63% of individual users were repeat users. The most prevalent repeat users were national and state and territory environment and primary industry agencies, on average, using the ALA in six out of the seven years surveyed.

Use by environmental and primary industry agencies was predicted, however, there was also a consistent pattern of usage by many other parts of government including regulatory, Indigenous land management, health and education, and fire management. This suggests that Living Atlas software can and does play an important role in the policy landscape.

Session: 6960773-6**7018753**

24/10/25 | 12:05

Room: Caldas

ORAL • EN

Integrating Biodiversity Data in Chile: The BIODATA-IEB Initiative

Presenter

Ricardo Segovia

Authors

Ricardo Segovia (Instituto de Ecología y Biodiversidad • Chile)

Juan Sáez-Hidalgo (Instituto de Ecología y Biodiversidad • Chile)

Francisco Squeo (Instituto de Ecología y Biodiversidad • Chile)

Alicia Marticorena (Universidad de Concepción • Chile)

Julián Caro (Instituto de Ecología y Biodiversidad • Chile)

Pablo Guerrero (Instituto Milenio BASE • Chile)

Abstract

The BIODATA initiative, led by the Institute of Ecology and Biodiversity (IEB) in Chile, is developing a dynamic, multi-taxon biodiversity inventory by integrating local biological collections and expert taxonomic knowledge with global biodiversity datasets. A pivotal step in this process involves digitizing, curating, and managing collection specimens databases. Utilizing the i-Biodata platform, nearly 150,000 specimens representing over 3,400 species from five Chilean herbaria have been digitized and indexed, employing the standardized taxonomy provided by the Catalogue of Vascular Plants of Chile. To assess the quality and usability of this local catalogue, it was compared to a global reference catalogue derived from the Catalogue of Life (COL), specifically filtered for species recorded in Chile according to GBIF data. This comparative integration highlighted significant discrepancies in species richness among several plant families, underscoring the importance of local taxonomic expertise in curating accurate biodiversity data. Subsequently, the locally curated and validated vascular plant index was integrated into the broader global multi-taxon index derived from the COL dataset filtered by GBIF. The resulting complementary biodiversity catalogue is accessible and editable by taxonomic experts across different taxa through an interactive web portal, providing an authoritative resource to support biodiversity research, conservation strategies, and environmental policymaking in Chile.

Session: 6960773-6**7020686**

24/10/25 | 12:15

Room: Caldas

ORAL • EN

From Advocacy to Action: Microservices as a New Pathway for Biodiversity Data Capacity Building

Presenter

Stephen Formel

Authors

Stephen Formel (Formel Data Services • United States)

Abby Benson (United States)

JJ Dearborn (Smithsonian Institution | Biodiversity Heritage Library • United States)

Kristen “Kit” Lewers (University of Colorado Boulder and NASA Goddard Space Flight Center • United States)

Abstract

Despite decades of advocacy for improved data stewardship in science, most biodiversity research projects still struggle to implement sustainable data management. This gap hampers data sharing, reduces reproducibility, and limits the global utility of biodiversity knowledge. Rather than repeating calls for full-time data managers on every project we propose an alternative data management model grounded in decentralization, collaboration, and service-oriented design.

While not completely novel, our approach reimagines biodiversity data management as a series of modular, professional microservice units akin to the software engineering concept of microservices. Inspired by gig economy principles, and the widespread use of freelance expertise in other sectors (e.g. construction, accounting), we suggest that data planning, cleaning, publishing, and preservation be treated as affordable, on-demand services, with an emphasis on affordable tasks and simple purchase mechanisms. This enables scientists to allocate modest resources for high impact results. At the same time, this model fosters a viable career pathway for data stewards, helping to build a distributed, resilient workforce.

We believe this approach contributes to capacity building, technical cooperation, and accessibility of knowledge about biodiversity (targets 20 and 21 of the Kunming-Montreal Global Biodiversity Framework), by building a culture of data stewardship rooted in community engagement and entrepreneurial agency. Importantly, we emphasize the benefits of leveraging individual skillsets and independent operation to support Targets 20 and 21.

We will present how a microservice based model can strengthen the global biodiversity data ecosystem, reduce bottlenecks in data publishing, and empower individuals to become independent contributors to open science. We invite collaboration across domains to co- create a resilient, inclusive system of data stewardship that is pragmatic, scalable, and globally impactful.

Session: 6960773-6**7016138**

24/10/25 | 12:25

Room: Caldas**ORAL • EN**

The BDQ Standard

Presenter

Arthur Chapman

Authors

Lee Belbin (Blatant Fabrications Pty Ltd • Australia)**Arthur Chapman** (Australian Biodiversity Information Services • Australia)**Paul Morris** (Museum of Comparative Zoology, Harvard University • United States)**John Wieczorek** (Rauthiflor LLC • Argentina)

Abstract

We explore the critical issue of biodiversity data quality through work undertaken by the Tests and Assertions Task Group (TG2) of the Data Quality Interest Group in developing a biodiversity data quality standard - BDQ.

The Task Group developed a suite of 110 core single-record tests and supporting ‘ecosystem’ for formal description of tests, their results, and their application for quality control and quality assurance for defined uses of data. The tests arise from the recognition that data quality is second only in significance to data availability for the research community and other stakeholders.

We initially reviewed tests used by the Atlas of Living Australia, the Global Biodiversity Information Facility, VertNet, iDigBio, CRIA and BISON. This review led to the development of criteria required for a concise description of the tests that evolved.

We provide an overview of the development of BDQ, which is based on the Data Quality Fitness for Use Framework, a set of use cases, a suite of vocabularies and Darwin Core. BDQ includes an introduction, quick reference guide, user’s guide, implementer’s guide, test validation data, guide to the Fitness for Use Framework Ontology, internal vocabularies, references, links to example implementations, supplementary information and the core tests and assertions in various formats (CSV, RDF/XML, Turtle, JSON-LD).

BDQ tests are classified as either VALIDATION (identifies data that conforms to requirements), AMENDMENT (suggested enhancement to make data compliant), ISSUE (flags potential issues) and MEASURE (numeric values, summary counts, etc.).

We discuss the use of BDQ for evaluating fitness for use for identified user-defined purposes, improving the quality of biodiversity data, its intended uses for quality control and quality assurance for data providers and users, and the plans for its ongoing maintenance. This work aims to enhance trust in biodiversity data and facilitate more informed research and decision making.

Session: 6960773-6

7014181

24/10/25 | 12:35

Room: Caldas

LIGHTNING TALK • EN

Latest additions to Audiovisual Core with examples

Presenter
Ed Baker

Authors
Ed Baker (Natural History Museum • United Kingdom)

Abstract
Audiovisual Core is the TDWG stadard for biodiversity media and has an active maintenance group. This talk provides an update on our activities in the year since the last conference to improve the Audiovisual Core standard, including our work on 3D representations, readiness for artificial intelligence, and what we plan to be working on for the next year. Some quick examples of new functionality will be provided.

Session

6799392

Symposium

24/10/25 | 10:45

Room: Valle

Genomic DSI as a Global Biodiversity Monitoring Tool: Integration, Standardization, and Equity

Organizers

Camila Mazzoni

Jonathan Ready

Robert Waterhouse

Physilia Chua

Katharina Heil

Andrew Crawford

Carolyn Hogg

Maria M. Zambrano

Joana Pauperio

Eduardo Eizirik

Angelica María Batista Morales

Maribet Gamboa

Description

Digital Sequence Information (DSI) encompasses a broad range of sequence-based data that are critical for biodiversity monitoring at species and population levels. Despite its transformative potential, integrating and standardizing DSI in biodiversity monitoring remains a challenge, particularly in tropical systems and the global south where genetic biomonitoring methods face unique obstacles.

Biodiversity genomics provides tools to produce high-quality genomic data, integrate it across datasets, and support its use in decision-making for biodiversity actions. However, methods like metabarcoding and species-specific detection techniques have generally been developed for well-characterized ecosystems with lower diversity in temperate climates. These approaches may translate poorly to tropical regions due to differences in reference dataset coverage, variation in evolutionary history and biological diversity, and distinct societal demands and capacities for biodiversity data usage. This session focuses on genomic DSI, highlighting its role in generating, analyzing, and applying data in organismal and environmental contexts, while addressing the challenges of adapting genetic monitoring methods to evolutionarily and functionally distinct systems.

Key discussions will explore innovations in data and metadata standards, tools for integrating genomic data into biodiversity infrastructures, strategies for democratizing DSI generation, challenges in adapting genetic monitoring methods to freshwater, terrestrial, and transitional environments, analysis to ensure equitable participation and benefit sharing, and case studies demonstrating reliable and FAIR data applications and its use in biodiversity monitoring and conservation policy.

The session was developed by GEO-BON and major biodiversity genomics initiatives, including the European Reference Genome Atlas, Earth BioGenome Project, DSI Scientific Network, ELIXIR, Biodiversity Genomics Europe, EMBL-EBI, GenoTropics Consortium, and the Threatened Species Initiative. The session will provide attendees with insights into how scaling and standardizing genomic DSI can bridge knowledge gaps, contribute to local capacity building for genetic biomonitoring and promote equity in biodiversity science and policy.

Session: 6799392**7014906**

24/10/25 | 10:45

Room: Valle

ORAL • EN

Engaging the ERGA community on the concept of non-monetary benefits in the context of DSI and the Cali Fund

Presenter

Robert Waterhouse

Authors

Robert Waterhouse (SIB Swiss Institute of Bioinformatics • Switzerland)

Abstract

As a community of researchers dedicated to the production and use of reference genomes for biodiversity, the European Reference Genome Atlas (ERGA) recognises the urgent need to engage the genomics research community on the concept of non-monetary benefits in the context of Digital Sequence Information (DSI) and the Cali Fund. Exactly how to proceed remains unclear, but with a large and diverse community ERGA represents a good testing-ground for further developing a meaningful path forwards involving fostering awareness, dialogue, and collaboration around equitable benefit-sharing. Non-monetary benefits are increasingly recognised as critical to fair access and equitable use of genetic resources, and could include efforts towards capacity-building, technology transfer, training, and data sharing, aligning well with the mission of ERGA. The Cali Fund, established to pilot benefit-sharing mechanisms linked to DSI, provides a practical framework to explore how such benefits can be implemented without hindering open scientific research. To effectively engage our community of researchers, ERGA has started to raise the topic of DSI and benefit-sharing firstly through webinars with domain experts, to be followed by workshops, surveys, and other consultations to gather insights and address concerns. These discussions highlight that many researchers value global collaboration and see the potential for non-monetary benefit-sharing to enhance research equity, especially for scientists in low- and middle-income countries. However, challenges remain, including ensuring that benefit-sharing policies do not create burdensome reporting requirements or barriers to data access. By activating the genomics community to consider the various options and debate their pros and cons, we aim to co-develop feasible, researcher-friendly approaches that align with the scientific ethos of openness while advancing global equity goals.

Session: 6799392**7009078**

24/10/25 | 10:55

Room: Valle

LIGHTNING TALK • EN

A Human Rights Approach to Benefit Sharing from the Use of Digital Sequence Information

Presenter

Alex Reep

Authors

Alex Reep (Alliance Bioversity-CIAT • United States)

Abstract

Digital Sequence Information (DSI) holds vast potential for biodiversity monitoring and conservation. Yet, its use can risk reinforcing historical inequities if not accompanied by fair and equitable benefit-sharing with Indigenous Peoples and Local Communities (IP and LCs). This study investigates IP and LC perceptions of benefit-sharing from the use of DSI derived from genetic resources stewarded in their territories. Results propose a human rights-based approach to the design and implementation of the multilateral mechanism and Cali Fund established at COP16.

This research was conducted under the Fulbright U.S. Student Program between October 2023 and May 2024 in five departments of Colombia. Semi-structured interviews were held with 22 individuals from Indigenous, Afro-descendant, and campesino communities. Participants were asked about what they consider to be “fair and equitable” benefit-sharing and their views on data governance. Interview and field note data were analyzed using qualitative coding and AI Assist with MAXQDA 24 software, and the Gioia et al. (2013) method supported the identification of themes by systematically recognizing patterns in study data.

Three key findings emerged. First, local context matters: definitions of fairness are deeply shaped by regional histories, environmental conflicts, and structural exclusion. Second, IP and LCs should be recognized not only as data providers, but as technology co-creators, offering unique ethnobiological knowledge essential to DSI-enabled innovation. Third, DSI governance must prevent biopiracy, ensuring free, prior and informed consent and protections for traditional knowledge associated with genetic resources.

This lightning talk presents a rights-based framework for benefit sharing that aligns with both the FAIR and CARE Principles and prioritizes local capacity strengthening. It advocates for ethical and collaborative innovation as researchers sequence the world’s biodiversity. Drawing on community perspectives, the talk emphasizes that effective DSI governance must be grounded in equity, transparency, and accountability—principles that resonate deeply with interviewees as biodiversity stewards.

Session: **6799392****7020754**

24/10/25 | 11:05

Room: Valle

LIGHTNING TALK • EN

Food Composition Data as a Global Public Good: Access & Benefit Sharing (ABS), Provenance, and Metadata Curation

Presenter

Sarah Brinkley

Authors**Sarah Brinkley** (The Periodic Table of Food Initiative, The Alliance of Bioversity-CIAT • Colombia)**Alex Reep** (The Periodic Table of Food Initiative • United States)**Colin Khoury** (The Periodic Table of Food Initiative • Colombia)**Esteban Neira-Monsalve** (Farmless B.V. • Colombia)**Katie Lee Riddle (Rongowhakaata)** (Te Kotahi Research Institute • New Zealand)**Mathieu Rouard** (The Alliance of Bioversity-CIAT • France)**Sunil Archak** (ICAR-National Bureau of Plant Genetic Resources (NBPGR) India • India)**Alejandro Lago** (Associate Professor of International Law, CUNEF University • Spain)**Isabel López Noriega** (The Alliance of Bioversity-CIAT • Spain)**Selena Ahmed** (The American Heart Association • United States)**Abstract**

Where was your food grown? By whom? And why is it meaningful? When traditional ecological knowledge and other metadata are collected alongside food composition data, we can begin to understand the full significance of foods. The Periodic Table of Food Initiative (PTFI)® is developing standardized tools, protocols, and training to generate and integrate diverse data across the spectrum of edible biodiversity. The PTFI enables decision-makers across disciplines to apply food composition knowledge in research, policy, and innovation. But for these data to serve as a global public good, we must support all knowledge holders—data contributors and users alike—in navigating a complex ethical, legal, and technological landscape.

The PTFI is committed to responsible access to genetic resources and associated traditional knowledge, while supporting equitable benefit-sharing under international agreements such as the Nagoya Protocol and the evolving Digital Sequence Information (DSI) framework of the Convention on Biological Diversity (CBD). Aligned with COP16 decisions, PTFI is implementing mechanisms to report the provenance of DSI derived from genetic resources—ensuring transparency, traceability, and accountability in line with global ABS guidelines and expectations.

To operationalize these commitments, the PTFI has developed a multi-tiered mechanism for ABS curation that tags and gates the DSI derived from diverse communities' food systems. The PTFI's ABS curation protocols determine which data are made public and are aligned with legal and ethical standards of data governance.

This oral presentation will demonstrate how data-driven efforts to map the world's edible biodiversity can be designed not only for scientific excellence and interoperability, but also to uphold principles of justice, transparency, and responsible data stewardship. We call on global biodiversity data managers to collaborate in building an open, ethical, and inclusive living data infrastructure that recognizes the value of both scientific and traditional knowledge in reshaping the future of food.

Session: 6799392**7016063**

24/10/25 | 11:10

Room: Valle

LIGHTNING TALK VIRTUAL • EN

Multi case study analysis of justice considerations in biodiversity genomics projects.

Presenter

Bob Kreiken

Authors

Bob Kreiken (Delft University of Technology • Netherlands)

Abstract

The large-scale production and utilization of genomic DSI as part of the Earth Biogenome Project has unprecedented scientific and bioeconomic benefits. To assess its known and unknown consequences, the Earth Biogenome Project community uses the ethical, legal and social issues (ELSI) method. However, the ELSI approach does not fully capture the distributive, procedural and recognitional dimensions of environmental justice that are invoked by biodiversity genomics. Particularly, how scientists relate to each other and other stakeholders is not well understood at regional and national levels, where ultimately the Earth Biogenome Project relies on. The incorporation of data justice helps to understand the justice considerations in genomic DSI generation, access, use and sharing. Building on a multi case study analysis of affiliated projects of the Earth Biogenome Project, this oral presentation discusses how projects each encounter and deal with different justice considerations, ranging from the fair recognition of contributors, species selection to biotechnological data use. The research highlights that we should think of genomic DSI and samples as culturally, politically and historically situated resources, particularly when DSI is abstracted in global databases, and opens up the conversation about more just sequencing and studying of Nature.

Session: 6799392**7020587**

24/10/25 | 11:15

Room: Valle

LIGHTNING TALK • EN

Everywhere everyone everything all at once: Integrating data infrastructures and analysis workflows for the upscaling to global genetic monitoring

Presenter**Jutta Buschbom****Authors****Jutta Buschbom** (Statistical Genetics • Germany)**Sharif Islam** (Naturalis Biodiversity Center • Netherlands)**Eva Häffner** (Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin • Germany)**Alexandra Pavlova** (Wildlife Genetic Management Hub, School of Biological Sciences, Monash University • Australia)**Abstract**

Effective decision-making on biodiversity restoration would greatly benefit from baseline data on intraspecific genetic diversity, its integration across species for each location, and efficient systems for monitoring changes of genetic diversity in response to dynamic environments and human management.

This requires large sets of well-curated information-rich FAIR and CARE Digital Objects, implemented as Digital Extended Specimens (DES) that are representing digitized field samples, their derived genomic data and associated information. These use-case driven sets of structured (meta)data from many providers need to be merged, modified and further extended on demand. Existing workflows and work environments have to be redesigned to accelerate this process and achieve seamless integration, and thus scale to the needs of efficient and effective worldwide monitoring under the UN Global Biodiversity Framework. Arising future digital ecosystems will need to be foremost flexible, requiring low investments by users, and be able to quickly integrate inter- to transdisciplinary data as well as existing powerful platforms and well-tested analytical pipelines and functionality.

Taking a practical, pragmatic approach, we are proposing a lightweight, general linking element that would allow existing platforms and tools to be connected easily. This approach would enable users to take advantage of the core strengths of existing products and the expertise of their associated communities, while quickly sharing data and their work between specialized solutions. At the same time, data would be FAIRified and CAREd-for, promoting attribution, transparency and responsibility. The linking element and transformation of data to FAIR digital objects with governance information are prerequisites for a transition to machine-actionable operations that are accelerating the different steps in a workflow.

The objectives of our initial use case are to analyze three basic measures of population-genetic diversity based on genome-wide sequencing data as a first step towards operationalizing genetic monitoring at scale.

Session: 6799392

7020771

24/10/25 | 11:20

Room: Valle

ORAL • EN

Microbes as Ecosystem Sensors

Presenter

Maria M. Zambrano

Authors

Maria M. Zambrano (Corporación Corpogen • Colombia)

Martha Lorena Medina (Corporación Corpogen • Colombia)

Abstract

The massive amount of digital sequence information on microbial genomic, functional, and taxonomic diversity worldwide reveals that microbes serve as sensors of change and are unique, given their capacity to connect environments and ecosystems and enable the flow of organisms, properties, and genes. The generation, access, and use of metagenomic and microbial sequence data provide a window of opportunity for monitoring biodiversity and understanding the impact of microbial life on human, environmental, and animal health.

However, technological and financial barriers compromise the implementation of modern technologies, especially in lower-income countries, hindering the capacity to leverage digital data for capacity building and decision-making processes. Ongoing efforts focused on microbial surveys across diverse ecosystems aim to enhance local capacity to provide and harness digital data as a critical element for understanding microbial life, its impact on the environment, and its effect at both local and global scales.

Session: 6799392**7006840**

24/10/25 | 11:30

Room: Valle

ORAL • EN

Mobilizing large scale metabarcoding datasets in Neotropical systems

Presenter

Jonathan Ready

Authors

Jonathan Ready (UFPA • Brazil)

Marcia Anjos (UFPA • Brazil)

Fabricio Rosa (UFPA • Brazil)

Alan Rodrigues (UFPA • Brazil)

Cintia Carvalho (UFPA • Brazil)

João Braúllio Sales (UFPA • Brazil)

Silvana Melo Sviggum (UiO • Norway)

Quentin Mauvisseau (UiO • Norway)

Hugo de Boer (UiO • Norway)

Abstract

In order to massively accelerate the production of occurrence data for many species and understand ecological associations and interactions large datasets were produced for many sample types across different habitats (water filters, spider webs, bulk insect traps, gut contents) using markers that target either vertebrates (12S) or general biodiversity (COI) combined with deep sequencing. Spider webs and gut contents of generalist predators/detritivores proved very effective at recovering diversity, recovering many of the same species as environmental samples or targeted sampling while also generating useful information on ecological interactions. While many sequences cannot currently be identified to species level, many can, and species of interest for conservation (both threatened and invasive species) or health risks were identified confirming the effectiveness of this genomic method for both general biodiversity and OneHealth surveillance.

Mobilizing this data into GBIF using the new metabarcoding toolkit has helped to visualize the outputs, guarantee the long term use of the data, future revision of taxonomic identities, and make the data accessible for effective future management.

Session: 6799392**7020600**

24/10/25 | 11:40

Room: Valle

ORAL • EN

Towards Scalable and Comparable Genome Analysis for Biodiversity Monitoring

Presenter

Camila Mazzoni

Authors

Camila Mazzoni (Leibniz Institute for Zoo and Wildlife Research • Germany)

Abstract

The transformative potential of genome-wide Digital Sequence Information (DSI) for biodiversity monitoring hinges on the ability to generate and integrate high-quality, standardized data among populations across diverse regions and diverse taxa within regions and ecosystems.

Yet, inconsistencies in sampling design, metadata, and analytical workflows often undermine comparability and scalability, especially in under-resourced contexts. Reference genomes are the basis for comparability at the species level, enabling consistent interpretation of genome data across studies, ecosystems, and geographical boundaries. Establishing shared standards for their production is therefore essential to support distributed and equitable genomic monitoring efforts that are responsive to global conservation challenges.

This presentation builds on the work of the genome stream of the Biodiversity Genomics Europe project and is further inspired by related initiatives under the Earth BioGenome Project (EBP) umbrella, including contributions from both European and South American consortia. It proposes a roadmap for harmonizing genomic practices—spanning sample collection, metadata structuring, laboratory protocols, and bioinformatics—in a distributed and inclusive way. Emphasis is placed on operationalizing FAIR (Findable, Accessible, Interoperable, Reusable) data principles and ensuring inclusive participation in DSI generation and use.

By focusing on reference genome production as a foundational layer—and its broad use as the anchor for population-based genomic datasets—we can enhance interoperability across genetic monitoring frameworks, strengthen DSI infrastructures, and foster actionable insights for biodiversity policy and practice.

Session

6960773-7

Symposium

24/10/25 | 10:45

Room: Cauca

Ecological Analysis & Modeling (Contributed Oral Presentations)

Organizers

Andre Zerger

Alice Hughes

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-7**7020396**

24/10/25 | 10:45

Room: Cauca

ORAL • EN

Effects of urbanization on frugivory Interaction Networks Between Birds and Plants in the Llanos Foothills, Villavicencio -- Meta

Presenter

Andrea Morales Rozo

Authors

Andrea Morales Rozo (Grupo de Investigación ECOTONOS, Universidad de los Llanos • Colombia)**Leidy Tatiana Gomez Pardo** (Grupo de Investigación ECOTONOS, Universidad de los Llanos • Colombia)**Juan Luis Parra Vergara** (Grupo de Investigación Ecología y Evolución de Vertebrados, Universidad de Antioquia • Colombia)**Luz Stella Suarez Suarez** (Grupo de investigación Biorioquia, Universidad de los Llanos • Colombia)**Juan Fernando Acevedo Quintero** (Grupo de investigación Ecología de Bosques Andinos Colombianos, Universidad Pedagógica y Tecnológica de Colombia • Colombia)

Abstract

Ecosystems are shaped by interactions between plants and animals, which can be studied through network analysis by quantifying structural properties and assessing species roles. This research evaluated how the structure of frugivory interaction networks changes in areas with varying degrees of urbanization, and the influence of functional traits on these networks in the city of Villavicencio. To this end, focal observations of fruiting plants were conducted between September 2021 and March 2022. The degree of urbanization was determined based on the percentage of built-up area, and the structure of the frugivory interaction networks was described using measures of modularity, nestedness, and centrality. Urbanization is hypothesised to act as a strong filter favoring generalist species and leading to networks with no modules and few central species. The influence of urbanization on nestedness and modularity was assessed using linear models, while generalized linear models were employed to evaluate the relationship between centrality and functional traits. The results showed that the structure of the networks was both nested and modular, composed predominantly of generalist species. Birds were characterized small, highly abundant, and with generalist feeding habits, typically consuming pioneer plants with rapid growth and prolonged fruiting periods. No significant relationship was found between the degree of urbanization and the structural metrics of the networks. However, significant relationships were observed between centrality and abundance in birds, and between centrality, abundance, and fruit type in plants. Even though effects of urbanization on network structure are not evident, effects on species and its roles are.

Continuous monitoring of the effects of urbanization on the structuring of these networks is recommended.

Session: **6960773-7****7020569**

24/10/25 | 10:55

Room: Cauca

ORAL • EN

Estimating the geographic distribution of the Queen Conch, *Aliger gigas* (Linnaeus, 1758), under different scenarios of climate change

Presenter

Daniel Rojas Ariza

Authors

Daniel Rojas Ariza (University of Kansas Biodiversity Institute • United States)

Claudia Nuñez-Penichet (Department of Fish and Wildlife Conservation, Virginia Tech • United States)

Abstract

The queen conch is a key native species of the Caribbean Sea and a primary source of income for thousands of fishers. Historically, it has been a highly valuable resource for the fishing sectors of countries like the Bahamas, Turks and Caicos, Honduras, and Nicaragua. Due to its high economic value, the species has been overfished across the region, and combined with limited larval dispersal, low recruitment, and poor population connectivity, its numbers have declined drastically. The queen conch is now classified as a threatened species. Despite this status, the potential impacts of climate factors on its distribution are not yet fully understood, posing a challenge to conservation efforts. To address this, it is essential to investigate the species' potential future distribution under projected climate conditions. Here, we integrate and leverage diverse types of information from multiple datasets encompassing occurrence records, climate data and marine habitats satellite data to develop ecological niche models estimating present and future distribution patterns of the queen conch under different climate change scenarios. Preliminary projections indicate major loss of suitable areas for *Aliger gigas* along the northern Atlantic coast of South America, the Lesser Antilles, and the coast of Central America. Under moderate to extreme climate change scenarios, the entire northern coast of South America is predicted to become unsuitable within 40 years. Conversely, a major proportion of present and future suitable areas are projected to persist or expand in the Bahama Banks, Cuba and Florida, regions that host some of the largest seagrass beds in the Caribbean, which are highly important for juvenile conch survival. Overall, results predict a northward shift in the species' range over the coming decades, with the extent of this shift depending on the severity of climate change impacts.

Session: 6960773-7

7014596

24/10/25 | 11:05

Room: Cauca

ORAL • EN

Characterizing landscape configuration effects on eastern spruce budworm infestation dynamics

Presenter

Tommaso Trotto

Authors

Tommaso Trotto (The University of British Columbia • Canada)

Nicholas Charles Coops (The University of British Columbia • Canada)

Alexis Achim (Université Laval • Canada)

Sarah Elizabeth Gergel (The University of British Columbia • Canada)

Dominik Roeser (The University of British Columbia • Canada)

Abstract

In North America, insect disturbances on forested lands are becoming more severe due to rapid climatic changes, posing increasing threats to forest biodiversity and resilience. Therefore, understanding the risk of outbreaks at the landscape level is a key priority. While host species abundance is a known driver of infestations, less is known about how the spatial organization of host species across the landscape affects infestation outcomes. To

explore this, we present a data integration approach that combines multi-temporal earth observation data from Landsat with forest inventory information to model spruce budworm (*Choristoneura fumiferana*, Clem) infestation risk across boreal Quebec, Canada. Our workflow bridges the gap between Landsat observations and biodiversity assessments that can inform forest managers, conservation planning, and spatially-targeted mitigation strategies. Using 13 years of Landsat data, we tessellated the landscape into 400 m grid cells and calculated configuration metrics capturing conifer patch area, shape, and aggregation. These metrics were combined with infestation reports from the forest inventories to train annual and time-integrated random forest models of infestation risk. Our findings revealed that landscapes with greater fragmentation of conifer stands were at a higher risk of severe infestations. In particular, we found that landscapes with smaller, irregularly-shaped, and more isolated conifer stands of more variable area increased the risk of infestations. This may be due to the spruce budworm's capacity for long-range dispersal and rapid saturation of suitable landscapes. Our findings underscore the power of integrating Landsat observations and inventory data, as well as advances our capacity to detect and model landscape-level

disturbance dynamics, with applications for biodiversity conservation in the face of expanding forest insect outbreaks. By operationalizing long-term Landsat data in forest health assessments, our work contributes to more informed, proactive decision-making across policy, research, and forest management sectors.

Session: **6960773-7****7013334**

24/10/25 | 11:15

Room: Cauca

LIGHTNING TALK • EN

Understanding Ecosystem Connectivity through Integrated Monitoring along a Forest--River--Wetland--Estuary--Marine Continuum in Hokkaido, Japan

Presenter

Masahiro Nakaoka

Authors**Masahiro Nakaoka** (Akkeshi Marine Station, Hokkaido University • Japan)**Tomonori Isada** (Akkeshi Marine Station, Field Science Center for Northern Biosphere, Hokkaido University • Japan)**Ippei Suzuki** (Akkeshi Marine Station, Field Science Center for Northern Biosphere, Hokkaido University • Japan)**Karibu Fukuzawa** (Nakagawa Experimental Forest, Field Science Center for Northern Biosphere, Hokkaido University • Japan)**Kouji Nakayama** (Faculty of Agriculture, Kyoto University • Japan)**Manqing Zhang** (Field Science Education and Research Center, Kyoto University • Japan)**Yoriko Sugiyama** (Hokkaido Forest Research Station, Field Science Education and Research Center, Kyoto University • Japan)**Kazuya Kobayashi** (Hokkaido Forest Research Station, Field Science Education and Research Center, Kyoto University • Japan)**Abstract**

Broad-scale studies on ecosystem connectivity are essential to understand how environmental changes – both natural and human-induced – in one ecosystem can cascade into adjacent systems via the lateral transport of materials and the movement of organisms. Simultaneous monitoring of terrestrial, freshwater, and marine ecosystems is crucial for this understanding, but it requires close collaboration among researchers across disciplines. Connectivity is particularly important in estuarine and coastal systems influenced by freshwater input, while freshwater ecosystems can also be shaped by marine-derived materials transported by fish and birds.

Eastern Hokkaido, Japan, still harbors relatively pristine ecosystems across land and sea, offering an ideal natural laboratory to study ecosystem connectivity with minimal anthropogenic disturbance. In the Bekanbeushi River watershed, we have been conducting long-term, concurrent observations of biodiversity and ecosystem dynamics across forest, freshwater, and marine environments. These efforts are part of a joint education and research program between Hokkaido University and Kyoto University, titled “The Forests-Rural-Sea Linkage Study.”

During this intensive field course, students explore biodiversity and ecosystem functions in forests, grasslands, rivers, estuaries, and coastal waters, focusing on their ecological linkages. For example, fish biodiversity comparisons between rivers in agricultural vs. forested areas reveal the impact of land use on freshwater ecosystems. Similarly, marine biodiversity surveys across salinity gradients in the brackish Akkeshi-ko estuary highlight the influence of freshwater input on coastal biodiversity.

Long-term data collected for >15 years indicate relatively stable ecosystem conditions, although recent increases in temperature and extreme precipitation events suggest that climate change may soon drive substantial shifts. Our next step is to make these monitoring data openly available and to apply them to local ecosystem management and biodiversity conservation practices.

Session: **6960773-7****7016057**

24/10/25 | 11:20

Room: Cauca

ORAL • EN

Multimodal survey reveals bio-regionality across the new Hermandad Marine Reserve

Presenter

Diana Pazmiño

Authors

Diana Pazmiño (Galapagos Science Center, Universidad San Francisco de Quito and University of North Carolina at Chapel Hill • Ecuador)

Corbin Jones (University of North Carolina at Chapel Hill • United States)

Diego Urquía (Department of Biology, University of North Carolina at Chapel Hill • United States)

Daniel Velasco (Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito USFQ • Ecuador)

Daniel Armijos (Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito USFQ • Ecuador)

Isabela Estrada (Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito USFQ • Ecuador)

María Antonia Izurieta (Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito USFQ • Ecuador)

María de Lourdes Torres (Laboratorio de Biotecnología Vegetal, Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito USFQ • Ecuador)

Susana Cárdenas (Instituto de Ecología Aplicada, Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito USFQ • Ecuador)

Alex R. Hearn (Galapagos Science Center, Universidad San Francisco de Quito and University of North Carolina at Chapel Hill • Ecuador)

Abstract

The Hermandad Marine Reserve (HMR), created in 2022, is a 60,000 km² pelagic Marine Protected Area that extends from the northeastern part of the Galápagos Marine Reserve to the maritime border with Costa Rica. It includes a core no-take zone (30,000 km²) and two strips at the edge of the no-take zone (30,000 km²), where longline is not permitted, and is key to protect endangered migratory species. Understanding spatial patterns of marine biodiversity in this area is important to advance our understanding of biogeography, but it is also crucial for assessing the impacts of the Reserve, and guiding conservation efforts. Here, we combined environmental DNA (eDNA) and Baited Remote Underwater Video Stations (BRUVS) to characterize biodiversity patterns across the HMR, with a focus on pelagic fauna communities. Fifteen locations across the HMR, and three additional seamount locations outside the Reserve were monitored during a research cruise in March 2024. By combining analyses of videos from BRUVS and eDNA data from the 12S and 16S fragments, we were able to detect a total of 96 species (BRUVS n=30; eDNA n=74), including ascidians, mammals, reptiles, birds, teleost and elasmobranchs. Both methods show significant differences in pelagic species composition between the West and Central-East regions of the HMR. Furthermore, BRUVS show different composition and high diversity in two locations outside of the HMR (Paramount and Darwin), highlighting the relevance of seamounts for pelagic fauna. This study provides the first characterization of pelagic biodiversity of the HMR, and the baseline for long-term monitoring efforts. Additionally, it demonstrates the sensitivity of the methods used, capable of detecting a range of species, from abundant commercially important fish to elusive highly endangered mammals and elasmobranchs that are present in this biological corridor.

Session: 6960773-7**7002102**

24/10/25 | 11:30

Room: Cauca

ORAL • EN

Enhancing transferability of species distribution models -- guidance through algorithm, variable, and ensemble modelling decisions

Presenter

Yu Hin Yau

Authors

Yu Hin Yau (The University of Hong Kong • China)

Alice Hughes (The University of Hong Kong • China)

Timothy Bonebrake (The University of Hong Kong • China)

Abstract

Species distribution models (SDMs) are useful tools to estimate species' distributions in unsampled, novel environments (e.g., future climates). However, data available often fail to represent the full range of viable environments due to various reasons, including sampling biases, biogeographic barriers and the availability of potentially suitable habitats. Therefore, many SDMs are likely based on truncated niche spaces and will have to extrapolate in unsampled environments, ultimately over- or under-estimating species' distributions, especially under climate change.

We generated four occurrence datasets for 1,567 species, deliberately truncating the input data by subsampling four different latitudinal ranges. These datasets were used to explore the consequences of niche truncation on SDM transferability (ability to accurately extrapolate in unsampled conditions) by comparing these truncated ranges with species distributions generated from the complete dataset. We also tested the ability of various algorithms, the use of various thresholds or variable selection to counteract truncated data on model accuracy.

Niche truncation resulted in 42% increase in mean SDM inaccuracy when 22% areas were unsampled. SDMs tend to overpredict species distributions when extrapolating in unsampled environments, distorting our estimation of climate change response and invasion risk. We suggest using a set of SDM algorithms tailored for modelling goals when extrapolating SDMs. We also recommend an inclusive approach in variable selection when ecological knowledge is insufficient to precisely identify the most relevant variables. Moreover, the choice of ensemble algorithms significantly impacts SDM transferability, which means that variation in predictions resulting from different methods should be clearly reported. While niche truncation is best dealt with using data more representative of species' full range of viable environments, decisions related to algorithm, variable and ensemble choices can improve model transferability.

Session: **6960773-7****7020849**

24/10/25 | 11:40

Room: Cauca

ORAL • EN

From Pixels to Parks: Upscaling Clustered SDMs Enables a Novel Correction for Sample Bias

Presenter

Noah Wightman

Authors

Noah Wightman (McGill University • Canada)

Laura Pollock (McGill University • Canada)

Brian Leung (McGill University • Canada)

Abstract

Species distribution models (SDMs) are widely used for ecological inference and conservation applications. However, sampling bias and spatial scaling challenges can both hinder the predictive accuracy of SDMs. Firstly, sampling bias arises because biodiversity data tend to be more abundant in certain environments (ie. citizen science data is concentrated near cities), and SDM predictions often reflect this bias rather than species ecology. Standard bias-correction methods are not always successful, so creative, data-driven solutions need to be explored. Secondly, it is often valuable to examine distributions and biodiversity patterns at both fine and coarse spatial grains, but there are pitfalls when converting SDM predictions to different spatial scales. Distributions can be “clustered” by drivers like unmeasured environmental variation, biotic interactions, and dispersal, which are not captured by standard SDMs. Nearby SDM predictions are therefore *not independent probabilities*, so it’s difficult to re-calculate predictions at different scales robustly. These two challenges intersect when we try to integrate data at multiple spatial scales to correct for sampling bias, for example by using national park species checklists as presence-absence data. Here, we propose a model which tackles both challenges simultaneously. We use a “clustering parameter” to adjust SDM predictions appropriately at coarser grains, then use the coarse-grained checklist data to adjust for sample bias. We test our model using simulations which vary both the amount of clustering and the amount of sample bias. Our model successfully distinguished error caused by clustering from error caused by sampling bias. It was able to integrate coarse-scale park checklist data to produce unbiased SDMs which outperformed standard methods. We further use these simulations to demonstrate that clustering is linked to beta- diversity and species-area curves. In conclusion, this method provides a framework for translating SDM predictions to different spatial scales, allowing us to integrate diverse data sources robustly.

Session: **6960773-7****7020982**

24/10/25 | 11:50

Room: Cauca

ORAL VIRTUAL • EN

Investigating the link between phylogenetic diversity and dilution effect through the invasion ecology of mosquito species *Culex pipiens* (Diptera: Culicidae)

Presenter

Michaela Seal

Authors

Michaela Seal (University of Calgary • Canada)

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Andrei Vasile (University of Calgary • Canada)

Alexandra Coker (City of Calgary • Canada)

John Soghigian (University of Calgary • Canada)

Abstract

The dilution effect hypothesizes that an increase in biodiversity can reduce the abundance of parasites per host, overall reducing the risk of disease. In the context of vector-borne pathogen transmission, the presence of diverse host species that are inefficient reservoirs regulate the levels of the pathogen in a system. However, there have been mixed findings of the dilution effect in literature. Recent studies suggest phylogenetic diversity may mediate the strength of the dilution effect. The complexity of the dilution effect may be untangled by examining the evolutionary identities of the species comprising a community rather than the absolute diversity. The recent arrival of invasive mosquito species *Culex pipiens* in Alberta, a Canadian prairie province, is an opportunity to study the unexplored interaction between phylogenetic diversity and vector-borne pathogen prevalence in a system with changing vector diversity and abundance.

Culex pipiens is a globally widespread invasive mosquito species well adapted to urban environments that is considered among the most important vectors of West Nile virus (WNV) and avian malaria in North America, as well as California serogroup viruses (CSGV) which are of growing concern under climate change. The objective of my study is to address the knowledge gap of the relationship between vector-borne pathogens and phylogenetic diversity by investigating the vector ecology of *Cx. pipiens* in central Alberta to understand if the species poses an increased risk of disease transmission. I will assess the diversity of native and invasive mosquitoes and present preliminary results of pathogen detection for WNV, avian malaria, and CSGV and their relationship to mosquito and avian host diversity across sites.

The findings of my research will guide local preventative measures in response to *Cx. pipiens* and will have broader implications for building resilience and competence in response to future invasive mosquito introductions in Canada.

Session: **6960773-7****7009952**

24/10/25 | 12:00

Room: Cauca

ORAL • ES

Vacíos en el conocimiento digital de la flora mesoamericana

Presenter

Angela P. Cuervo-Robayo

Authors

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Santiago Ramírez-Barahona (Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México • Mexico)

Susana Magallón (Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México • Mexico)

Abstract

La disponibilidad digital de datos sobre plantas vasculares ha cambiado la investigación botánica y la conservación, pero su utilidad depende de la calidad y cobertura de la información. Para evaluar las limitaciones actuales, analizamos 3 578 777 registros de presencia correspondientes a 32 522 especies de plantas vasculares distribuidas en Mesoamérica, combinando los nombres taxonómicos estandarizados por el *World Checklist of Vascular Plants* de Kew con los datos públicos de GBIF. Medimos tres dimensiones de los datos —espacial, filogenética y temporal— y cartografiamos su distribución espacial.

Los resultados revelan una cobertura deficiente y heterogénea. Primero, la caracterización de la diversidad de especies es incompleta: numerosas gradillas carecen de registros recientes o presentan escaso número de especies respecto al total esperado. Segundo, los registros provienen principalmente de colectas anteriores a 1980, lo que limita la detección del efecto de las dinámicas actuales de la biodiversidad frente al cambio global. Tercero, la representación filogenética es baja, con linajes enteros poco muestreados, dificultando estudios macroevolutivos y de biogeografía histórica.

Al superponer las tres dimensiones, se identificaron “puntos calientes” de brechas de información que abarcan aproximadamente un tercio de la región, mientras que menos del 15 % de Mesoamérica cuenta con cobertura adecuada en los tres ejes. Estas carencias comprometen la robustez de los análisis de filogeografía espacial, la modelación de distribuciones de especies y la priorización de áreas de conservación basada en presencias digitales.

Las zonas detectadas constituyen oportunidades prioritarias para invertir en digitación de colecciones, expediciones botánicas focalizadas, secuenciación de referencia y programas de monitoreo. Reforzar y actualizar estos componentes incrementará la representatividad taxonómica, geográfica y temporal de los datos disponibles, potenciando investigaciones futuras y la planificación de la conservación de la flora mesoamericana en el corto y mediano plazo.

Session: 6960773-7

7021004

24/10/25 | 12:10

Room: Cauca

ORAL • ES

Índice de Singapur sobre la Biodiversidad de las Ciudades - Evaluación para Bogotá, D. C. - Colombia-

Presenter

Sara Lucía Colmenares Trejos

Authors

Iván Darío Melo Cuéllar (Secretaría Distrital de Ambiente • Colombia)
Sara Lucía Colmenares-Trejos (Secretaría Distrital de Ambiente • Colombia)
Juliana Rodríguez Ortiz (Secretaría Distrital de Ambiente • Colombia)

Abstract

El conocimiento profundo de la biodiversidad urbana depende de datos confiables, continuos y comparables. El Índice de Singapur sobre la Biodiversidad de las Ciudades (CBI), se basa precisamente en este principio: traducir información ecológica, institucional y social en indicadores medibles que permitan conocer el estado de conservación y orientar decisiones de política pública. Para Bogotá D. C., la aplicación de este índice ha representado un ejercicio estratégico de sistematización y análisis de datos obtenidos mediante monitoreo estandarizado de la biodiversidad urbana, protocolos técnicos y reportes institucionales.

Durante su primera evaluación, realizada por la Secretaría Distrital de Ambiente para el año 2023, Bogotá obtuvo 81 de 112 puntos posibles. El componente de gobernanza fue el mejor calificado, con 45 de 56 puntos, gracias a políticas públicas formuladas y en implementación, participación ciudadana, educación ambiental y colaboración interinstitucional, sin embargo, se evidencian vacíos en la valoración económica de la biodiversidad y retos en la asignación presupuestal.

En biodiversidad nativa, con 24 de 36 puntos, destacan indicadores que reflejan aumentos en especies de plantas y artrópodos nativos, así como avances en restauración ecológica; estos resultados se sustentan en monitoreos periódicos y bases de datos organizadas por grupos biológicos. Persisten retos en conectividad ecológica y en seguimiento de aves endémicas. En servicios ecosistémicos, con 12 de 20 puntos, la regulación hídrica y climática obtuvo puntuaciones bajas, revelando la necesidad de integrar mejor los datos sobre funcionalidad ecológica.

Los resultados del índice no solo son una radiografía del estado actual de la biodiversidad urbana, sino también una oportunidad para fortalecer sistemas de información ambiental y garantizar que los datos guíen la gestión adaptativa. La consolidación de bases de datos abiertas, integradas y periódicas es clave para avanzar hacia una ciudad más verde, resiliente al clima y que se gestiona basada en evidencia científica.

Session: 6960773-7**7031433**

24/10/25 | 12:20

Room: Cauca

ORAL VIRTUAL • EN

Accelerating Actions on Ecosystem Restoration to Achieve Target 2 of the Kunming-Montreal Global Biodiversity Framework

Presenter

Adelola Temitope

Authors

Carmen Morales (FAO • Spain)

Adelola Temitope (FAO • Nigeria)

Abstract

To support the UN Decade on Ecosystem Restoration and Target 2 of the Kunming-Montreal Global Biodiversity Framework, a resource guide, developed by FAO, SER, CBD, and CIFOR-ICRAF, was launched at CBD COP16 in 2024. The guide, 'Delivering restoration outcomes for biodiversity and human well-being', provides CBD Parties and stakeholders a detailed look into the key components and intended outcomes of Target 2 and resources to assess opportunities, plan, implement, monitor and report ecosystem restoration. The resource guide features case studies from pilot countries. In 2025, FAO started to work with pilot countries to help them develop capacity in planning, monitoring and reporting restoration. As the first milestone of the pilot work, four national consultations were delivered in 2025 in Brazil, Peru, Kenya and Philippines to understand these countries' capacities and gaps in restoration target setting, monitoring and reporting. Various stakeholders participated in the national dialogues and engaged in discussions covering a wide range of topics related to Target 2. As the country pilot work evolves, FAO and CBD have partnered with subregional technical support centres to organize workshops and training of trainers sessions to support more countries. FAO is also promoting the restoration approaches of Indigenous Peoples, recognizing their vital role in achieving restoration goals. The FAO Indigenous Peoples Unit, in collaboration with Indigenous Peoples' organizations, launched the Indigenous Peoples Biocentric Restoration Initiative. Led by Indigenous Peoples, this initiative centers Indigenous Peoples' knowledge and cosmogony and promotes the restoration of ecosystems through the strengthening of their food and knowledge systems. Success stories, progress, and lessons learned in aligning national and sub-national ecosystem restoration efforts with Target 2 will be shared in this session. These reflections will contribute to scaling up ecosystem restoration and support the implementation of the KM-GBF Target 2.

Session: 6960773-7

7020554

24/10/25 | 12:30

Room: Cauca

ORAL • ES

Datos geográficos, filogenias y provincias biogeográficas Neárticas: Un análisis biogeográfico cladístico integrativo

Presenter
Willie Corona

Authors
Willie Corona (Universidad Nacional Autónoma de México | Facultad de Ciencias | Grupo de biogeografía de la conservación • Mexico)
Tania Escalante (Universidad Nacional Autónoma de México | Facultad de Ciencias | Grupo de biogeografía de la conservación • Mexico)

Abstract
Las plataformas de datos espaciales abiertos de biodiversidad constituyen una herramienta fundamental en biogeografía. Al integrar información espacial de especies con sus filogenias, es posible proponer relaciones de áreas que pueden ser usadas en la conservación. Existe incertidumbre sobre las relaciones entre las provincias biogeográficas que conforman la región Neártica, así como de su monofilia. Para contrastar la hipótesis de la monofilia de 29 provincias, analizamos mediante biogeografía cladística, algunos grupos monofiléticos de mamíferos y plantas con distribución norteamericana. En total seleccionamos 11 filogenias: cinco de mamíferos *Lepus*, *Microtus*, *Mephitidae*, *Sylvilagus* y *Vulpes*, dos de angiospermas de los géneros *Cypripedium* y *Fraxinus* y cuatro gimnospermas de los géneros *Abies*, *Juniperus*, *Picea* y *Pinus*. La información espacial de las especies fue descargada mediante portales de datos abiertos como GBIF, Data Basin, IUCN, entre otras. Los areagramas fueron contruidos al sustituir el nombre de las especies en las filogenias por las provincias en las que se distribuyen. A partir de un Análisis de Parsimonia de Brooks, se obtuvieron tres areagramas generales igualmente parsimoniosos, por lo que se aplicó un consenso estricto. Un clado fue reconocido tanto al centro-norte como al centro-oeste y sur de Norteamérica, el clado hermano se ubicó al centro-este. La provincia hermana de los dos clados anteriores fue Texas, seguida de la provincia Comanche, hermana de los clados previos. Finalmente, el grupo hermano de los anteriores clados se ubicó tanto al norte como al noroeste. Las provincias neárticas no fueron monofiléticas, ya que la provincia de Chihuahua se relaciona más con el Neotrópico. Tampoco se reconoció monofilia en las siguientes escalas de regionalización biogeográfica. Estos resultados sugieren que es importante considerar las relaciones evolutivas de las provincias recuperadas con estos grupos para proponer nuevos esquemas de regionalización biogeográfica, así como de estrategias de conservación que permitan mantener procesos biogeográficos.

Session

6796507-2

Symposium

24/10/25 | 14:00

Room: Ballroom A

Unlocking Biodiversity data Potential in Latin America: Tools and Practices of Data Integration (Part 2)

Organizers

Marius Bottin

Ricardo Segovia

Juan Manuel Saez Hidalgo

Description

Biodiversity data holds immense potential for addressing critical environmental challenges, but its true power lies in integration. Combining disparate datasets across various sources enables us to uncover complex ecological patterns, monitor species distributions, and inform conservation strategies. Networking among specialists developing biodiversity data integration strategies is therefore essential to harness regionally diverse ecosystems through common and innovative data management approaches.

This session invites Latin American researchers, data managers, and developers to showcase their work on biodiversity data integration, facilitating the sharing of experiences and advancements for establishing concrete regional collaboration agendas. We aim to foster a dynamic exchange of perspectives on current approaches, best practices, open-source application development, and remaining challenges. Presentations are encouraged to address:

- Developments of open source tools applications and tools for the integration of data, which facilitate data sharing and interoperability
- Dataflows using existing tools to integrate or promote the use of large datasets
- Research studies using various data types or various datasets

Session: 6796507-2

7020227

24/10/25 | 14:00

Room: Ballroom A

ORAL • ES

Biodiversidad urbana en México y riesgos conjuntos por cambio climático, efectos de isla de calor y expansión urbana

Presenter

Julian A. Velasco

Authors

Julian A. Velasco (Instituto de Ciencias de la Atmósfera y Cambio Climático, Universidad Nacional Autónoma de México • Mexico)

Constantino González-Salazar (Mexico)

Abstract

Las ciudades concentran altas densidades humanas y un alto consumo energético per cápita, lo que genera impactos en la biodiversidad y los ecosistemas. Sin embargo, también pueden funcionar como reservorios de biodiversidad. En países de altos ingresos se conocen bien los factores ecológicos, evolutivos y socioeconómicos que configuran la biodiversidad urbana, lo que permite diseñar estrategias de planificación para su conservación. En contraste, en ciudades latinoamericanas se desconocen los factores que determinan los patrones de biodiversidad y cómo interactúan con estresores como el cambio climático, la isla de calor urbana y el cambio de uso de suelo. En este estudio se actualizó una base de datos integrando información de diferentes sectores incluyendo biodiversidad, socioeconómica, isla de calor, cambio climático para más de 350 ciudades mexicanas con el fin de entender: 1) el efecto de la escala en la jerarquía de factores socioambientales que determinan la biodiversidad de vertebrados terrestres, y 2) cómo clasificar las ciudades según su exposición a estresores antrópicos para priorizar acciones de conservación. Los resultados muestran que la escala es el principal factor que determina la riqueza de especies, modulando el efecto de variables como el tamaño de áreas protegidas urbanas, número de ecorregiones y PIB. Las ciudades del noreste de México podrían estar en mayor riesgo por la combinación de estresores, por lo que deben ser priorizadas.

Estos hallazgos permiten orientar políticas de planificación urbana que ayuden a frenar la pérdida de biodiversidad ante la expansión futura de las ciudades.

Session: 6796507-2

7023698

24/10/25 | 14:11

Room: Ballroom A

ORAL VIRTUAL • EN

A Novel Trait-Based Avian Response Index of Ecosystem Integrity for Neotropical Forests: Toward Scalable, Actionable Biodiversity Monitoring

Presenter

Jeremy Dickens

Authors

Jeremy Dickens (Center for Development Research (ZEF) • Germany)

Alexander Lees (Manchester Metropolitan University • United Kingdom)

Yadvinder Malhi (School of Geography, Oxford University Centre for the Environment • United Kingdom)

Christian Borgemeister (Germany)

Jan Henning Sommer (Germany)

Abstract

Monitoring ecosystem integrity at local scales remains a major challenge, particularly in tropical forests, where biodiversity is high, data are sparse, and anthropogenic pressures are intensifying. Existing indicators often underrepresent animal communities and below-canopy ecological processes, limiting their effectiveness—especially in degraded or secondary habitats.

To address this, we present a novel metric—provisionally termed the **Avian Trait-Response Index of Ecosystem State (AviRIES)**—that translates biodiversity data into an indicator of ecological integrity across Neotropical moist forest landscapes by leveraging established relationships between species traits (e.g., habitat affinities, foraging behaviour, life history, and morphology) and their responses to ecosystem stressors. Using a structured approach, we assigned scores to all regional bird species based on their responses to both direct (e.g., degradation, conversion) and indirect (e.g., isolation, habitat area) stressors. These scores are aggregated into site-level metrics, providing a rapid, scalable, and accessible means of ecosystem assessment with actionable insights.

Species scores align with observed population trends and extinction risks, enabling early identification of at-risk species and supporting proactive conservation planning. Field applications across Amazonian land-use gradients demonstrated the index's sensitivity to both ecological degradation and recovery, with strong correlations to established forest health indicators. Notably, its divergence from metrics such as carbon balance highlight its complementary value in capturing overlooked dimensions of biodiversity and ecosystem functioning. Applications across biogeographic regions, survey methods, seasons, and repeated samples confirm the index's robustness and generalizability.

By converting biodiversity observations into standardized, trait-informed indicators, AviRIES facilitates data integration, enhances interoperability across monitoring systems, and supports open data sharing. It offers a practical tool for tracking conservation and restoration progress, making it a strong candidate for inclusion in global frameworks such as the **Global Biodiversity Framework** and the **Sustainable Development Goals**.

Session: 6796507-2**7014433**

24/10/25 | 14:23

Room: Ballroom A

ORAL • ES

Datos integrados revelan retrocesos desde elevaciones bajas en aves con distribución restringida a lo largo de los Andes septentrionales

Presenter

Wilderson Medina

Authors

Wilderson Medina (Tropical Mountains Research Foundation • Colombia)

Ryan Huang (University of Pretoria • United States)

Stuart Pimm (Duke University • United States)

Abstract

Estudios locales en los trópicos han demostrado cambios en la distribución altitudinal de aves en respuesta al aumento de la temperatura. Sin embargo, no se sabe si estos cambios suceden a nivel regional para especies de rango restringido. Este grupo de especies es particularmente vulnerable a eventos climáticos extremos y a la deforestación, los cuales se han acentuado en las últimas décadas en los Andes septentrionales. Se usaron datos de ciencia ciudadana tomados de eBird y GBIF para documentar la distribución de aproximadamente 200 de estas especies. Se analizó si estos datos pueden dar indicios de los cambios de su distribución altitudinal con el tiempo al comparar la presencia observada y la esperada en umbrales de los extremos de la elevación durante dos periodos: antes y después de 2005. Se esperó una cantidad menor de observaciones por debajo del umbral mínimo y una mayor cantidad por encima del umbral máximo. También se analizaron los efectos de la deforestación en elevaciones más bajas dentro de los rangos de distribución de las especies y se comparó la pérdida relativa de bosque con la prevalencia entre datos observados y esperados en todo el rango altitudinal. En las elevaciones más bajas los retrocesos de las especies fueron ubicuos e involucraron una reducción del 23 al 40% de prevalencia de observaciones. En las elevaciones más altas los incrementos de prevalencia no fueron uniformes. Los retrocesos ocurrieron a lo largo de un espectro amplio de especies, desde las que predominan en las tierras bajas hasta las que predominan en las tierras altas. Ya que la deforestación no se relacionó con el retroceso, se asume que un clima más cálido es la explicación más parsimoniosa para estos cambios. Es de suma importancia monitorear la adaptación de estas especies vulnerables frente a los nuevos retos ambientales.

Session: 6796507-2**7020173**

24/10/25 | 14:35

Room: Ballroom A

ORAL VIRTUAL • ES

PhenChile: avances del sistema de monitoreo fenológico nacional

Presenter

Roberto Chávez

Authors

Roberto Chávez (Pontificia Universidad Católica de Valparaíso • Chile)

Diego Valencia (Conaf • Chile)

Ignacio Díaz-Hormazábal (Conaf • Chile)

Jorge Herreros (Ministerio de Medio Ambiente • Chile)

Jose Lastra (Wageningen University and Research Centre • Netherlands)

Javiera Aguayo (Chile)

Pablo Stuardo (Pontificia Universidad Católica de Valparaíso • Chile)

Sebastián Bruna (Pontificia Universidad Católica de Valparaíso • Chile)

Marcela Riquelme-Solar (Chile)

Francisca Díaz (Chile)

Abstract

El monitoreo de la fenología foliar mediante teledetección es una de las maneras más sencillas y eficientes de detectar y evaluar geográficamente los efectos del cambio climático en la vegetación. Por esta razón, GEO-BON ha incluido la fenología como una de las Variables Esenciales para el monitoreo de la Biodiversidad. Cambios en los ciclos fenológicos anuales pueden modificar patrones biogeográficos a gran escala que afectan la biodiversidad, el crecimiento de los bosques, la dinámica de plagas, la agricultura y la disponibilidad de alimentos. Por esta razón existen diversas iniciativas nacionales e internacionales para desarrollar sistemas operacionales de monitoreo fenológico basados en imágenes satelitales, así como redes de observación terrestre con cámaras time-lapse o "Phenocams". En Chile, un país con 4.000 kilómetros de extensión, una alianza entre la Pontificia Universidad Católica de Valparaíso, el Servicio Nacional Forestal Conaf y el Ministerio del Medio Ambiente han desarrollado un sistema de monitoreo fenológico y de detección de disturbios extremos. La plataforma web se basa en índices de vegetación obtenidos mediante teledetección y un flexible algoritmo probabilístico no paramétrico (el paquete R `npphen`) capaz de reconstruir cualquier tipo de fenología anual utilizando datos satelitales y cuantificar su variación interanual mediante percentiles de la distribución de frecuencias de referencia (RFD). Las anomalías fenológicas negativas con $RFD > 0,95$ activan una "alerta roja" que se muestra en la aplicación web tan pronto como los datos satelitales están disponibles. Además, se está construyendo una red Phenocam que capturan fotos RGB cada 30 minutos las que son transmitidas por red 4G o internet satelital al servidor central. En este trabajo, presentamos la aplicación web lanzada en 2024, junto con avances recientes y un análisis de oportunidades y desafíos futuros.

Session: 6796507-2**7015609**

24/10/25 | 14:48

Room: Ballroom A

ORAL • EN

A FAIR tool for assessing the environmental impact of energy transition policies

Presenter

Maite Irazabal

Authors

Julio López Paneque (LifeWatch ERIC • Spain)

Ana Mellado (LifeWatch ERIC • Spain)

Abstract

Unlocking the potential of integrated data sources is essential to understanding and mitigating the environmental impacts of the global energy transition. As countries accelerate their shift to renewable energy, the integration of biodiversity and environmental issues into energy policy becomes increasingly important. This presentation introduces a prototype tool developed under the EULAC ENERGYTRAN project, co-designed by European and Latin American research infrastructures and centers, to support evidence-based policymaking through data integration and workflow-based analytics.

The tool enables users to compute and analyze a set of environmental indicators related to energy transition by integrating diverse open data sources (OLADE and Eurostat) from Latin America, the Caribbean, and Europe. Following the FAIR (Findable, Accessible, Interoperable, Reusable) principles, it promotes transparent, reproducible, and cross-domain research. Embedded within a LifeWatch ERIC Virtual Research Environment, the tool supports the onboarding and composability of scientific workflows, allowing users to replicate and adapt analyses across contexts. By connecting regionally distributed data, the tool provides a practical example of how integrated data systems could inform sustainability assessments and guide policy decisions.

Session

6798998-2

Symposium

24/10/25 | 14:00

Room: Ballroom B1

Sampling with intention: optimizing strategies for monitoring biodiversity (Part 2)

Organizers

Laura Pollock

Katherine Hebert

David Rolnick

Tanya Berger-Wolf

Description

Biodiversity is changing, but the nature and cause of these changes remains an open question for the majority of taxa on the planet. Knowing how biodiversity is changing, how species are responding to threats, and how we monitor requires data. The core of the Global Biodiversity Framework is a monitoring framework that converts a variety of datastreams into indicators of progress towards biodiversity targets. The ideal version of this—intentionally designed, well-funded structured surveys and frequent optimised monitoring—is rarely possible. But the vast streams of incoming data from satellites, UAVs, camera traps, acoustic records, eDNA, telemetry, and community science are already building a dynamic evidence base. The question is how to make these datastreams maximally effective to capture biodiversity and its changes. In this session, we will bring together scientists and conservation practitioners to showcase the cutting-edge science on AI and adaptive sample optimization, examples of successful approaches in management and practice, and perspectives on how to incentivise users to collect biodiversity data where we need it most. We will mix theory and practice to highlight actionable ways to build effective biodiversity data streams in different ecosystems, to ensure we are well-equipped to bend the curve of biodiversity loss.

Session: 6798998-2**7014625**

24/10/25 | 14:00

Room: Ballroom B1

ORAL • EN

Contextualizing biodiversity data gaps in conservation decisions to inform targeted monitoring

Presenter

Melissa Chapman

Authors

Melissa Chapman (ETH Zurich • Switzerland)

Abstract

Biodiversity data is notably sparse, with well-documented disparities across space and time that reflect not only taxonomic preferences and accessibility of different places, but also socioeconomic inequities. However, assessment and discussion of these data gaps are rarely contextualized in the specific conservation actions that data might support or inform – actions that often happen within highly constrained decision spaces. For example, opportunities to expand protected areas to meet GBF target 3 are largely limited to currently unprotected, undeveloped, and otherwise suitable land and ocean areas. Restoration efforts are similarly limited to degraded landscapes or seascapes and are subject to numerous socioeconomic constraints. Decisions concerning managing invasive species or protecting species of particular conservation concern might rely on just a subset of taxon-specific data.

In this talk, I show how data disparities within decision spaces reflect and refract global data disparities, providing insight into how biases may be more relevant to certain subsets of conservation applications. I argue that situating data gaps within their decision-making context is essential for targeting monitoring investments where data offer the highest value of information and for evaluating model performance and improving downstream conservation planning tools.

Session: 6798998-2**7012266**

24/10/25 | 14:10

Room: Ballroom B1

ORAL • EN

Optimizing sampling to detect species range shifts

Presenter

Michael Catchen

Authors

Michael Catchen (Université de Montréal • Canada)**Timothée Poisot** (Université de Montréal • Canada)

Abstract

As climate and land-use change drive shifts in species distributions, identifying where and how ranges are changing is critical for informed conservation planning and environmental management. However, the vast spatial extent of most species ranges makes comprehensive sampling infeasible. Effective monitoring of range shifts therefore requires prioritizing sampling locations that are most likely to provide as much information on the state of current species' ranges as possible. Monitoring range shifts presents several unique challenges that should shape survey design: (1) Species absence records are often rare, but necessary for the most effective prediction of range boundaries, meaning absences are typically more valuable than presence data (2) The temporal resolution of records matters—recent observations are far more valuable for detecting current range limits than older ones; and (3) Species distribution models (SDMs) built from sparse data benefit from careful consideration of sampling density in environmental as well as geographic space. This is complicated by the fact that the density of points in environmental space is itself shifting under global change, potentially resulting in unique combinations of environments that do not exist in the present. This talk will focus on how we can use simulation to generate virtual species with realistic distributions undergoing range shifts to benchmark methods for optimal range monitoring for biodiversity conservation.

Session: 6798998-2

7014487

24/10/25 | 14:20

Room: Ballroom B1

LIGHTNING TALK • EN

ForestWeb3- Mobilising, harmonising and incentivising forest biodiversity and environmental monitoring data through Web 3.0 technology

Presenter

Robert Lewis

Authors

Robert Lewis (Norwegian Institute for Nature Research • Norway)

Jonas Lembrechts (University of Antwerp • Belgium)

Sigrid Engen (Norwegian Institute for Nature Research • Norway)

Chunli Li (University of Bergen • Norway)

Peter Walker (Stockholm Environment Institute • Estonia)

Abstract

In an era of converging ecological crises and digital innovation, ForestWeb3 introduces a decentralized, Web3 fundamental approach to biodiversity monitoring that integrates long-tail biodiversity data and microclimate sensing, with converging IoT sensor technologies, blockchain-based data governance framed within a lens of novel financial incentive mechanisms. The overarching legacy goal of ForestWeb3 is to foster trans-national opportunities for forest biodiversity stewardship and monitoring, one that is decoupled from extant dependencies upon basic science funding and one which introduces new actors committed to safeguard biodiversity and protect nature.

Here in this session, we introduce actionable pathways for mobilizing new actors in biodiversity and environmental monitoring by aligning technological infrastructure with emerging regenerative-finance (ReFi) principles. ForestWeb3's WP2 lays the foundation for systems in which contributors, such as private forest landowners, can be rewarded for verifiable ecological data through nature-backed digital asset schemes.

At the core of this approach is the convergence of affordable, modular IoT sensing devices and decentralized Web3 architectures. These modular IoT sensor units autonomously collect and transmit high-frequency environmental data, such as temperature, humidity, and light, directly into tamper-evident digital records. Deployed as part of a Decentralized Physical Infrastructure Network (DePIN), they enable distributed actors to contribute born-digital ecological data at scale, with minimal configuration or technical expertise.

By reducing the barriers to participation and embedding trust, transparency and control (fundamental properties of decentralized technologies) directly into the data pipeline, ForestWeb3 opens up biodiversity and microclimate monitoring to a broader set of contributors. Through this, ForestWeb3 supports a shift toward dynamic, incentive-aligned data ecosystems, capable of powering next-generation indicators, feeding into global biodiversity frameworks, and enabling new forms of ecological stewardship rooted in transparency and distributed value creation.

Session: 6798998-2**7020821**

24/10/25 | 14:25

Room: Ballroom B1

LIGHTNING TALK • EN

Uncertainty-driven sampling priorities: Mapping where new iNaturalist observations matter most for California vascular plants

Presenter

Avery Hill

Authors

Avery Hill (California Academy of Sciences • United States)

Rebecca Johnson (California Academy of Sciences • United States)

Abstract

Volunteer-collected biodiversity data, like those from iNaturalist, are increasingly recognized for their utility in ecosystem monitoring and biogeographical research efforts. Species Distribution Modeling (SDM) is a popular method to wield these expansive and expanding data while mitigating some of the biases inherent to volunteer-collected data. The vast majority of iNaturalist data is sampled opportunistically by users and—with the exception of targeted data collection campaigns—users often make observations of charismatic species at convenient locations, which can be redundant in the context of SDM. Therefore, there is a large opportunity to provide accessible, data-driven estimates of localities and taxa where observations would be more impactful for myriad research and conservation questions. Here we demonstrate a unique approach to produce sampling-prioritization maps by calculating and mapping the uncertainty of habitat suitability predictions from SDMs, which has been shown possible using MaxEnt bootstrapping and analytical methods. With California vascular land plants as our case study, we trained MaxEnt models for a diversity of species and calculated the variance of habitat suitability predictions for each grid cell in California. The species-level maps of SDM prediction variance indicate ‘hotspots’ for sampling prioritization, which are stacked across species to produce cumulative priority areas. We then compared these maps to California land ownership classes and OpenStreetMap trails data and identified areas that are both sampling priorities and accessible. Altogether, this work helps guide targeted iNaturalist data collection efforts for users and potential campaign organizers and is an important step towards collecting more meaningful biodiversity data with the one of the largest communities of participatory scientists in the world.

Session: 6798998-2**7020911**

24/10/25 | 14:30

Room: Ballroom B1

LIGHTNING TALK • EN

Optimizing sampling and monitoring of species interactions within Biodiversity Observation Networks

Presenter

Gabriel Dansereau

Authors

Gabriel Dansereau (Université de Montréal • Canada)

Abstract

Optimal monitoring strategies should be designed to efficiently monitor all essential facets of biodiversity. Yet, species interactions are often overlooked in monitoring designs compared to spatial coverage and species richness, partly due to the inherent difficulty of sampling and monitoring interactions compared to species distributions. Here, we used simulations to test the efficiency of monitoring species interactions and species richness within Biodiversity Observations Networks (BONs). We tested several methods for designing and optimizing BONs to monitor species interactions and examined efficiency when increasing the number of monitored sites. We showed that the required sampling effort is considerably higher for interactions, especially when considering that interaction realization and detection realistically depend on species abundance. Thus, expectations to monitor a relevant proportion of interactions within a BON should be lower than expectations to monitor its species. However, from a single-species perspective, optimizing monitoring designs based on a known species range proved an efficient strategy to retrieve its interactions, outperforming designs based on total species or interaction richness. Only optimizations based on detailed knowledge of where realized interactions occurred allowed better performance, which likely represents an unrealistic level of information to attain. Among the algorithms tested, Uncertainty Sampling was the most efficient at optimizing BON design on species information. Therefore, our results offer insights into defining realistic expectations for interaction monitoring. With the right target and optimization strategy, available information, such as species ranges, can guide observation network designs to monitor species interactions with a reasonable number of sites.

Session

6798502-3

Symposium

24/10/25 | 14:00

Room: Ballroom B2

Scaling AI For and Across Biodiversity: Data Collection and Curation in AI-Driven Biodiversity Research

Organizers

Sanson Poon

Arianna Salili-James

Ben Scott

Rukaya Johaadien

Michal Torma

Nicky Nicolson

Kit Lewers

Wouter Koch

David R. Williamson

Description

Artificial Intelligence (AI) is revolutionising the way biodiversity data are managed, studied, and preserved, offering groundbreaking possibilities for research, curation, conservation, policy-making and public engagement. Digital representations of organisms are central in biodiversity data collection, curation and use. It is these representations, rather than the physical organisms themselves, that are increasingly the basis for research. Digital representations allow the use of machine learning, AI, and computer vision to measure the physical properties of organisms and to classify them taxonomically and phenologically, on an unprecedented scale.

While AI-driven innovations are emerging across institutions and disciplines, a critical question remains: how can these advancements be successfully embedded and scaled to maximise impact? This session explores cutting-edge AI applications, from large-scale digitisation and automated species identification to advanced data management and predictive analytics. We will examine strategies for integrating AI across institutional frameworks, addressing challenges in adoption, collaboration, and sustainability. We welcome talks investigating the complexities of maintaining these services in the long term, addressing the financial burdens of API access and the rapid evolution of AI models and services that can quickly render solutions obsolete. By tracing the AI journey within our organisations, we aim to define best practices that unlock its full potential, as well as to understand what others are working on, and what we can learn from other domains. Finally, we are also interested in topics including:

- Novel data collection and analysis techniques or novel uses of established ones
- Data collection, digitization, standardization and curation for future applications
- Practical implications of AI use on data quality, interpretability, and legal aspects

Session: 6798502-3

7020879

24/10/25 | 14:05

Room: Ballroom B2

ORAL • EN

AI-assisted exploration, curation, and extension of biodiversity data using iChatBio

Presenter

Michael Elliott

Authors

Michael Elliott (ACIS Lab, University of Florida • United States)

Manuel Luciano (ACIS Lab, University of Florida • United States)

José Fortes (ACIS Lab, University of Florida • United States)

Abstract

The development of large language models that can interact with their environment through function-calling mechanisms has led to the development of agentic systems – artificial intelligence (AI) systems that can understand natural language requests, coordinate one or more function-calling AI agents to full those requests, then report the outcome of their efforts in natural language. As research tools, agentic systems have the potential to transform how researchers interact with scientific data. Such systems allow users to express what information they need (e.g., “What collections contain specimens of *Cattleya trianae*?”) without specifying where or how to find it, offloading these labor-intensive tasks to AI agents.

General-purpose agentic systems can struggle to make effective use of scientific data and retrieval tools due to lacking domain expertise. iChatBio (<https://ichatbio.org>) is an agentic system specially designed to assist biodiversity researchers with discovering, processing, and analyzing biodiversity-related information. This presentation will discuss how iChatBio approaches the following use cases:

- **Exploration:** includes finding, retrieving, summarizing, and comparing biodiversity data from diverse sources across the Internet
- **Curation:** includes filtering unwanted records from datasets, fixing spelling and formatting errors, combining duplicate records into one, and inferring missing field values from related fields
- **Extension:** includes linking specimen records to related records, genetic data, literature, and more, to form extended specimen records

Each use case above involves the orchestration of several specialized agents. Each specialized agent provides iChatBio with additional capabilities, such as retrieving data from a specific data provider (via an online Application Programming Interface (API)), processing occurrence records, or extracting information from images. Through such agents, iChatBio currently supports interactions with iDigBio (<https://idigbio.org>), GBIF (<https://gbif.org>), iNaturalist and BHL (<https://biodiversitylibrary.org>), among other resources, with more agents being added regularly. New agents can also be contributed by members of the community using the iChatBio Software Development Kit (iChatBio SDK).

Session: 6798502-3**7018530**

24/10/25 | 14:15

Room: Ballroom B2**ORAL VIRTUAL • EN**

KIEBIDS: a modular framework for scalable information extraction from written records in natural history collections

Presenter

Christian Bölling

Authors

Christian Bölling (Museum für Naturkunde Berlin – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany • Germany)**Théo Leger** (Museum für Naturkunde Berlin – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany • Germany)**Joachim Snellings** (Museum für Naturkunde Berlin – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany • Germany)**Margot Belot** (Museum für Naturkunde Berlin – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany • Germany)**Franziska Schuster** (Museum für Naturkunde Berlin – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany • Germany)

Abstract

Written records in the context of natural history collections, such as object labels, accession catalogs, or expedition and travel reports, represent an outstanding data source due to their content and historical depth. The data that can be derived from this material for historical periods, such as information on the taxonomic treatment of objects and the occurrence and habitats of biological species, are of essential importance for biodiversity research.

To date, this data remains largely inaccessible for computational knowledge engineering approaches, as manually processing the sources and converting the information into structured, interoperable data formats is a labor-intensive challenge due to the volume, heterogeneity complexity of the documents – conditions under which curatorial resources are generally insufficient. Artificial Intelligence (AI) based methodologies can significantly accelerate the process and make it economically scalable.

We present KIEBIDS, a framework for implementing and executing AI-based application workflows for information extraction from written records in natural history collections. The framework is based on the principles of adaptability and modularity for individual workflows.

Workflows are implemented as a sequence of five functional steps: (i) preprocessing of document images, (ii) layout analysis to segment images into relevant regions such as text blocks and lines, (iii) syntax-level text recognition, (iv) semantic parsing to detect categories of entities (e.g., taxonomic names, persons, places), and (v) entity disambiguation and linking, in which recognized entities are identified by linking them to authority records.

The extracted data is made available in PAGE-XML format for downstream use. The modular structure with standardized interfaces between functional modules allows each step of the information extraction process to be adapted to varying input data, information retrieval goals and updated implementations of functions (e.g., through a newly trained model or an external application accessed via application programming interfaces (APIs), supporting scalable deployment and efficient maintainability.

Session: 6798502-3**7013541**

24/10/25 | 14:20

Room: Ballroom B2**LIGHTNING TALK • EN**

Biodiversity datasets as linked open data for research and conservation

Presenter

El-Amine Mimouni

Authors**El-Amine Mimouni** (Quebec Center for Biodiversity Science | Department of Biological sciences, McGill University | Biodiversité Québec • Canada)**Guillaume Larocque** (Quebec Centre for Biodiversity Science | Department of Biological sciences, McGill University | Biodiversité Québec • Canada)**Vincent Beauregard** (Biodiversité Québec | Département de Sciences biologiques, Université de Sherbrooke • Canada)**Fanie Pelletier** (Quebec Centre for Biodiversity Science | Département de Sciences biologiques, Université de Sherbrooke • Canada)**Dominique Gravel** (Biodiversité Québec | Département de Sciences biologiques, Université de Sherbrooke • Canada)**Andrew Gonzalez** (Quebec Centre for Biodiversity Science | Department of Biological sciences, McGill University • Canada)**Abstract**

Biodiversity data are inherently complex, spanning multiple spatial and temporal scales, sampling methodologies, and data types. Despite progress in data generation capacities and storage, much of this information remains siloed and difficult to integrate due to a lack of standardization across disciplines, making integration and reuse a challenge.

To address this issue, we are developing a semantic web platform that publishes and connects biodiversity data as linked open data, enabling their integration, discovery, and reuse across research domains. Our approach builds on established community standards, namely Darwin Core and Ecological Metadata Language (EML), to structure and semantically annotate biodiversity data.

These annotations are expressed using Resource Description Framework (RDF) and aligned with ontologies from both biodiversity informatics and the broader semantic web, enabling datasets to be interlinked and queried while preserving sampling context and supporting provenance tracking, promoting transparent reuse, proper attribution, and seamless integration with global biodiversity aggregators therefore respecting FAIR principles.

We are piloting this system with Québec-based biodiversity datasets, using open-source tools and academic researcher-driven governance. This pilot demonstrates how semantic technologies can enable “living ecological data”: datasets that are not only open, but richly described, semantically connected, and capable of supporting long-term, cross-disciplinary ecological research. By exposing data to AI models through semantic descriptions, this approach also helps bridge the gap between ecological data and predictive analytics.

Session: 6798502-3**7017172**

24/10/25 | 14:30

Room: Ballroom B2**LIGHTNING TALK VIRTUAL • EN**

ChatGPT as a Semantic Engineering Assistant: Lessons from Ontology Design in the Agricultural Biodiversity Domain

Presenter

Filipi Miranda Soares

Authors

Filipi Miranda Soares (University of Sao Paulo • Brazil)

Antonio Mauro Saraiva (University of Twente • Brazil)

Luís Ferreira Pires (University of Sao Paulo • Netherlands)

Debora Pignatari Drucker (University of Twente • Brazil)

Kelly Rosa Braghetto (Embrapa Agricultura Digital • Brazil)

Luiz Olavo Bonino da Silva Santos (University of Sao Paulo • Netherlands)

Dilvan de Abreu Moreira (University of Twente • Brazil)

Fernando Elias Corrêa (University of Sao Paulo • Brazil)

Alexandre Cláudio Botazzo Delbem (University of Sao Paulo • Brazil)

Abstract

Modeling species names in biodiversity ontologies is particularly challenging in multilingual contexts, where semantic conflation often occurs. A notable example is the term *Pimenta*. In Brazilian Portuguese, it refers to *Capsicum* sp. (chili peppers), while its direct translation (pepper) to English often denotes *Piper nigrum* (black pepper). Resources like AGROVOC and Agrotermos mistakenly equate *Pimenta* and “pepper,” reinforcing taxonomic confusion by treating them as multilingual equivalents despite botanical differences. This illustrates the broader challenge of preventing semantic drift in cross-cultural agricultural vocabularies.

In developing the Agricultural Product Types Ontology (APTO), which incorporates terms from AGROVOC and Agrotermos, we used generative AI — specifically ChatGPT-4 — as a semantic engineering assistant. We tested two approaches: (1) prompt-based queries with a browser plugin accessing the GBIF API, and (2) a ChatGPT-generated Python script for converting GBIF taxonomy data into OWL format.

These AI-supported methods automated the construction of APTO’s “Organism” module, integrating taxonomic hierarchies and synonyms (Soares et al., 2025a). ChatGPT effectively identified mismatched synonyms — e.g., outdated Agrotermos terms versus current GBIF labels

— and reduced manual labor in ontology development. However, concerns about scalability, reproducibility, and hallucinations persist, highlighting the need for expert oversight.

This case study shows how generative AI can support — but not replace — human-led ontology development. It also emphasizes AI’s potential role in biodiversity informatics, particularly for managing evolving, multilingual taxonomies. All tools and source code are available via Zenodo (Soares et al., 2025b).

Session: 6798502-3**7020029**

24/10/25 | 14:35

Room: Ballroom B2**LIGHTNING TALK • EN**

Using Galaxy-Ecology as a sustainable Biodiversity common virtual research environment: Focus on integration, access and automation of AI algorithms

Presenter

Yvan Le Bras

Authors

Yvan Le Bras (MNHN Data Terra PNDB Biodiversity Data Hub UAR 2047 DoHNÉE • France)

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Nicolas Buisine (MNHN Data Terra PNDB Biodiversity Data Hub UAR 2047 DoHNÉE • France)

Jian-Sheng Sun (MNHN Data Terra PNDB Biodiversity Data Hub • France)

Arthur Barreau (Université Rennes 1 MNHN UMR ISYEB • France)

Nadine Le Bris (Sorbonne Université • France)

Björn Grüning (Freiburg university • Germany)

Abstract

Galaxy platform is a web solution originally developed 16 years ago to facilitate high performance computing access and computational workflows creation by life science researchers. During last 10 years, evolutions of the Galaxy platform made it notably possible 1/ to attain high degree of FAIRness for a computational point of view thanks to conda, containers orientations, 2/ to create Galaxy training network and related infrastructure, 3/ to address needs of new communities as “Climate”, “Ecology” and more recently “Earth Science” 4/ to propose innovative ways of integrating synchronous and asynchronous scientific workflows and 5/ to integrate state of the art approaches notably on modeling and artificial intelligence domains.

From genetics to satellite remote sensing data passing through occurrences as environmental data, Galaxy-Ecology provides functionalities to access data files and peer reviewed scripts to visualize and analyze it. Capitalizing on Galaxy solution and already administrated sustainable facilities allows us to provide access to such functionalities without need of dedicated funding and reproducible reanalysis through established workflow.

We here want to illustrate relevance of this strategy particularly on scaling AI for and across Biodiversity.

Session: 6798502-3**7020886**

24/10/25 | 14:40

Room: Ballroom B2**LIGHTNING TALK VIRTUAL • EN**

Hybrid scenarios for identification, or how to combine deep learning and symbolic AI

Presenter

Régine Vignes Lebbe

Authors

Régine Vignes Lebbe (France)

Bouquin Sylvain (Sorbonne Université • France)

Conruyt Noel (Université de La Réunion • Réunion)

Abstract

The identification of biological specimens is a task for which computer aided methods have been proposed since the beginning of the computerisation of taxonomic data in the 1970s. The construction of keys, whether static or dynamic, is part of the family of symbolic AI methods based on a symbolic, textual representation of knowledge in the form of logical rules. The keys are decision tree.

Computer-aided identification using decision trees is increasingly being replaced by automatic identification (e.g. Pl@ntnet, Birdnet) via the application of statistical AI such as deep neural networks.

Hybrid statistical and symbolic AI methods make it possible to combine the performance of the first one with the explicability of the latter. We describe several hybrid scenarios combining image-based deep learning and symbolic decision trees and we classify these scenarios into three categories.

- In the first category, statistical AI is essentially used to accelerate identification in reducing and focusing the knowledge base of the decision tree.
- In the second category, the AI image acts as an agent verifying the answers given by the decision tree. In case of inconsistency, the user is prompted for verification, or the key displays new explanations and illustrations.
- In the third category, statistical AI and symbolic AI interact, or even alternate, to advance identification: the symbolic AI chooses the classification models that are best able to discriminate the remaining taxa with deep learning ; then the application of these classification models provides new values to advance the decision tree.

These scenarios are being studied in a number of different applications, including coral identification using underwater monitoring videos, wild bee identification using a combination of wing images and morphological characteristics, and the search for herbarium specimens closest to an illustration.

Session

6960773-10

Symposium

24/10/25 | 14:00

Room: Tolima

Collection Management & Digitization (Contributed Oral Presentations)

Organizers

Marie Grosjean

David Fichtmueller

Description

Contributed oral sessions provide an essential platform for presenting innovative research that advances the field of biodiversity informatics while addressing emerging challenges at the intersection of data science, conservation, and policy. These sessions accommodate presentations that align with the broader themes of the Living Data conference but do not fit within the scope of pre-organized symposia.

The Academic Committee has organized contributed submissions into thematic sessions to foster focused discussion and knowledge exchange among researchers working on related topics. Each thematic session brings together diverse perspectives and methodologies, creating opportunities for cross-pollination of ideas and collaborative problem-solving. While space for contributed oral presentations is limited due to the robust program of organized sessions, these presentations represent cutting-edge work that contributes significantly to our collective understanding of biodiversity data mobilization, management, and application.

We encourage active participation and engagement during these sessions, as they showcase the breadth and dynamism of the global biodiversity informatics community.

Session: 6960773-10**7020649**

24/10/25 | 14:00

Room: Tolima

ORAL • EN

Tools and skills for digitising herbaria

Presenter

Elspeth Haston

Authors

Elspeth Haston (Royal Botanic Garden Edinburgh • United Kingdom)

Abstract

The drive to digitise natural science collections has created a need for the development of digitisation tools as well as the upskilling of existing staff in the use of digital technologies. Digitisation programmes may use existing software and equipment which may be sourced from other communities and disciplines, sometimes requiring modifications and additional documentation. In other cases, new equipment or software requirements have been identified. Where this results in the development of custom-designed tools their accessibility and sustainability need to be considered.

Digitising natural history collections involves a number of complex processes and tasks which can be integrated into pipelines, often incorporating both human, automated and AI workflows. The changing roles of collection staff to include digitisation is resulting in the urgent need to upskill existing staff as well as provide resources to support the training of new staff, students and volunteers. This may include fundamental training in data structure, standards and management, as well as specialist training in the use of custom-designed equipment and software.

This presentation looks at the tools and skills required for digitising herbaria and how these are being developed and maintained.

Session: 6960773-10**7019882**

24/10/25 | 14:10

Room: Tolima

ORAL • EN

Digitisation 101: RGB Kew's blueprint to getting 8.5 million plant and fungal specimens online

Presenter

Sidrah Ikram

Authors

Sidrah Ikram (Royal Botanical Gardens, Kew • United Kingdom)

Olivia Mitrovits (Royal Botanical Gardens, Kew • United Kingdom)

Sarah Cheseldine (Royal Botanical Gardens, Kew • United Kingdom)

Udayangani Liu (Royal Botanical Gardens, Kew • United Kingdom)

Robert Turner (Royal Botanical Gardens, Kew • United Kingdom)

Abstract

Royal Botanic Gardens, Kew has embarked on a four-year Digitisation Project to provide a science-based solution to address the pressing global challenges of biodiversity loss, climate change and food security. By making over 8.5 million plant and fungal specimens freely accessible by 2026, we aim to enhance scientific research and public understanding of these issues.

We present an overview of the processes we undertook and the difficulties we faced, so that it will help serve as a blueprint for other organisations planning to undertake similar initiatives. This includes the early stages of strategic planning, securing funding and procuring a supplier to help achieve this ambitious plan. Digitisation on a large scale has proven to be extremely complexed as there are numerous resources and workflows needed to digitise a specimen, including imaging, transcribing, quality assurance and data cleaning. Each workstream came with its own set of challenges and problems to overcome. Scientific institutions can often forget the importance of change management, stakeholder engagement and communications, all of which played a vital role in the success of our project.

We have developed a new Integrated Collections Management System (ICMS) to standardise our data across 12 distinct collections, as well as our newly digitised records. This aims to enhance collaboration between our curators, researchers and scientists. Additionally, we are building an open data portal, which will allow us to share our collection data to researchers, conservationists and policymakers around the world. By harnessing the power of data, we can strengthen our efforts for safeguarding the future of biodiversity for generations to come.

Large-scale digitisation is key to unlocking the wealth of information in our world. We hope that our experience and learnings will assist other Herbaria, Fungaria and research institutions in the preparation of their own digitisation efforts.

Session: 6960773-10**7020813**

24/10/25 | 14:20

Room: Tolima

ORAL • ES

Ideación, diseño e implementación de un sistema de gestión de datos de biodiversidad y su importancia para una organización

Presenter**Jorge Homero Márquez Taffo****Authors****Jorge Homero Márquez Taffo** (Cienciambiental • Chile)**Stephanie Orellana Bello** (Cienciambiental • Chile)**Soledad Kremer** (Cienciambiental • Chile)**Francisca Muñoz Narbona** (Cienciambiental • Chile)**Riva Quiroga** (Cienciambiental • Chile)**Marcela Torres-Gómez** (Cienciambiental • Chile)**Fabián San Martín** (Cienciambiental • Chile)**Sergio Moraga** (Cienciambiental • Chile)**Antonio Tironi** (Cienciambiental • Chile)**Alex Oporto** (Cienciambiental • Chile)**Abstract**

Las organizaciones y empresas que trabajan con datos de biodiversidad no suelen darle la importancia necesaria a su gestión. Conceptos como trazabilidad, orden, estándares, entre otros, si bien son conocidos, no siempre se aplican de manera sistemática en su tratamiento y análisis, lo que puede afectar tanto la calidad de estos como la de los productos derivados.

La implementación de un sistema de gestión de datos resulta crucial cuando comienzan a acumularse una gran cantidad de datos obtenidos en el desarrollo de estudios de campo, a lo largo del tiempo y el espacio geográfico, registros provenientes de diferentes componentes: flora, vegetación, criptógamas, fauna, entomofauna, biota acuática y calidad de agua. La situación es más compleja si estos derivan en distintos tipos de análisis y forman parte de documentos y planillas entregables, en diferentes formatos, a la autoridad y clientes.

En este trabajo se quiere exponer el complejo proceso de idear, diseñar e implementar un sistema de gestión de datos de biodiversidad dentro de una organización, así como las soluciones tecnológicas y procedimentales desarrolladas para abordar este desafío. El enfoque no solo considera el orden y tabulación de los datos, sino también la definición de criterios, la adopción de estándares y el aseguramiento de la trazabilidad a lo largo de todo el flujo de trabajo. Asimismo, se abordará el reto de resguardar la calidad de los datos, desde su colecta en terreno hasta su uso en los entregables finales, considerando que en este flujo participan distintas personas de la organización.

Este proceso, la implementación continua del sistema, junto con el uso de herramientas y procedimientos, han sido fundamentales para facilitar el tratamiento de los datos. Estos esfuerzos han permitido validar formularios, agilizar procesos, cumplir con estándares y protocolos, tanto internos como nacionales, y generar entregables automatizados y de alta calidad.

Session: 6960773-10**7020735**

24/10/25 | 14:30

Room: Tolima

ORAL • EN

Curating the coral record: bias, gaps and challenges of natural history collections datasets

Presenter

Catalina Merino

Authors

Catalina Merino (Museo Nacional de Historia Natural • Chile)

Nadiezhda Santodomingo (Natural History Museum • United Kingdom)

Kenneth G. Johnson (Natural History Museum • United Kingdom)

Abstract

Natural history collections (NHCs) are critical archives of global biodiversity, yet their scientific potential remains constrained by uneven digitization and systemic biases. Using stony corals (Scleractinia), a well-documented group of high ecological and conservation relevance, as a study model, we analysed 176,279 specimen records from the Global Biodiversity Information Facility (GBIF) to assess how effectively NHCs capture coral diversity and distribution patterns. Our findings reveal that specimen collection peaked in the 1970s (6,037 records per year) but has declined sharply since 2005, with recent biodiversity data increasingly reliant on observational records that often lack vouchered specimens. Although NHCs include 92% of known coral species, half of all records are concentrated in just 8.6% of taxa, and geographic coverage remains uneven, with significant underrepresentation in regions such as the South China Sea and northern Madagascar. Additionally, only 34% of institutions maintain over 90% completeness for collection dates and coordinates. However, a targeted analysis of the Natural History Museum, UK (NHMUK) demonstrates that many incomplete records contain sufficient metadata to support retrospective recovery, underscoring the transformative potential of curated digitization. Despite these limitations, NHCs offer substantial opportunities for enhancement through digitization tools, taxonomic reconciliation, and prioritized georeferencing, which can transform incomplete records into robust datasets for ecological research. Our study highlights the urgent need to revitalize physical collections, standardize digitization practices, and fully integrate NHCs into modern biodiversity data infrastructures to address critical gaps in marine conservation.

Session: 6960773-10**7012677**

24/10/25 | 14:40

Room: Tolima

ORAL • EN

Untangling attribution in biodiversity data records

Presenter

Arturo Ariño

Authors

Arturo Ariño (University of Navarra, BIOMA Institute for Biodiversity and Environment • Spain)**María Imas** (University of Navarra, BIOMA Institute for Biodiversity and Environmental Research • Spain)**Ana Amézcuca** (University of Navarra, BIOMA Institute for Biodiversity and Environmental Research • Spain)**Angel Chaves** (University of Navarra, BIOMA Institute for Biodiversity and Environmental Research • Spain)

Abstract

The exactness, fitness-for-purpose (FFP) and reliability of primary biodiversity data can be enhanced by additional data beyond the basic taxon-location-date triad. Often, the only available data source are the labels in legacy specimen collections. The time-consuming digitization process seems most efficient if all potentially available information can be collected at once with a single event of specimen handling, as opposed to separate events to capture different segments of data (e.g. taxon names, localities and dates, and later on additional data or images). There is, however, a delicate compromise between producing a faster catalogue for immediate use and housekeeping and an accurate, wider-FFP database where all data have been thoroughly checked.

Recognizing potential sources of error at digitization time and estimating the prevalence of such errors on created catalogues may inform digitization practices and help making choices. During a routine dataset integration procedure, the quality and reliability of the data capture of names of locations and researchers was analyzed in order to ensure correct attribution. The dataset consisted on transcribed label data of about 25K specimens from three targeted insect orders collected over six decades, and included about 2500 locations and 3600 distinct collector strings. But captured names, both of locations and collectors, could be (i) unidentified; (ii) misinterpreted from the handwriting; (iii) ambiguous, referring to more than one entity; (iv) duplicated under multiple spellings and transcriptions; or (v) misplaced or misattributed to another entity.

By using indexing and cross-referencing techniques and mining ancillary sources, the roster of names was more than halved but, by far, the most time-consuming task was positively identifying and disambiguating the actual collector for proper attribution. We will present a summary statistics of the types of errors found in the dataset and the solution options, that could be used as a reference for similar cleanups.

Session: 6960773-10**7020454**

24/10/25 | 14:50

Room: Tolima

ORAL • EN

Mobilising legacy georeferencing efforts

Presenter

Ashleigh Whittaker

Authors

Ashleigh Whittaker (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

Efforts to digitise our natural history collections have increased and improved over time, using high-volume workflows to produce accessible specimen records. Each record provides evidence that a species occurred at a point in space and time. However, there is variation in what data is recorded at the time of collection, for example locality information does not always include GPS coordinates.

The Royal Botanic Gardens, Kew will soon have a fully digitised herbarium and fungarium collection which will support research by providing freely accessible, standardised data to a wide user base. Post-digitisation, follow-on activities will enhance the digital specimen record, such as the addition of georeferencing data. Georeferencing extends beyond a record's taxonomic identification and collection event metadata to add a spatially mappable representation of the collection event, for Kew this typically includes coordinates and a measurement of error (Chapman and Wieczorek 2020).

Georeferencing has been categorised as an enhancement to a digital specimen record (MIDS Task Group 2025), however without the addition of georeferencing data some records are unusable. Analysis of spatial data underpins global conservation policy and action through outputs including species distribution models and IUCN Red List assessments, among many others (Tulloch et al. 2018).

With a newly digitised collection, Kew's legacy datasets from conservation assessment projects will be consolidated, standardised and incorporated to augment centrally managed specimen records. Georeferencing is a time-consuming and subjective process that is often inconsistent within, and between, institutions - limiting its usability. Unlocking this wealth of georeferenced data will facilitate a more efficient use of typically limited resources as well as reduce the duplication of georeferencing efforts.

This presentation will outline how we approached integrating longstanding georeferencing workflows with a newly digitised collection, alongside the knowledge gained from exploring approaches to georeferencing the entirety of Kew's collection.

Session

6798214

Symposium

24/10/25 | 14:00

Room: Caldas

Standards for all: Darwin Core in multiple languages

Organizers

Esteban Marentes Herrera**Paula Zermoglio****Ana Carolina Peralta****Camila Andrea Plata Corredor**

Description

The Darwin Core Standard (DwC) is the most widely used standard to share, use and reuse biodiversity data globally. Provides a glossary of terms, identifiers, labels and definitions, aimed at facilitating biodiversity data sharing. Unfortunately, most of its normative information and associated documents are still currently available only in English. This constitutes a barrier for wider use in non-English-speaking countries, because it adds an additional layer of complexity, and hinders participation.

The community has acknowledged this issue and there have been several initiatives to translate DwC materials. Previously, translations of term definitions were available and linked to the official Quick Reference Guide, but were disconnected as they were not part of the standard and were having trouble being up to date. Other initiatives have provided translations, such as Portuguese, Spanish, and a joint effort between GBIF and TDWG to manage translations for more than 12 languages, using the Crowdin platform.

This session will explore different translation initiatives that help local users learn, appropriate and use DwC. By showcasing experiences we will explore the possibility of creating a Task Group within TDWG to continue working on broadening DwC use based on diversifying available languages and managing translations in the long term.

Session: 6798214**7020284**

24/10/25 | 14:00

Room: Caldas

ORAL VIRTUAL • EN

Expanding Access: Reflections on the French Translation of Darwin Core

Presenter

Elie M. Saliba

Authors

Elie M. Saliba (Muséum National d'Histoire Naturelle • France)

Sophie Pamerlon (PatriNat (MNHN-OFB-CNRS-IRD) • France)

Matthew Blissett (GBIF Secretariat • Denmark)

Ben Norton (Independent • United States)

Abstract

The most widely adopted Biodiversity Information Standards (TDWG) vocabulary is the Darwin Core (DwC) standard (Darwin Core Maintenance Group, 2023). Accessibility to non-English-speaking communities is crucial to the standard's success, given its global reach and comprehensive scope. The objective is to promote equitable participation in biodiversity informatics by the broader internationalization initiatives of the TDWG. The initial comprehensive translation of the documentation was finalized and published in the French language in May 2025. The translation can be accessed at <https://dwc.tdwg.org/fr/>.

Darwin Core's maturity and extensive legacy use present translation challenges, in contrast to recently ratified standards (e.g., Latimer Core) that capitalize on the most recent infrastructures. During the translation process, tensions emerged between preserving the traditional meaning of long-used terms and modernizing the language to enhance clarity and inclusivity. This work prompted specific editorial and methodological inquiries:

- What is the appropriate approach to translating terms that are deprecated or have ambiguous definitions?
- How can linguistic precision be preserved without introducing inconsistencies with the current data implementations?
- What is the most effective method for integrating translated content into documentation workflows while simultaneously guaranteeing ongoing maintenance?

This talk will outline the methodology employed for the French translation of Darwin Core, encompassing strategies for addressing semantic problems and conforming to established standards. We will provide practical insights and recommendations for future translation initiatives to foster sustainable, multilingual documentation practices throughout TDWG.

Darwin Core Maintenance Group. 2023. Darwin Core List of Terms. Biodiversity Information Standards (TDWG).

Session: **6798214****7018533**

24/10/25 | 14:07

Room: Caldas

ORAL VIRTUAL • EN

Bridging Language Barriers: Lessons from the French Translation of Latimer Core

Presenter

Elie M. Saliba

Authors

Elie M. Saliba (Muséum National d'Histoire Naturelle • France)

Jutta Buschbom (Statistical Genetics • Germany)

Sharon D. Grant (Field Museum of Natural History • United States)

Janeen M. Jones (Field Museum of Natural History • United States)

Ben Norton (Independent • United States)

Maarten Trekels (Meise Botanic Garden • Belgium)

Sarah Vincent (Natural History Museum • United Kingdom)

Kate Webbink (Field Museum of Natural History • United States)

Abstract

Internationalization of standards documentation is essential to pursuing global interoperability through the adoption of data standards. Ratified in 2025, the Latimer Core (LtC) standard focuses on the representation and discovery of natural science collections (Woodburn et al. 2023). The first complete translation of the LtC standard documentation was completed in French, facilitating access to the standard for francophone communities.

The process of implementing the translations into an established workflow within the TDWG infrastructure raised several interesting linguistic questions and imposed several unanticipated technical challenges.

The linguistic questions, linked to the French language, include:

- How can labels that are inherently more verbose in French and other languages than in English be rendered without compromising the conciseness essential to technical vocabularies?
- How do we decide how many anglicisms are acceptable, and where to put the limits on language purism?

Examples of technical challenges, some of which remain a work in progress, include:

- How can we accurately document the process of translating a data standard from its beginning to its implementation?
- What constitutes a sufficient minimum for a functional translation? How much of the standard documentation needs translation?
- How can terminological consistency be maintained across standards, a factor all the more important given the ever-increasing number of inter-standard bridges being created?

These questions and challenges underscore the inherent complexity of translating technical standards, a task that extends beyond linguistic equivalence. The overarching lesson is that translations should be perceived as a collaborative endeavor that significantly enhances the accessibility, interoperability, and global significance of the TDWG framework.

In this presentation, we will describe the process of translating standards documentation within the TDWG infrastructure and explore the lessons learned along the way, especially those with wider implications for similar activities in the future and recommendations to avoid future pitfalls.

Woodburn et al. (2023): <https://doi.org/10.3897/biss.6.91159>

Session: **6798214****7013927**

24/10/25 | 14:14

Room: Caldas

ORAL • EN

Tools that Speak Your Language: A Multilingual Approach to Lowering Barriers in Biodiversity Data Sharing

Presenter

Melissa Jean-Yi Liu

Authors

Melissa Jean-Yi Liu (Taiwan Biodiversity Information Facility, Biodiversity Research Centre, Academia Sinica • Taiwan)**Jhu-Jyun Jhang** (Taiwan Biodiversity Information Facility, Biodiversity Research Centre, Academia Sinica • Taiwan)**Zhen Yao** (Taiwan Biodiversity Information Facility, Biodiversity Research Centre, Academia Sinica • Taiwan)**Chun-I Chang** (Taiwan Biodiversity Information Facility, Biodiversity Research Centre, Academia Sinica • Taiwan)**Daphne Z Hoh** (Taiwan Biodiversity Information Facility, Biodiversity Research Centre, Academia Sinica • Malaysia)**Mao-Ning Tuanmu** (Taiwan Biodiversity Information Facility, Biodiversity Research Centre, Academia Sinica • Taiwan)

Abstract

Many researchers and data holders in Taiwan are willing to share their biodiversity data, but are often discouraged by English-only documentation and complex publishing workflows. Even after attending workshops, participants frequently struggle due to language barriers and the lack of real-time support. To address these challenges, the Taiwan Biodiversity Information Facility (TaiBIF) recently introduced two tools to support local users.

The TaiBIF Open Data Toolkit (ODT) is an all-in-one platform that guides users through every step of creating a Darwin Core (DwC) dataset

— from template generation to data editing, cleaning, and validation. A key feature of ODT is its support for translating DwC terms, helping users map local or non-standard field names to standardized DwC vocabulary. First introduced at TDWG 2024, ODT was designed to be beginner-friendly and to reduce reliance on multiple tools. Since its launch, it has continued to evolve, with new features such as column swapping, fuzzy and regex text filtering, and automatic taxonomic lookup via API.

Digital TaiBIFer, an AI-powered multilingual helpdesk built on ChatGPT, was developed from a prototype that won third prize in GBIF's 2024 Ebbe Nielsen Challenge. Available 24/7, Digital TaiBIFer offers real-time assistance by suggesting dataset types, explaining Darwin Core terms, and mapping data fields to the standard.

To further promote community participation, TaiBIF has launched both Traditional Chinese and English interfaces for ODT and is building a collaborative translation system. We are actively seeking volunteers and partner institutions to help reduce language barriers and make biodiversity data more globally accessible.

Session: 6798214**7020392**

24/10/25 | 14:23

Room: Caldas

ORAL • EN

Translate to Focus on What Really Matters: Our Biodiversity -- SiB Colombia's Journey

Presenter

Camila Plata

Authors

Camila Plata (Catalogue of Life • Colombia)

Esteban Marentes (SiB Colombia – Instituto Humboldt • Colombia)

Dairo Escobar (ANDI • Colombia)

Ricardo Ortiz-Gallego (SiB Colombia – Instituto Humboldt • Colombia)

Abstract

Our modern world keeps working as it surfs on an ocean of data, and one of the first steps to make that data usable into our digital world is to structure it under a common standard. For biodiversity data, the most important standard has been the Darwin Core (DwC). As the popularity and use of DwC has grown over the years, many GBIF nodes across the world, such as SiB Colombia, became the bridge between the standard and data publishers.

Although Colombia is one of the hotspots of world biodiversity, back in 2003 when it became a GBIF node most of the data produced by the country was far from ready to be published in a standardized manner – a data-sharing culture was needed. And that culture spoke a language that was foreign to most biologists, the Darwin Core.

To take on the challenge of fostering the culture of standardizing biodiversity data, the node needed to simplify, and exemplify the standard as much as possible. One of the first barriers identified was language, so the first DwC translations to Spanish began around 2012. This task evolved over a decade from a single Excel spreadsheet with header notes, to 11 normative and non-normative interactive spreadsheets along with a Spanish implementation of the standard documentation in biodiversidad.co, the Colombian GBIF hosted-portal. The team also actively contributed to the Crowdin translation of eight guidelines on how to use the Darwin Core standard and how to effectively publish data through GBIF.

Here we will tell the story on how SiB Colombia along with its community navigated the Spanish translation of Darwin Core, and how it has impacted the usage of the standard not only within the country but also across the Latin American and Caribbean region as the translated spreadsheets crossed borders.

Session: 6798214**7017146**

24/10/25 | 14:33

Room: Caldas**ORAL • EN**

Translating Darwin Core and other TDWG standards using Crowdin

Presenter

Matthew Blissett

Authors

Matthew Blissett (GBIF Secretariat • Denmark)

Daniel Noesgaard (GBIF Secretariat • Denmark)

Abstract

Users of data standards benefit when the labels and definitions are available in their own languages. Providing translations of data standards may increase the amount of data published in that language and remove barriers to its use.

The Global Biodiversity Information Facility (GBIF) has used the Crowdin platform for over 10 years to manage translation of software, documents and the GBIF.org website. Building on this experience, we have collaborated with Biodiversity Information Standards (TDWG) to use Crowdin for the translation of the Darwin Core, Humboldt Core and Latimer Core standards.

This presentation will explore how we have engaged members of the community, including students, through various activities including supporting translation “hackathons”, outreach to graduate programmes and by awarding badges to volunteers translators.

We will explain how the translators use the system and how users and developers can access the translated standards. We will also demonstrate some features of Crowdin for managing translation workflows, including integrations with Github and Contentful, which may be useful for a possible Task Group.

Session

6799398

Panel

24/10/25 | 14:00

Room: Valle

Fireside chat: Modeling the way forward for the Global Biodiversity Framework

Organizers

Mark Urban

Santiago Velazco

Natalie Briscoe

Greta Bocedi

Damaris Zurell

Description

The Kunming-Montreal Global Biodiversity Framework sets ambitious goals and targets and charts an ambitious plan for reversing global biodiversity declines. The Framework identifies indicators to track progress toward targets, but its monitoring-based indicators can only retrospectively evaluate biodiversity status and trends. The GBF does not mention 'model' or 'prediction' anywhere in its text. This backward-looking approach risks the continued decline of global biodiversity by failing to provide timely warnings that existing actions are insufficient to meet GBF goals. Also, incorporating forward-looking models can identify and design efficient actions, making success more feasible within social and economic constraints. In this open discussion, we will address some of the following questions: How can modeling best support the goals and targets of the GBF? What is needed to facilitate modeling - better data, better models, more resources, all of the above? What are the most important next steps to incorporate modeling into future iterations of the GBF? These are just some starter questions. We look forward to an open discussion of this topic based on the audience's participation.

Session

6799775

Panel

24/10/25 | 14:00

Room: Cauca

Challenges in incorporating species population data: connecting data to conserve biodiversity

Organizers

María Claudia Franco

Carlos Alberto Galvis

Edna Julieth Penagos Carvajal

Maria Piedad Baptiste

German Forero

Cristina López

Description

Biodiversity loss is progressing at an alarming rate, with extinction rates up to 1,000 times higher than natural rates. Population information on fauna and flora species is key to assessing the status of biodiversity and guiding species conservation actions and policies. Despite the vast amount of data generated, its impact remains limited by the lack of standardization, accessibility and collaboration. In order for data to truly contribute to conservation, it must be accessible, interoperable and useful for decision-making. This session will explore strategies to improve the collaboration among stakeholders, the generation of information, as well as practices for standardization and availability of data to facilitate effective reporting and use of data for promoting decision making.

We invite discussions of how open standards can accelerate action in favor of biodiversity. Successful network monitoring models and strategies to transform local efforts into global impact will be discussed, including case studies from highly biodiverse but understudied regions. One such region is the Orinoquia, where the lack of structured data limits its conservation. Challenges such as data fragmentation and the need for a common language in its management. The potential of open-source tools to improve interoperability and strengthen information management in key landscapes will also be analyzed. The objective is to promote strategic alliances, promote access to live data, transform information into practical knowledge for biodiversity management, and consolidate a roadmap for conservation based on integrated and accessible data for all stakeholders and social actors.



LIVING
DATA
2025

Huila room / *Salón Huila*

Daily Sessions Workshops

*Sesiones
Diarias de Talleres*

Session

6798781

Workshop

21/10/25 | 11:15

Room: Huila

The Essential Biodiversity Variables Cube: a standard for spatiotemporal biodiversity data

Organizers

Nestor Fernandez

Henrique M. Pereira

Lina Estupinan

Description

Essential Biodiversity Variables (EBVs), a framework initially conceptualized by GEO BON, hold significant potential for supporting biodiversity assessments across scales ranging from sub-national to global levels. However, realizing the full potential of EBV data requires a breakthrough in making data from diverse sources interoperable to ensure widespread use. This session will discuss advances towards a new standard for EBVs, known as the EBV-Cube standard. This standard aims to facilitate access to multiple EBV data products, organized under a consistent data structure with standardized annotations across different EBV classes. The development of this new standard also seeks to support the dissemination of EBV data products through the GEO BON Data Portal, following best practices in data management and ensuring access via services. The session will also aim to promote the formation of a working group dedicated to the continued development of this standard under the auspices of GEO BON and TDWG.

Session

6803041

Workshop

21/10/25 | 14:00

21/10/25 | 16:00

Room: Huila

Room: Huila

Liberating and re-use of data imprisoned in scientific literature

Organizers

Donat Agosti

Laurence Bénichou

Tim Hirsch

Description

Biodiversity research results are contained in the ever-growing corpus of scientific publications, traditionally stored in, or provided through, academic libraries. Access to this literature can be difficult in terms of both findability and accessibility. In the digital age, this barrier can and should be lifted by opening publications to machine access, ensuring the data they contain adheres to the FAIR principles. This workshop provides a hands-on demonstration of the existing workflows to liberate data from legacy publications, as well as to publish in a semantically-enhanced way and to reuse the data. It will also highlight the benefits and opportunities provided by accessible, semantically-enhanced literature in the biodiversity domain.

The workshop will have three parts:

1. Introduction by means of a hand-on exercise to the applied concepts, using existing workflows to convert a publication including biodiversity-related data from a PDF to a machine actionable format, for dissemination to GBIF, the Biodiversity Literature Repository, ChecklistBank, and OBIS;
2. Explanation of how to find, access and use the data, including for potential new data metrics, or use of the resources for AI applications to support for example IPBES and, potentially, generation of essential biodiversity variables;
3. Demonstration of services enabling direct semantic publishing.

Session

6799300-1

Workshop

22/10/25 | 14:00

22/10/25 | 16:00

Room: Huila

Room: Huila

Hip to be cubed: using the new GBIF SQL Download API

Organizers

Pieter Huybrechts

Lissa Breugelmans

Maarten Trekels

Andrew Rodrigues

Matthew Blissett

Description

GBIF released a new API that allows you to query species occurrences using Structured Query Language (SQL). But what is it used for and how do you use it?

In this workshop we will demonstrate how you can use this exciting new tool for questions that were previously difficult or expensive to answer. There is a lot of occurrence data available, but you often only need it in aggregated or summarized form for further analysis. For example, rather than raw occurrence records, you want to know the species occurrence counts for cells of a spatial grid for which you have land use or other environmental data.

This training is aimed at people both completely new to SQL, as well as those already familiar but wanting to learn more about the specifics of this tool.

After a short introduction to SQL, the standard language for database querying, we will dive into several practical exercises to demonstrate the capabilities of the API. Finally, we will build a biodiversity cube and match it to a reference dataset via spatial join to a reference grid. We will also touch upon the new user interface for the API which you can use without prior knowledge of SQL.

This exciting new service helps to bridge the gap between the large amounts of available observational data and the need for environmental data in multiple dimensions aggregated to spatial reference grids. It is a task that previously required access to significant resources and experience. The service makes this functionality accessible to a broad audience, repeatable, and easy to cite and reference via the DOI created for every query.

This workshop receives funding from the B-Cubed project (European Union's Horizon Europe Research and Innovation Programme (ID No 101059592)).

Session

6799240

Workshop

23/10/25 | 10:45

Room: Huila

Towards a standard for exchanging passive acoustic monitoring (PAM) data

Organizers

Sanne Govaert

Juan Sebastián Ulloa Chacón

Julia Wiel

Esteban Marentes Herrera

Description

Passive Acoustic Monitoring (PAM) is a powerful tool for biodiversity monitoring. However, a major bottleneck is the lack of a universal accepted standard for data exchange. This hinders data sharing, large-scale studies, and the publication of open and FAIR data to platforms such as GBIF.

We assessed if Camtrap DP, a standard for exchange and archival of camera trap data (<https://doi.org/10.1002/rse2.374>), can be adapted to fit PAM data. We will introduce the proposed changes that allow Camtrap DP to cover both camera trapping and acoustic data.

This hands-on session will guide you through mapping a demo dataset to the three core tables of the proposed new version of Camtrap DP: deployments, media, and observations. You can participate in our accessible non-coding group or utilize a prepared R Markdown script.

We will end with outlining the community-driven development process and explain how you can contribute to its finalization and adoption.

This workshop is also an opportunity to engage with experts and stakeholders involved in collecting, using and adopting best practices for sharing PAM data.

Session

6803173

Workshop

23/10/25 | 14:00

23/10/25 | 16:00

Room: Huila

Room: Huila

Learning novel tools for integrating freshwater biodiversity and high-resolution hydrographical data

Organizers

Thomas Tomiczek

Yusdiel Torres Cambas

Vanessa Bremerich

Afroditi Grigoropoulou

Merret Buurman

Jaime Garcia Marquez

Paula Torre Zaffaroni

Description

In order to save time during the workshop, we kindly ask the participants to pre-install all necessary software depending on their operating system, using the installation guides found here:

<https://glowabio.github.io/hydrographr/articles/hydrographr.html>

This workshop introduces cutting-edge advancements in global high-resolution freshwater datasets and teaches participants the skills to integrate such datasets into ecological models. Participants will learn how to process and efficiently use open and interoperable hydrographical network data (Hydrography90m), lakes (HydroLakes/NASA SWOT) and range-wide environmental data (Environment90m) accessible through the user-friendly GeoFRESH web application and the hydrographr R-package, developed at the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB). GeoFRESH and hydrographr leverage powerful open-source geospatial processing tools in the backend, to support large-scale freshwater ecological analyses. The workshop will address key challenges in freshwater research, e.g. integrating large species occurrence databases into predictive modelling workflows, overcoming data scaling issues, and processing continuous environmental data at the sub-catchment level. Through hands-on demonstrations, participants will engage in practical, real-world exercises and gain insights into the potential of large-scale, high resolution datasets for improving freshwater ecological modelling. Participants will leave with a deeper understanding of how to acquire, process, and analyze freshwater data, encouraging them to share their new knowledge within their communities. This collaborative approach aims to foster long-term use and further development of these data-driven tools for advancing management, monitoring and the overall conservation of freshwater ecosystems globally.

Session

6798919

Unconference

24/10/25 | 09:00

24/10/25 | 09:00

24/10/25 | 10:45

Room: Cauca

Room: Huila

Room: Huila

Living Data Unconference 2025

Organizers

Yi-Ming Gan
Deborah Paul
Esteban Marentes Herrera
Nicky Nicolson

Description

Your chance to take control of the conference programme! At an unconference you are either learning or contributing: learn about new domains and share your expertise in your own, while exploring ideas inspired by the main Living Data event. This is your chance to find others with similar interests, explore subjects in greater depth or propose new areas that haven't been mentioned yet - sowing the seeds for new collaborations.

Share your latest ideas and topics during the event itself on a topic board where others can indicate their support. Come along to the session to pitch and support ideas. With a little guidance from the organizers, we will work together to propose, select, and prioritize the discussion group topics, then self-organize into focused groups to learn, find synergy and gain new insights. We will end by reporting back to the whole group (e. g. needs you discovered, something you learned). We encourage you to ensure that the outputs of your discussions have a life beyond the session as short writeups or position statements to gather more participants and move forward together.



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www.livingdata2025.com/on-demand.html

Virtual On-Demand Sessions

Sesiones

Virtuales a la Carta

Session: 6960773**7013325**

Virtual | On demand

Room: Virtual

LIGHTNING TALK VIRTUAL • EN

Rescuing the past to prepare for the future: environmental data rescue as a key activity of open science

Presenter

Diane Srivastava

Authors

Diane Srivastava (Canada)

Abstract

In the rush to implement new standards and programs for future data collections, it can be easy to overlook the treasure trove of environmental data that has already been collected, and can serve as essential baselines for global change, but is being lost at an astonishing rate. The Living Data Project has rescued close to a hundred environmental and biodiversity datasets by pairing data custodians with paid graduate students that we custom train. I describe how we prioritize data for rescue, and the key steps in the data rescue process, ending with recommendations for others wanting to start their own data rescue programs.

Session: 6960773**7014245**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

From collections to decision-making: The CETAF/DiSSCo Specialisation Tool in support of European biodiversity data integration

Presenter

Laura Tilley

Authors

Laura Tilley (Consortium of European Taxonomic Facilities • Belgium)**Patrick Semal** (Royal Belgian Institute of Natural Sciences • Belgium)**Franck Theeten** (Royal Museum for Central Africa • Belgium)**Ana Casino** (Consortium of European Taxonomic Facilities • Belgium)**Wouter Addink** (Naturalis • Netherlands)

Abstract

The CETAF/DiSSCo Specialisation Tool, developed in collaboration between the Consortium of European Taxonomic Facilities (CETAF) and the Royal Belgian Institute of Natural Sciences (RBINS), plays a strategic role in the DiSSCo Research Infrastructure by harmonising the collection-level documentation of institutional specimen holdings and streamlining the extraction of information from natural science collections. Based on the CETAF Registry, this tool collects structured data from natural science institutions across Europe via Google Forms and Sheets, and exports them into a Django/PostgreSQL backend data storage with options for, curation, enrichment, and exchange through a JSON API.

The API supports integration with key DiSSCo services such as the European Loans and Visits System (ELViS) and the Collection Digitisation Dashboard (CDD), using common standards like Latimer Core. It provides essential functions for mapping institutional capacities, enabling the identification of Centres of Excellence and facilitating evidence-based decision-making at both institutional and infrastructure levels.

Data is aggregated, normalised, and transformed for export to external publishers like GRSciColl, using automated workflows, and data visualisation software (like Grafana). Database and API keep history of data, for diachronic analysis. Output data can be transformed from one structure (e.g LatimerCore) to another (e.g DarwinCore) using parameters capturing JSON paths in a configuration file. The system architecture ensures sustainability, flexibility, and alignment with FAIR principles. It also supports pre-filled update forms and future migration to CETAF-hosted infrastructure for long-term maintenance.

The Specialisation Tool benefits a wide user base, including researchers, collection managers, institutional decision-makers, communities from related disciplines, and policy makers. It enhances discoverability and standardisation of institutional data and collections, supporting the relevance of natural science collections and contributing directly to DiSSCo's mission to unify Europe's scientific collections into a cohesive, accessible, and strategically governed digital infrastructure.

Session: 6960773**7020559**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Wildlife in the Anthropocene: Golden Jackals (*Canis aureus*) as Sentinels, Vectors and Amplifiers of Zoonotic Diseases

Presenter

Gila Kahila BarGal

Authors

Gila Kahila BarGal (The Hebrew University • Israel)

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Abstract

In Israel, rabies virus, a life-threatening zoonotic pathogen, remains a persistent public health concern, particularly among wild canids. Adopting the “One Health” approach, which integrates human, animal, and environmental health, we studied the role of the golden jackal (*Canis aureus*) as a potential reservoir and vector of rabies and other infectious zoonotic agents. As a synanthropic species, golden jackals live in close proximity to human populations, thereby increasing the risk of cross-species zoonotic pathogen transmission. The research focused on the golden jackals as a potential carrier of zoonotic diseases, analyzing their fecal and fur microbiota, gut resistome, the prevalence of various pathogens, including evidence of rabies, and host genetics (immune system genes). We also explored associations between rabies and other pathogens, golden jackal traits, and environmental variables. The cohort consisted of 100 specimens from the North of Israel. The results revealed a significant diversity of zoonotic pathogens, microbiome (fur and gut), and antibiotic resistance, highlighting their role in disease transmission dynamics. Importantly, the study uncovered the association between genetic variation, pathogens, animal traits, and environmental factors. The proximity of golden jackals to humans and their role as a companion species underscores their critical role as sentinels, indicators of diseases and antibiotic resistance, and amplifiers of the rabies virus. This emphasizes the importance of ongoing GJ surveillance, monitoring, and the development of preventive health strategies. The management of the GJ populations will not only prevent outbreaks but also have an impact on biodiversity conservation.

Session: 6960773**7012938**

Virtual | On demand

Room: Virtual

LIGHTNING TALK VIRTUAL • EN

Controlled access to sensitive biodiversity data in OpenObs

Presenter

Alice Ainsa

Authors

Alice Ainsa (France)

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Abstract

The dissemination of biodiversity data is essential for conservation systems, scientific research, and public information. However, sensitive data – concerning species that simultaneously meet the following three criteria: a risk of voluntary infringement, intrinsic sensitivity of the species and the likely effect of information dissemination – must be shared with caution to avoid harming the elements they refer to. This is the guiding principle behind the controlled management of these data in national systems like SINP (National Inventory of Natural Heritage), which promotes differentiated access depending on the user's profile and intended use.

Following this approach, the French national portal for biodiversity data, OpenObs,, presented at several TDWG conferences, notably in 2023 (DOI: 10.3897/biss.7,112179), is planning to introduce a new feature that will allow users to submit a nominative and reasoned request to view the precise locations of sensitive data, for a specific taxonomic group and geographic area. A dedicated request form has been developed, and the processing of these requests will be handled by platform administrators. If approved, the user will have access to the precise data under a strict license of use, the SINP Closed License for the Communication of Basic Exchange Data https://inpn.mnhn.fr/docs/demandes_sinp/Licence_ferme_SINP.pdf, which does not authorize the redistribution of these data.

This new feature is based on several recent developments in OpenObs: the integration of duplicated location fields (precise and blurred), and a conditional display system based on the access status. These new features may also be of interest to the ALA (Atlas of Living Australia) community, which shares similar concerns and needs regarding the management of sensitive data.

Session: 6960773**7019810**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Specimens, Sprints, and Scrum Masters: Project Management at the Museum für Naturkunde

Presenter

Caitlin Thorn

Authors

Caitlin Thorn (Museum für Naturkunde Berlin • Germany)

Jessica Zimmermann (Museum für Naturkunde Berlin • Germany)

Abstract

Project Management: Scrum, Agile, Kanban, sprints. These words might sound out of place in a natural history museum, but at the Museum für Naturkunde Berlin (MfN), we're experimenting with project management tools that can work beyond the tech world.

Our Digital Catalog Infrastructure team includes developers, data managers, media managers, and digitization managers, all working toward building and maintaining the systems that support the museum's digital data landscape. To manage this complexity, we introduced Scrum practices in a workplace not traditionally built for agile methods.

As certified Scrum Masters, we adapted agile principles to fit our museum context: introducing short iterations (sprints), structured meetings, and sprint planning boards to organize priorities and improve communication across groups.

This presentation shares our lessons learned: What worked, what didn't, and how we balanced flexibility with structure to keep the team aligned. We aim to show that, with the right approach, agile methods can bring clarity, focus, and momentum to even the most traditional scientific institutions.

Session: 6960773**7020589**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Sounds of Life: a FAIR platform to unlock the potential of acoustic biodiversity data for discovery and interoperability

Presenter

Homo Julien

Authors

Homo Julien (Foxcub • France)

Darty Kevin (Foxcub • France)

Kilouchi Shadia (CNRS UMR Passages • France)

Abstract

Environmental acoustic data, whether derived from bioacoustics or ecoacoustics, offer unique opportunities to detect species, monitor biodiversity trends, and explore the sonic dynamics of ecosystems. Yet their scientific and operational potential remains underexploited, hindered by fragmented practices, lack of shared standards, and limited pathways for publication and reuse.

Sounds of Life (SoL) is a platform aligned with the FAIR principles (Findable, Accessible, Interoperable, Reusable), designed to unlock this potential through structured metadata, collaborative tools, and interoperability with global biodiversity data infrastructures. It supports the description, annotation, and publication of both targeted recordings (e.g., animal vocalizations) and large-scale soundscapes rooted in ecoacoustic approaches. Built on the Darwin Core standard and integrated with systems like GBIF, SoL enables rich metadata enrichment across species, equipment, geolocation, acoustic context, and temporal resolution, linking datasets to taxonomic, geographic, and environmental references.

This framework highlights key interdisciplinary challenges: aligning heterogeneous vocabularies across scientific communities (ecology, engineering, conservation), addressing taxonomic uncertainty, documenting soundscapes meaningfully, and ensuring traceability and reusability across platforms. SoL addresses these through an extensible metadata model, controlled vocabularies, and export pipelines designed for both human and machine readability.

The platform provides a multilingual, interdisciplinary environment where users annotate recordings spectrally, describe sound types and scenes, and prepare datasets for publication or analysis. While SoL does not yet include integrated artificial intelligence, it is AI-ready, ensuring that curated data can serve as a solid foundation for future analyses, training, or decision-support systems.

In response to priorities raised by the global bioacoustics community, including those from a recent international horizon scan, SoL supports the mobilization of acoustic data for conservation. It fosters discovery and reuse, connects local observations to interoperable infrastructures, and helps integrate acoustic approaches into policy, research, and field-based action, positioning itself as a key contributor to biodiversity science.

Session: 6960773**7014157**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

A hierarchical typology and geospatial assessment of South Africa's springs for biodiversity reporting

Presenter

Heidi van Deventer

Authors

Heidi van Deventer (Council for Scientific and Industrial Research (CSIR), South Africa • South Africa)**Christel Hansen** (University of Pretoria • South Africa)**Callum Tyrer** (University of Pretoria • South Africa)

Abstract

Mapping and monitoring of ecosystem biodiversity are important for reporting to the Global Biodiversity Framework (GBF) by 2030. The GBF reporting, however, poorly recognises the diversity of springs that may exist. The aim of our project was to map the biodiversity of South Africa's 6 940 springs that has been mapped and compiled in the 2018 National Biodiversity Assessment. Our objectives were (i) to define a hierarchical typology that can describe the biodiversity; (ii) assess the biodiversity using a diverse number of geodatasets related to the typology; (iii) evaluate whether threats to springs can be represented and (iv) how protected these springs are.

Preliminary outputs show that four levels of a hierarchy can describe characteristics of springs, including at the top level the realms, second one the biomes, at the third level the Ecosystem Functional Groups, and at the fourth level, site, or local characteristics. Applying the framework to the springs showed that most springs (93%) are predominantly surrounded by terrestrial ecosystems, with only 7% associated with units from the National Wetland Map, and only six mapped within the Estuarine Functional Zones. Most of the springs (55%) are within the Temperate upland rivers MHT and Southern Temperate Highveld FEOw, whereas <22% are in the other four MHTs and five FEOws.

Only 90 springs (1.3%) are thermal.

Available data show that 21% of the springs may be degraded or transformed, with only 12% of all springs located in National Protected Areas and World Heritage Sites. However, since mapping was done using available datasets, these results are an underrepresentation of potentially degraded and transformed springs.

The framework developed can potentially be applied globally, should countries have mapped their springs. Therefore, the reporting and monitoring of springs using geospatial methods should be considered for the GBF.

Session: 6960773**7014350**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Critical analysis of environmental characterization practices through integrated analysis of biodiversity data published in an open-access database

Presenter

Paula Castellões

Authors

Paula Castellões (CLS Brasil • Brazil)

Luciana Frazão (Brazil)

Cristine Moraes (Brazil)

Leonardo Marques da Cruz (CLS Brasil • Brazil)

Abstract

To conserve and restore the planet's marine biodiversity, it is necessary to undertake a critical analysis of the efforts made on the data generated so far. The present paper focuses on the analysis of phytoplankton biodiversity in the water column, whether or not it is restricted to the photic layer, based on data obtained from several Environmental Baseline Studies (EBS), submitted to environmental licensing processes for O&G exploration in Brazil. As part of the environmental licensing process, all studies are subject to technical analysis and approval by the licensing environmental agency, guided by technical guidelines. Despite that, the phytoplankton biota sampling strategy is

not standardized. Samples should be taken from each water mass and the subsurface, but some projects are approved, under justification, sampling only at the photic layer. BDCA (Environmental Characterization Database - bdca.com.br) is a Brazilian system that allows the storage, consultation, and sharing of environmental data in the marine environment. There are currently ten registered EBSs carried out in deep and ultra-deep areas in Brazilian offshore sedimentary basins that include phytoplankton biota. Only four of them sampled phytoplankton in all identified water masses, while the others restricted sampling to until 300m. Although the highest densities and species richness occur in the euphotic zone, studies that included deep-sea analysis have also recorded the occurrence of healthy microphytoplankton cells between 600 and 2,000m. These results contribute both to a more comprehensive view of deep ocean biodiversity and to their role in biogeochemical cycles and their ecosystemic services. By reanalyzing environmental data shared in open access databases, it was possible to identify these gaps in knowledge of marine biodiversity, and we hope that it will also be possible to refine global projections and propose improvements in the methodologies and guidelines adopted by decision-making bodies.

Session: 6960773**7020236**

Virtual | On demand

Room: Virtual

LIGHTNING TALK VIRTUAL • EN

How lack of standardization and complexity is affecting the finding of general trends: a case study from an ecological meta-analysis

Presenter

Romullo Guimarães Lima

Authors

Romullo Guimarães Lima (Federal University of Ceara, Brazil • Brazil)

Bruno Eleres Soares (University of Regina • Canada)

Abstract

Year after year, a plethora of studies is being published on different ecological topics. Since early 2000's, functional diversity has been quantified to assess how human impacts affect diversity. Thus, it would be expected that a large pool of articles could be used to produce current meta-analyses to assess large-scale patterns and synthesize the effects of human impacts on this dimension of biological diversity. Despite that, problems such as lack of standardization between studies, high methodological complexity, poor data reporting reduce the number of usable articles. Here, using a recently published meta-analysis from 18 years of study on how functional diversity is affected by humans, we discuss these issues by reviewing papers that could have been included in the meta-analysis but that were eventually excluded due to several problems. With this, we expect to understand what is refraining us from finding more robust general patterns of environmental change and how we could tackle these problems as a scientific community.

Session: 6960773**7014050**

Virtual | On demand

Room: Virtual

LIGHTNING TALK VIRTUAL • EN

Supporting Scientists, Building Engagement and Working Together to Enable Evidence - Challenges and Opportunities

Presenter

Oliver Williams

Authors**Oliver Williams** (Centre for Environment, Fisheries and Aquaculture Science (Cefas) • United Kingdom)**Laura Hanley** (Cefas • United Kingdom)**Abstract**

Cefas has supported science and scientists within the biodiversity realm for many years. We share our thoughts on the ways we promote engagement on FAIR data initiatives which are central to our science delivery and strategic ambitions. We work collaboratively with others, nationally and globally, to share best practice and build a community of data professionals who can support each other. We hope to spark conversations on shared challenges and benefits, sharing ways that we can work together to build solutions that can meet our own institutional needs as well as those required for a global approach for biodiversity data.

Session: 6960773**7015950**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Designing Policy Interfaces: Spatial Data Usability and Interactive Governance in a Marine Protected Area

Presenter

Folco Soffietti

Authors

Folco Soffietti (Iuav University of Venice • Italy)**Gianni Sinni** (Iuav University of Venice • Italy)**Francesco Musco** (Italy)

Abstract

This study analyses the digital interface of the Gironde and Pertuis Marine Nature Park management plan as a model for integrating spatial data into policy through user-centred design. In contrast to static regulatory documents, the Gironde platform presents a modular, Web-GIS- based solution that supports stakeholders—including policymakers, developers, and institutional users—in exploring management objectives, spatial stakes, and implementation actions through interactive navigation.

Using document analysis, UX evaluation, and a semi-structured expert interview with a former officer of the French Office for Biodiversity, this study explores the platform's design logic and governance functions. The interface, although not legally binding, aligns with EU marine spatial planning (MSP) standards by enabling access to structured spatial data layers, dynamic map generation, and task-specific data storytelling. Features such as relational linking between ecological stakes ('enjeux'), policy actions, and geographies exemplify the platform's operational capacity and alignment with the MSP Directive (2014/89/EU) and the INSPIRE Directive (2007/2/EC).

Importantly, the study argues that good design is not merely aesthetic but fundamental to the usability and legibility of environmental data. As noted by Soares et al. (2022) and Henderson (2024), the usability of digital products is defined by their ability to match user goals with efficient and intuitive interaction pathways. The Gironde case illustrates how design principles—such as modular information architecture, cognitive load management, and iterative user testing—can translate complex spatial planning into accessible formats, enhancing data interoperability and decision support.

As EU Member States evolve their MSP implementation tools, the Gironde portal offers a replicable design model that bridges legal frameworks and user experience. It demonstrates how spatial data, interface design, and digital governance coalesce to foster more transparent, adaptive, and stakeholder-relevant marine policies.

Session: 6960773**7018859**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Modeling global spatial patterns of species richness using GBIF data and environmental variables

Presenter

Franco Magni

Authors

Francisco J Galdames G (Lemu Earth • Chile)

Franco Magni (Lemu Earth • Chile)

Stephan M Funk (Lemu Earth • Chile)

Pablo Gonzalez (Lemu Earth • Chile)

Christian Peña (Lemu Earth • Chile)

Abstract

An accurate estimation of species richness is critical for effectively guiding conservation prioritization efforts. However, there remains no universally accepted standard or globally recognized baseline for actual species richness at any location. We present a global estimation of species richness, computed using species occurrence data from the Global Biodiversity Information Facility (GBIF), the most extensive and comprehensive repository of global species occurrence records.

For our modeling approach, we used occurrence data from thousands of terrestrial species in combination with different environmental data layers. Species richness was calculated using estimations of species distributions derived from environmental suitability analyses. We applied a weighting scheme based on species rarity, using the range-size rarity concept, which assigns greater importance to species with more restricted geographic distributions. This modelling approach increases the utility of the species richness estimation by identifying areas with high concentrations of rare and potentially threatened species.

The use of this type of data enables continuous refinement and improvement of species richness calculations, taking advantage, for instance, of the continually expanding data volume within GBIF. This constant increase in data is driven by growing contributions from automated monitoring systems such as camera traps and extensive citizen science initiatives, ensuring that species richness calculations remain current, dynamic, and highly relevant for ongoing conservation efforts.

Session: 6960773**7019920**

Virtual | On demand

Room: Virtual

LIGHTNING TALK VIRTUAL • EN

Springs as Overlooked Biodiversity Hotspots: A Call for Global Conservation Action

Presenter

John Simaika

Authors

John Simaika (International Water Management Institute • Sri Lanka)

Abstract

Springs are largely understudied and are because of this, forgotten ecosystems, often excluded from conservation planning. Global knowledge on springs is patchy and biased with some areas well documented, while others remain nearly invisible in biodiversity data. Springs, being at the groundwater-to-surface water interface, harbour unique, often highly localized and endemic biodiversity. This biodiversity remains often undescribed and poorly assessed. Much of this biodiversity remains undescribed and poorly assessed, leaving springs and their ecological value largely unknown at the global scale. Threats to these ecosystems include climatic change, over-extraction, pollution, habitat fragmentation and land-use change. In the absence of conservation policy, which would mandate the monitoring and management of spring habitats, the degradation and loss of springs is now a silent crisis. New technologies and emerging tools promise to put springs on conservation agendas. Remote sensing is needed to identify and delineate springs, and to monitor hydrological and land cover changes. In situ, environmental DNA (eDNA) will be useful for rapidly identifying and monitoring species, including rare and cryptic taxa. Automated sensors can collect much needed data continuously on water quality. Historical data and long-term ecological records, where available, could inform conservation management. Harmonized data collection, analysis and reporting standards and interoperable systems could further support spring conservation and management through easy-to-share formats and readily available reporting standards in an easily accessible way. These spring data could be integrated into existing biodiversity observation networks. These efforts, to leverage data and technology are far easier to accomplish now than they might have been just a decade ago and are needed to close this enormous knowledge gap on springs. There is an urgent need for springs to be put international and national agendas, and for policies to explicitly recognize spring ecosystems, their importance to human livelihoods. And their rich biodiversity.

Session: 6960773**7020693**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Demonstration of the Integration of Earth Observation data into Ecosystem Services Accounting in the European Union

Presenter

Mayra Zurbaran Nucci

Authors

Mayra Zurbaran Nucci (European Commission – Joint Research Centre • Italy)

Abstract

The European Union's amended Regulation 691/2011 on European environmental economic accounts emphasizes the importance of environmental accounting in informing policy decisions. The Integrated Natural Capital Accounting (INCA) project, which operationalizes the System of Environmental Economic Accounting Ecosystem Accounting (SEEA EA), supports this regulation by enabling the generation of ecosystem services accounts in a spatially explicit way. This presentation will showcase the results of integrating Earth Observation (EO) data into natural capital accounts for various ecosystem services, including Crop Provision, Wood Provision, Local Climate Regulation, Global Climate Regulation, Crop Pollination, Air Filtration, and Nature-Based Tourism, as well as voluntary services such as Flood Control and Soil Retention, within the context of the INCA project.

Our results demonstrate the successful integration of EO data into ecosystem services accounting, providing a robust and comparable framework for decision-making. We will present the outcomes of this integration, highlighting the potential of EO data to enhance the accuracy and reliability of natural capital accounts.

This presentation will provide an opportunity to learn about the latest developments in integrating EO data into ecosystem services accounting, and how this can support informed policy-making for biodiversity conservation, climate change mitigation, and sustainable development. The results contribute to the ongoing discussion on the role of EO data in supporting sustainable development and environmental protection.

Session: 6960773**7020372**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

From Sensors to Stories: Reimagining Biodiversity Data through Digital Narratives

Presenter

Alinta Kiri Krauth

Authors

Alinta Kiri Krauth (University of Bergen • Norway)

Jason Nelson (University of Bergen • Norway)

Robert Lewis (Norwegian Institute for Nature Research • Norway)

Abstract

As ecological data infrastructures become increasingly complex, there is an urgent need to explore their role beyond scientific domains. This presentation reports on on-going research exploring the potential of Nordic region biodiversity data as a generative material for creative generative narratives. We explore this through a mixed-methods practice-led examination of how creative practice can transform ecological data into multisensory experiences, stories, and artistic expressions that aim to resonate with broader publics. Through this, we propose a reimagining of biodiversity data as part of a living, participatory ecosystem of cultural materials.

We report specifically on ongoing research in the Nordic Forest Research supported ForestMicroClim project (SNS132) as a case study in generative narrative engagement with Nordic forest microclimate data: a collaboration between The Norwegian Institute for Nature Research, invited digital artists and writers, and the Center for Digital Narrative research institution. In this context, art|science stakeholder collaboration plays a crucial role, and we argue that creative practice in this context functions not as a tool of science communication alone, but as a mode of inquiry in its own right that brings value to science organizations.

The outcomes of this project will be the use of generative narrative and poetry as a creative methodology for translating and reimagining ecological data into interactable formats. We have so far found that unlike static visualization or traditional storytelling, generative literary forms using algorithmic processes enable dynamic, non-linear engagements with complex systems. We believe this offers a unique mode of encountering biodiversity data that resists reductive interpretation. It invites participants to dwell in potential uncertainty and engage with ecological data as layered, entangled, interpretable, and open-ended.

Session: 6960773**7020974**

Virtual | On demand

Room: Virtual

LIGHTNING TALK VIRTUAL • EN

Fighting Poaching through High Precision Real-Time Gunshot Detection Using Deep Learning and Cross-Device Communication

Presenter

Naveen Dhar

Authors

Naveen Dhar (United States)

Abstract

Poaching remains a global issue despite increased surveillance and collaborative efforts. The advancement of low-cost Autonomous Recording Units has enabled acoustic monitoring over large spatial and temporal scales. However, high false-positive rates and large file sizes of existing classifiers have rendered real-time acoustic detection of poaching impractical. I propose a low-footprint acoustic gunshot detection model and a cross-device communication pipeline to reduce false positives, suitable for on-device, real-time rainforest gunshot detection.

A custom deep neural network consisting of 2D and 1D convolution layers followed by a Long-Short Term Memory layer was trained on open-source rainforest/gunshot audio from Belize, with depthwise-separable convolutions to reduce size. A novel approach to reduce false positives is the use of cross-device communication (CDC). I propose the Sensor Analysis and Integration Layer (SAIL), a custom probability weighting function designed to leverage information from multiple sensors and map three or more predictions into a final prediction. CDC was simulated by performing three sound-attenuation augmentations on every waveform in a test dataset of 7190 files, emulating a three-sensor array for each waveform. The proposed gunshot detection network produced confidence probabilities for each augmented waveform, which were then fed to the SAIL function. To evaluate SAIL under varying sensor placements, three simulation configurations were created, each increasing in augmentation, or sensor array, variance, and ten simulations were run per configuration, totaling thirty.

SAIL achieved a statistically significant average FPR reduction of 29%, from 0.126 to 0.09, compared to non-simulation classification.

Additionally, the proposed network achieved a validation F1 of .89 at 598KB; a competitive performance at 1/50th the size of leading classifiers. Combined with the significant FPR reduction across all simulations, SAIL and efficient deep learning present great promise in addressing the major obstacles currently preventing acoustic monitoring from becoming a cost-effective solution for long-term, large-scale, real-time poaching detection.

Session: 6960773**7019869**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

The number of human-simulated predators influences the escape behaviour of bird species in a West African protected area.

Presenter

Ngozi Okafor

Authors**Ngozi Okafor** (A. P Leventis Ornithological Research Institute (APLORI), University of Jos Biological Conservatorry • Nigeria)**Abstract**

Continuous human presence in protected and recreational areas can adversely affect the wildlife population. Birds perceive the approach by humans as predatory and mostly flee in response, which can be energetically costly, and leads to disruption of foraging activities and interactions with conspecifics. This study used Flight Initiation Distance (FID) to assess bird responses to multiple versus single human approaches. We examined how the number of persons approaching the study bird species influenced the relationship between FID and factors such as flock characteristics, habitat features, bird orientation, and alert distance. A total of 668 FID approaches were conducted on ten bird species belonging to nine families at Rennajj fish farm, Jos, Nigeria. Our findings reveal that the number of persons approaching the study birds significantly affected their risk assessment and escape behaviour as they initiated flight earlier when approached by multiple persons. Focal birds positioned on water and ground exhibited significantly higher FID values than those in the tree or shrub habitats indicating high visibility and vigilance by birds on the ground and water. Furthermore, study birds fled at significantly shorter distances during three-person approaches when oriented backwards implying an increased vulnerability to predators approaching from the rear. We conclude that the number of persons approaching the study of bird species, and environmental and spatial cues play significant roles in the threat perception of wild birds. These factors should be integrated into wildlife management to manage human disturbance effectively.

Session: 6960773**7014892**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Looking backward in the future -- how open-access data is informing current biodiversity work in Fiji.

Presenter

Mereia Tabua

Authors

Mereia Tabua (NatureFiji- MareqetiViti • Wallis and Futuna)

Yumiko Baba (Auckland War Memorial Museum • New Zealand)

Abstract

Between 2021 and 2023, 17,991 occurrence data points across seven datasets of flora and fauna were mobilized from natural science collections in Fiji and made available publicly via the Global Biodiversity Information Facility. This mammoth task was a joint collaborative effort between the University of the South Pacific (USP), the Ministries of Agriculture and Forestry in Fiji and Auckland Museum in New Zealand through support and funding from the Biodiversity Information for Development Programme (BID-PA-2020-006-NAC).

While the published dataset represents less than half of the entire holdings at the South Pacific Regional Herbarium (SUVA) and the Biodiversity Center at USP, they date back to the early 1930s and serve as a baseline representation of Fiji's unique natural heritage, some of which are endemic and/or considered threatened under the IUCN Red List for Threatened Species. Fijian biodiversity specialists were integral to the publishing of the datasets as they ensured that the information pertaining to each occurrence record was correct and accurate, while ensuring sensitive locality information was withheld, making the data valuable and reliable for use and interpretation by the wider global scientific community.

These datasets are also an invaluable resource for Fiji's local species conservation organisation NatureFiji- MareqetiViti (NFMV). The datasets are useful to inform the validation process of 55 proposed Key Biodiversity Areas in Fiji, an on-going project of NFMV. It is also useful for current efforts to collate, update, and publish the diversity of understudied Fijian mosses, using records mobilized through the BID program from duplicate specimens that were sent from other internationally recognized herbaria. In this talk, we will showcase a continuous ripple effect of open-access data made available through the GBIF BID programme and how important these data are for the local NGOs and policymakers in the biodiversity conservation field in Fiji.

Session: 6960773**7015987**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Geospatial Mapping of Wetland Ecosystems to Inform Biodiversity Policy in the Sudan and South Sudan

Presenter

Rayan Madani

Authors

Rayan Madani (Higher Council of Environment, Rural and Urban Development • Sudan)

Abstract

Wetlands ecosystems in the arid zone provide multiple ecosystem services ranging from provisioning and regulating to cultural. As wetlands are habitats for many living organisms and a vital resource for the livelihoods of surrounding communities—especially in developing countries—understanding their ecosystem function begins with identifying and classifying them. This research aims to identify and classify wetlands in Sudan and South Sudan to provide updated information that could support future management and conservation plans. The research involved: selecting wetlands from literature, digitizing boundaries based on Google and Bing Aerial base maps, categorizing them by area and location, and calculating their areas and surrounding land use using different land use maps from the European Space Agency with the zonal histogram technique. This resulted in 48 maps for 12 wetlands, each showing land use, area, location, types, etc. Analysis revealed varying degrees of land use impact, with anthropogenic factors causing disturbance in some wetlands. These preliminary insights are necessary for setting conservation policy goals, as maps can provide crucial data for restoration and management.

Session: 6960773**6992098**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • EN

Freshwater biodiversity risk exposure of Natura 2000 sites to industrial pollution

Presenter

Szilard Erhart

Authors

Szilard Erhart (JRC • Italy)

Abstract

While every protected and conserved area can be exposed to pollution, some may suffer more. We develop methods to analyze their freshwater biodiversity risks from industrial sites around Europe. This study is novel as it is the first attempt at linking the European Pollutant Release and Transfer Register to the geographic data of Natura 2000 sites. Furthermore, we applied the improved characterization factors in the Environmental Footprint database published by the European Commission Joint Research Centre. The proximity of biggest industrial facilities to Natura 2000 sites, which is the largest network of protected areas in the world, can affect freshwater biodiversity risks in Europe and globally. We quantify hazards in the recent past and at the Natura 2000 site level. We find that European protected natural areas are exposed to more eutrophication and biodiversity risks mostly from the Sewerage and water treatment sector in the most industrialised European regions especially in the Benelux states, Southern Germany, in Northern Italy and South-West France. 370 of the E-PRTR facilities were located less than 500 m away from the border of Natura 2000 sites with protected freshwater species, 126 of which less than 100 m away and 51 within Natura 2000 sites. River basin districts of the Danube, Ebro and the Elbe were estimated to be most affected by pollutant releases with ecotoxicity and eutrophication impact potential in 2019. Approximately 3 % of industrial facilities reporting to the E-PRTR pollutant releases into water are closer to foreign Natura 2000 sites with freshwater fish or amphibian species than to the closest Natura 2000 site in the country where they are located. All this calls for improved monitoring and respective prevention measures in some key regions of Europe along with coordinated international biodiversity loss mitigation efforts.

Session: 6960773**7019747**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • ES

Cartografías de la vida: infraestructuras éticas de datos en territorios megadiversos

Presenter

Milena-Jael Silva-Morales

Authors

Milena-Jael Silva-Morales (Ecological LAB • Colombia)**Yasmín Navarrete** (Instituto de Filosofía y Ciencias de la Complejidad • Chile)

Abstract

El giro infraestructural en las ciencias de la biodiversidad ha permitido escalar la observación de lo vivo hacia nuevas dimensiones: desde la secuenciación ambiental hasta el modelado automatizado, pasando por arquitecturas de datos que interconectan sensores, satélites, comunidades y algoritmos. Sin embargo, esta expansión ha consolidado modelos de organización del conocimiento que, en muchos casos, reproducen relaciones asimétricas en la definición de qué se registra, quién interpreta y para qué se utilizan los datos.

Este trabajo propone el concepto de infraestructuras éticas de datos como marco analítico para reconsiderar el papel de los países megadiversos en la gobernanza digital de la biodiversidad. Más allá de la dialéctica entre apertura y soberanía, lo que se plantea es una ecología del dato que reconozca su dimensión política, territorial y ontológica. Se parte de una revisión bibliométrica de data papers relacionados con biodiversidad, así como de estudios de caso sobre el uso de tecnologías emergentes como el eDNA comunitario, sistemas de clasificación algorítmica y repositorios globales.

Los resultados muestran que, pese a la creciente visibilidad de los datos abiertos, persisten brechas estructurales en términos de trazabilidad contextual, agencia local y participación en la toma de decisiones. Frente a ello, se plantea una aproximación situada que articule ética, arquitectura institucional y corresponsabilidad territorial, permitiendo que las infraestructuras sean diseñadas desde, y no solo en, los territorios donde se genera el conocimiento biológico.

Esta propuesta se inscribe en la necesidad de reconfigurar el relato dominante sobre los datos vivos: no como herramientas de control sobre lo vivo, sino como instrumentos de cuidado, reciprocidad y construcción colectiva de futuros sostenibles. La interoperabilidad, para ser legítima, requiere primero justicia.

Session: 6960773**7007595**

Virtual | On demand

Room: Virtual

ORAL VIRTUAL • ES

Harnessing Ocean Science and Technology in Sudan: Community Engagement and Species Discovery to Combat Climate Change

Presenter

Khalid Mohammed

Authors

Khalid Mohammed (Institute of Marine Research • Sudan)

Abstract

This presentation explores the innovative efforts of Sudanese ocean scientists in fostering community engagement and advancing marine biodiversity research through the development of a mobile application. Recognizing the critical role of oceans in climate regulation and local livelihoods, Sudanese researchers have initiated programs to involve coastal communities in ocean conservation and climate resilience. Central to this initiative is a user-friendly app designed to document and identify local ocean species, empowering communities to participate actively in biodiversity monitoring. This citizen science approach not only enhances species discovery, including potentially new or undocumented marine organisms, but also raises awareness about the impacts of climate change on Sudan's coastal ecosystems. By integrating traditional knowledge with modern technology, these efforts aim to bridge scientific research and community action, fostering sustainable practices and informed decisionmaking. The presentation will highlight the project's methodology, community engagement strategies, key discoveries, and the potential of digital tools to address climate challenges in developing regions. Ultimately, this work demonstrates how local scientific capacity, combined with innovative technology, can contribute significantly to global climate adaptation efforts and marine conservation in Sudan and similar contexts. The ocean species discovery included:

- Citizen-Led Research by engaging citizens in data collection and research can accelerate ocean species discovery and prompt conservation.
- Technology Integration by leveraging technologies like mobile apps and online platforms can facilitate citizen participation in ocean conservation efforts.
- Education and Awareness by raising awareness about ocean species can inspire community-led conservation initiatives.

The Best Practices that succeeded this presentation represented at:

- Community-Centred Approaches, Educational and Feedback and Collaboration and Partnership.



Wednesday / Miércoles 5:30 p.m.

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Poster Session Main Hall & Virtual

Sesion de Posters

Hall Principal & Virtual

Posters Session

7010265

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

The impact of crowdsourcing projects in the digitisation effort of European herbaria.

Authors

Giulia Micai (Natural History Museum Vienna • Austria)

Heimo Rainer (Natural History Museum Vienna • Austria)

Wouter Addink (Naturalis • Netherlands)

Anton Güntsch (Berlin Botanical Garden and Botanical Museum • Germany)

Abstract

In the frame of the TETTRIs (Transforming European Taxonomy through Training, Research and Innovations) project, we've been using crowdsourcing annotation platforms to involve citizen scientists into digitisation campaigns that aim at extracting label data from botanical specimens physically deposited in various European herbaria.

The digitisation of herbarium specimens significantly enhances access to the collections for researches located all over the world and facilitates large-scale studies. Furthermore, digitisation helps preserving the physical specimens by reducing the need for handling and transportation.

Digitization also allows novel uses of metadata in combination with digital materials: for example, herbarium label data have been used to study shifts in plant phenology and to generate species distribution models (since accurate models rely on large numbers of data points that can efficiently be achieved via the repositories of digitized herbarium records).

Through the joint use of different crowdsourcing annotation platforms, we've been able to reach different communities of volunteers who helped overcoming linguistic barriers that might make data extraction difficult on a local scale, and make the information on the labels machine-readable, searchable and safely stored.

Since the beginning of the project, we've been able to launch and complete 8 digitisation campaigns on three European crowdsourcing annotation platforms (Die Herbonauten, Les Herbonautes and DoeDa), delivering specimen labels written in German, French and Dutch languages to the corresponding linguistic communities. This contributed creating an extended community of volunteers involved in more than one annotation platform at the same time, promoting knowledge exchange.

Posters Session

7020494

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Data for a purpose, data for life.

Authors

Nestor Galindo-Ruiz (Terrasos S.A.S. • Colombia)

Felipe Diaz Salazar (Terrasos S.A.S. • Colombia)

Jennifer Bedoya (Terrasos S.A.S. • Colombia)

Abstract

Climate change is an increasingly urgent issue, and restoration strategies—such as rehabilitating or recovering vegetation cover—are emerging as valuable tools for mitigating its impacts. These approaches not only support biodiversity conservation but also enhance other ecosystem services. However, a key challenge in implementing conservation strategies is the lack of reference frameworks and the context-specific nature of their success. Moreover, the short duration of most studies limits our understanding of their long-term effectiveness, often due to funding constraints or limited research opportunities. As a result, restoration efforts are frequently reduced to simply planting native species.

True ecological restoration, however, aims to achieve high ecological integrity—meaning ecosystems can sustain themselves and regulate their trophic networks without external intervention. Biodiversity projects play a vital role in enhancing habitat quality, but it is crucial to define clear criteria to evaluate their effectiveness, particularly in terms of the magnitude and relevance of ecological changes.

To address this, Terrasos has adapted the NARIA Framework, a standardized methodology for assessing and quantifying biodiversity gains. This tool consolidates data from biotic indicators, offering insight into ecosystem resilience. It enables the tracking and quantification of ecological changes over time, particularly through changes in vegetation cover at individual sampling units.

The framework facilitates a detailed understanding of restoration progress using the concept of “quality hectares” and supports the evaluation of conservation goals. Crucially, it also enables the long-term collection and analysis of ecological data, allowing for scalable assessments of biodiversity trends across varying territorial contexts.

Posters Session

7020556

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

DATOS GEOGRÁFICOS DE LA FLORA EUDICOTILEDÓNEA LEÑOSA DE LOS ANDES DEL NORTE Y CENTRO: SESGOS Y RIQUEZA

Authors

Pablo Andrés Gil Leguizamón (Universidad Pedagógica y Tecnológica de Colombia, Doctorado en Ciencias Biológicas y Ambientales, Grupo SisBio • Colombia)

María Eugenia Morales Puentes (Universidad Pedagógica y Tecnológica de Colombia, Doctorado en Ciencias Biológicas y Ambientales, Grupo SisBio • Colombia)

Jorge David Mercado Gómez (Universidad de Sucre, Grupo Evolución y Sistemática Tropical • Colombia)

Tania Escalante Espinosa (Universidad Nacional Autónoma de México, Grupo de Biogeografía de la Conservación • Mexico)

Abstract

Comprender la riqueza, historia evolutiva y biogeográfica de los bosques Andinos ha sido un tema central desde la ecológica y conservación. Estos estudios dependen de datos de colecciones biológicas y repositorios digitales que presentan sesgos Wallaceanos y Linneanos. El objetivo de este estudio fue analizar los sesgos y riqueza de la flora Eudicotiledónea leñosa del bosque andino. Se elaboró una base de datos con registros de GBIF y TROPICOS, se realizó una estandarización taxonómica (con APG IV y WFO) y validación de datos geográficos. Los registros y riqueza se analizaron mediante correlaciones muestreo-riqueza y déficit de información, mediante celdas (1x1°), en países y cuencas hidrográficas. En total se obtuvieron 645,793 registros en 37 países: el 1% no presentaron coordenadas, 57% estaban duplicados, 13% presentaron imprecisiones de georreferenciación y 29% cumplieron con la evaluación geográfica y taxonómica. A partir de 2,661 nombres científicos, se identificaron 675 sinónimos y 159 con jerarquías infraespecíficas, quedando finalmente una lista de 74 familias, 424 géneros y 1,986 especies. Las familias Melastomataceae, Rubiaceae, Malvaceae, Myrtaceae y Primulaceae, concentran el 21% de géneros, y 20% de especies. Los géneros *Miconia*, *Berberis*, *Symplocos*, *Weinmannia*, *Ilex*, *Saurauia* y *Brunellia* agrupan el 17% de especies. El coeficiente de Spearman reveló una correlación negativa y los estimadores no paramétricos predicen entre 89–178 especies no registradas. El mayor número de registros se concentró en Ecuador y Colombia, seguido de Perú, Bolivia, Brasil y Venezuela. Los registros de distribución se concentran en 472 cuencas (20 con 60% de registros y 14–52% de especies). Los Andes del Centro y Norte, el Escudo guyanés, Panamá y Costa Rica, mostraron alta concentración de registros y riqueza; las celdas ubicadas en Perú, Bolivia y Venezuela tuvieron bajo número de registros, sugiriendo falta de esfuerzo de recolección y necesidad de más inventarios.

Posters Session

7014914

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Community engagements to support Fisheries Information and Management System (FIMS) in Kenya artisanal fisheries for policy and decision making

Authors

Fatuma Mzingirwa (Kenya marine and Fisheries Research Institute • Kenya)

Elizabeth Mulwa (Kenya Fisheries service • Kenya)

Paul Lukwenda (Kenya Fisheries Service • Kenya)

Abstract

Kenya has developed a national Fisheries Information Management System (FIMS) with the aim of achieving data collection, seamless data integration, enhancing data sharing and data security, improving data accessibility and increasing end user productivity to ultimately support better decision making. Beach Management Units (BMUs) which are community based organizations legally mandated to co-manage fisheries at the local level play a crucial role in data collection for national planning. These BMUs receive specific training in collecting data from artisanal fishers on aspects such as fish species, quantities, sizes, gear types and fishing effort. Several methods are employed by the community during data collection including traditional manual data forms and digital tools like mobile application such as Open Data Kit (ODK), SmartFish and KoboCollect App. Data gathered at the community level is intended to feed into the national system which is designed as an open access platform that collects, stores and displays fisheries information. This integrated data has significant potential for informing crucial fisheries management activities including stock assessments, development of enforcement strategies, allocation of fishing rights and formulation of both local and national fisheries policies. However smooth and consistent collection and reporting of data by the communities face several challenges such as limited internet access and digital infrastructure in remote areas, capacity gaps in collection and analysis, fragmented data systems across counties and institutions and inconsistent funding and political support for these activities. Addressing these challenges is crucial because community engagement in data collection helps to create awareness on the importance of data for sustainable fishing and the value of accurate information. Further, It enhances data reliability and coverage, strengthen co-management practices, improves compliance with regulations and builds trust between the government and local fisheries to support evidence based decisions for the long-term sustainability.

Posters Session

7015388

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

El estudio “Las Aves de las Flores”

Authors

Daniela España (ASOCOLFLORES • Colombia)

Carlos Ariel López Zuleta (Asociación Bogotana de Ornitología, ABO • Colombia)

Pedro Arturo Camargo Martínez (Asociación Bogotana de Ornitología • Colombia)

Sergio Andrés Collazos González (Asociación Bogotana de Ornitología • Colombia)

Abstract

El estudio “*Las Aves de las Flores*”, desarrollado por la Asociación Bogotana de Ornitología y Asocolflores, caracterizó la avifauna presente en 29 fincas floricultoras de Cundinamarca y Antioquia entre septiembre y octubre de 2024. Las fincas se agruparon en tres bloques geográficos: dos en la Sabana de Bogotá y uno en el Oriente Antioqueño. Se utilizó una metodología basada en conteos por puntos de radio variable, combinando registros visuales y auditivos, lo que permitió una detección eficiente en hábitats heterogéneos.

Cada finca fue dividida en unidades de paisaje para analizar la relación entre hábitat y presencia de aves. Se aplicaron estimadores de riqueza no paramétricos (Chao 2, ACE, ICE) y se evaluaron la composición taxonómica, riqueza, abundancia, diversidad alfa y preferencias de hábitat, según categorías ecológicas y grupos funcionales.

El estudio registró 158 especies de aves, con mayor riqueza en el Oriente Antioqueño. Se identificaron 41 especies comunes entre ambas regiones, reflejando un núcleo compartido en estos sistemas productivos. Entre las especies registradas se encuentran endémicas, casi- endémicas, migratorias y amenazadas, lo que resalta el valor ecológico de las fincas floricultoras.

Se destaca la presencia de la Tingua moteada (*Porphyriops melanops bogotensis*), endémica del altiplano cundiboyacense y en peligro de extinción. Su abundancia aumentó notablemente en comparación con el estudio de 2010, atribuible a la mejora del hábitat en los reservorios de aguas lluvias, a las buenas prácticas agrícolas y ambientales y los procesos de la creación de corredores ecológicos para mejorar la conectividad del paisaje en las fincas floricultoras.

En conclusión, este estudio constituye una línea base para entender la avifauna en sistemas floricultores colombianos. Los resultados subrayan la relevancia de estas áreas para la conservación y sugieren implementar estrategias que equilibren la producción floricultora con la protección de la biodiversidad, con énfasis en especies amenazadas

Posters Session

7019955

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Completeness, reusability, and preservation of the biodiversity data shared in Ecology & Evolution following journal policies

Authors

Bruno Soares (University of Regina • Canada)**Romullo Lima** (Universidade Federal do Rio de Janeiro • Brazil)

Abstract

Transparent, reusable, and well-preserved datasets are essential for advancing biodiversity science and conservation. By adopting data availability statements, *Ecology & Evolution* (E&E) aimed to promote greater transparency and additional value in the research it publishes by enabling the reuse of biodiversity data. This presentation will assess three core characteristics of the data shared in E&E following the establishment of these policies: completeness, reusability, and preservation. While more datasets are being openly shared, many still lack raw data, sufficient metadata, or use proprietary formats. In addition, the common usage of platforms such as GitHub for sharing data and code pose risks for long-term preservation given the lack of unique digital identifiers, thus hampering the long-term potential for reproducibility. To tackle this issue, Ecology & Evolution should reassess the requirements for data sharing and the support given to authors in this direction. By aligning journal policies and author support with preservation infrastructure, we can strengthen the potential for the scientific community to advance a more open and integrated science.

Posters Session

7020820

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

A Comparative Analysis of Scientific Publications and Open Data on the GBIF Platform as an Assessment of Data Availability Gaps

Authors

Oleg Borodin (University of Tartu • Estonia)

Abstract

Currently, there are repositories of open scientific data, including those related to biodiversity. The most well-known initiative in this regard is implemented by the Global Biodiversity Information Facility (GBIF).

The GBIF platform provides access to biodiversity information on a global scale and integrates data from a wide range of sources – museum collections, scientific publications, various open data sources including DNA data, and citizen science initiatives that accumulate species occurrence records using mobile technologies, among others.

Thanks to its continuously improving infrastructure, the active work of experts involved from around the world, and programs aimed at expanding and strengthening the GBIF community, GBIF currently provides open access to more than 3.1 billion occurrence records, and this number continues to grow.

At the same time, there are extensive amounts of information that are still not available through GBIF. This is particularly true for narrowly taxonomic or regional biodiversity platforms, institutional databases, immense lists of scientific publications, and so on.

Information already published in scientific literature – such as journal articles, monographs, conference abstracts, scientific reports, preprints, dissertation abstracts, full dissertations, and so on – is of critical importance. In many cases, these data align with the principles of open scientific data, though some do not, particularly according to the Panton Principles.

This presentation showcases the results of an analysis of the representation of such biodiversity data in GBIF. The analysis was conducted using several taxonomic groups as examples, at the scale of Europe, Eurasia, and from a global perspective. The potential causes of the identified data gaps and possible ways to address them have been examined.

Posters Session

7020332

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

The utility of combining deep learning with metabarcoding to model biodiversity dynamics at a national scale

Authors

Adrian Baggström (Uppsala University • Sweden)

Tobias Andermann (Uppsala University • Sweden)

Abstract

To make informed decisions on how to effectively protect biodiversity, we need knowledge of its spatial and temporal dynamics. By combining detailed biodiversity surveys, geospatial data, and machine learning, we can model biodiversity with the aim of gaining insights into how these complex patterns behave. Here, we present a biodiversity modeling approach that utilizes metabarcoding-derived biodiversity data, remote sensing, and convolutional neural networks (CNNs). We apply CNNs to predict seasonal arthropod richness across Sweden and compare the results with other statistical models commonly used in spatial modeling. The biodiversity data used to train the models constitutes a state-of-the-art metabarcoding dataset composed of arthropod bulk samples, collected weekly from 198 locations, alongside 25 environmental features describing each site's conditions. We find that CNN models do not outperform the other models in the applied performance metrics despite their conceptual advantage of incorporating contextual information. Most of the tested models capture the seasonal trends, resulting in similar performance metrics. However, when sense-checking the spatial predictions, we find that the CNNs predictions yield ecologically more sensible patterns that distinguish different habitat types, as opposed to the other approaches. We conclude that while CNNs offer structural advantages for processing complex spatial data, their predictive performance does not surpass less complex statistical models when applied to datasets of limited size. Nonetheless, as metabarcoding biodiversity datasets continue to grow through large-scale sampling efforts, CNNs constitute a promising modeling approach to capture the complex correlations between biodiversity dynamics and the surrounding multidimensional environmental matrix.

Posters Session

7020944

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Altered particle MCMC: Enhancing bayesian SDMs for autocorrelated temporal species data

Authors

Qiyue Lyu (United States)

Abstract

Species distribution models (SDMs) traditionally rely on temporally aggregated species occurrence data, assuming static environmental conditions and stable species-habitat relationships. However, these assumptions are often violated, especially in dynamic environments where abiotic and biotic factors fluctuate. While recent advances in dynamic SDMs incorporate processes such as dispersal and demographic processes, they remain susceptible to biases from temporally autocorrelated occurrence data, leading to overfitting and inflated niche estimates. To overcome this, I implemented a novel altered particle Markov Chain Monte Carlo (pMCMC) algorithm within a Bayesian SDM framework. This innovative pMCMC method improves upon conventional MCMC by sequentially updating parameters and latent states, utilizing data from the next timestep to refine posterior estimates for the current timestep. My research aimed to answer two critical questions: 1) Does this new algorithm improve model performance for species occurrence datasets exhibiting high temporal autocorrelation compared to other commonly used SDMs? and 2) How does this improvement vary across different spatial resolution scales (1km², 15km², 100km²)? I simulated 1000 hypothetical taxa, each with varying degrees of temporal clumping in their distributional data. The accuracy of four SDMs in modeling these species distributions was then compared: Bayesian Logistic SDM with altered pMCMC, a Bayesian Logistic SDM with standard MCMC, Maximal Entropy Modeling (Maxent), and Random Forest. Results showed the pMCMC model achieved the highest average accuracy in scenarios where species occurrence exhibited high temporal autocorrelation, followed by Maxent and Random Forest. For species whose data had lower temporal autocorrelation, all models performed comparably. Furthermore, the pMCMC-fitted model showed greater performance in fine spatial scale scenarios, but this advantage plateaued at coarser spatial scales as the temporal signal became increasingly averaged out. These findings highlight the altered pMCMC algorithm as a significant advancement for handling temporally autocorrelated occurrence data, encouraging its usage in dynamic, fine-scale ecological applications.

Posters Session

7011700

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Extracting Species-Level Threat Data from Heterogeneous Conservation Literature: Towards a Scalable Approach Using LLMs

Authors

Adam Ulicny (Czech University of Life Sciences • Czechia)**Ivo Kadlec** (Czech University of Life Sciences • Czechia)**Petr Keil** (Czech University of Life Sciences • Czechia)**Florencia Grattarola** (Czech University of Life Sciences • Czechia)

Abstract

Large language models (LLMs) are increasingly being used to automate knowledge extraction from unstructured text. We explore their large scale application in parsing species threat assessments from conservation literature, such as national Red Lists. Conservation status data is often buried in lengthy, unstructured PDFs, making it time-consuming to track and analyze species-level assessments. Despite advances in natural language processing (NLP), few tools can extract structured data across diverse document formats with sufficient accuracy. We present a concept of an end-to-end pipeline that tests a combination of techniques, including species name recognition, contextual chunking, and both local and remote LLM APIs (e.g., Gemini, Ollama) to extract relevant data. Outputs are subject to automated checks and manual validation to ensure quality. Preliminary results show us species name and threat level data from a 600 page PDF can be extracted in around 30 seconds. This approach balances automation with human oversight, enabling efficient and scalable parsing of documents. The pipeline serves as a practical framework for researchers seeking to extract various kinds of species-level data from existing literature.

Posters Session

7020491

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Banco de Hábitat del Alto San Juan -- Yerre cuy: a long-term commitment to research over a 30-year period

Authors

Nestor Galindo-Ruiz (Terrasos S.A.S. • Colombia)**Aristarco Mosquera** (ASOCASAN • Colombia)**Ingrid Lozada Perdomo** (Terrasos S.A.S. • Colombia)

Abstract

The Community Council of Alto San Juan, ASOCASAN, is located in the municipality of Tadó, Chocó. This community is known for engaging in traditional activities such as selective timber harvesting, wildlife hunting, small-scale mining, agriculture, among others. These are all low-intensity, subsistence-level activities, usually scattered throughout the territory, which helps to minimize their residual impact. Despite the limited scale of these practices, the strong cohesion among the council members has enabled them to perceive changes and a decline in the landscape matrix within their territory. Key concerns include the density of existing trees, soil quality, water quality, and the decreasing abundance of fish and wildlife species present in their daily surroundings.

With this level of awareness and commitment to territorial sustainability, the Local Council of Angostura has taken the initiative to become a pioneer in biodiversity conservation through an unprecedented undertaking. This has led to the creation of the first Habitat Bank operated by a local community. As a demonstration of their commitment, they have established strategic alliances with various organizations such as IIAP and Terrasos for the official registration of the project.

Moreover, as part of asserting their sovereignty over the territory, they have opted for the voluntary biodiversity credit market as a financial mechanism to ensure legal, financial, and technical management—following the Protocol for the Issuance of Biodiversity Units developed by Terrasos.

As a biodiversity hotspot initiative, this project will generate open-access data for 30 years, enabling the observation of how this territory responds to climate change, while also documenting how low-intensity natural resource use practices, such as agroforestry systems, align with the generation of biodiversity gains.

Posters Session

7020793

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

FAIR Food: Interoperable Food Composition Data for Biodiversity-Driven Food Systems

Authors

Sarah Brinkley (The Alliance of Bioversity-CIAT • Colombia)

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Marie-Angélique Laporte (The Alliance of Bioversity-CIAT • France)

Abstract

Food Composition Databases (FCDBs) are foundational to understanding the quality and diversity of the global food supply. FCDBs inform research, policy, and interventions across nutrition, health, agriculture, and sustainability sectors. However, the complexity and variability of edible biodiversity—such as how foods are grown and consumed across different geographies—often hinders interoperability, reuse, and integration into food composition data generation workflows. Meeting FAIR Data Principles (Findable, Accessible, Interoperable, and Reusable) in this domain requires robust, standardized metadata frameworks.

In response, The Periodic Table of Food Initiative (PTFI) has developed its Core Metadata schema to support the generation of high-quality, reusable food composition data. This schema includes 45 mandatory metadata elements spanning the food collection, specific food specimen-level information, and information on derived samples. It incorporates established ontologies such as the Food Ontology (FoodOn) and the NCBI Taxonomy to enhance semantic interoperability and ensure alignment with existing data standards across biodiversity-adjacent disciplines.

This presentation outlines the structure and rationale of the PTFI Core Metadata and demonstrates how its implementation improves food systems data harmonization, reproducibility, and cross-study comparisons. By enabling consistent and meaningful metadata collection, this work supports the integration of food compositional data into a broader ecosystem of living data infrastructures, advancing insights into the complex links between food, health, and planetary sustainability.

We invite collaborators, data stewards, and institutions to join a global effort to harmonize and make interoperable food composition data—ensuring that the rich biochemical diversity of the world's foods is visible, usable, and impactful across disciplines and borders.

Posters Session

7008169

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Trait-Based Assessment of Polychaete Community Function and Ecosystem Resilience in the Saudi waters of the Arabian Gulf

Authors

Jayachandran Paravanparambil Rajakumar (Applied Research Center for Environment and Marine Studies, King Fahd University of Petroleum & Minerals • Saudi Arabia)

Joydas Thadickal V. (Applied Research Center for Environment and Marine Studies, King Fahd University of Petroleum & Minerals • Saudi Arabia)

Manokaran Seerangan (Applied Research Center for Environment and Marine Studies, King Fahd University of Petroleum & Minerals • Saudi Arabia)

Jayanath Gopi (Applied Research Center for Environment and Marine Studies, King Fahd University of Petroleum & Minerals • Saudi Arabia)

Jima Mantodi (Department of Marine Biology, Microbiology and Biochemistry, Cochin University of Science and Technology • India)

Manikandan Karuppasamy P. (Applied Research Center for Environment and Marine Studies, King Fahd University of Petroleum & Minerals • Saudi Arabia)

Mohamed Asharaf Thattathazhath (Applied Research Center for Environment and Marine Studies, King Fahd University of Petroleum & Minerals • Saudi Arabia)

Qasem Ali M. (Environmental Protection Department, Saudi Aramco • Saudi Arabia)

Alghamdi Hamed (Environmental Protection Department, Saudi Aramco • Saudi Arabia)

Lozano-Cortés Diego (Saudi Arabia)

Abstract

Functional traits are quantifiable biological characteristics that influence species fitness, ecological interactions, and contributions to ecosystem functioning. This study investigates how habitat heterogeneity shapes the functional structure and diversity of macrobenthic polychaete communities along the Saudi Arabian Gulf, from Khafji to Ras Abu Qamis. Functional diversity was assessed using indices such as functional dispersion (FDis), functional richness (FRic), and Rao's quadratic entropy (RaoQ). Multivariate techniques including RLQ and fourth-corner analyses were used to explore trait-environment relationships across shallow, intermediate, and deep benthic habitats.

Results revealed a more even distribution of functional traits and significantly higher functional diversity ($p < 0.01$) in shallow and intermediate habitats compared to deeper areas. The polychaete communities were predominantly composed of small-sized, infaunal, tube-building, and carnivorous species. To evaluate ecological resilience, functional redundancy (FRed), functional over-redundancy (FORed), and functional vulnerability (FVuln) were calculated. Sediment properties, particularly grain size, explained 27 percent of the variation in functional diversity, as demonstrated through variance partitioning analysis. Coarser sediments (lower phi values) were positively associated with functional diversity. These relationships were further validated using structural equation modeling. The findings underscore the critical role of sediment characteristics and environmental conditions in shaping benthic functional organization. They also demonstrate the value of trait-based ecological indicators for assessing biodiversity and ecosystem resilience in the Arabian Gulf, a region characterized by extreme environmental conditions and increasing anthropogenic pressures. The outcomes of this study provide important baseline information to inform conservation planning and ecosystem management strategies, particularly in data-limited arid marine environments.

Posters Session

7012455

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Vacíos y sesgos en el conocimiento de invertebrados marinos de México: evaluación taxonómica, espacial, temporal y nuevas prioridades de muestreo

Authors

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Abstract

Las lagunas de conocimiento sobre la biodiversidad pueden distorsionar los análisis biogeográficos y dar lugar a interpretaciones erróneas, con consecuencias negativas para la conservación y la gestión de los ecosistemas. En México, el estudio de los invertebrados marinos ha estado limitado históricamente por obstáculos físicos, económicos y sociales. Aquí evaluamos la cobertura taxonómica, geográfica y temporal de la información digital disponible para cuatro grupos de invertebrados marinos —esponjas, cnidarios, equinodermos y moluscos

— con el fin de identificar vacíos y sesgos de conocimiento y proponer áreas prioritarias de muestreo. Reunimos 121 502 registros correspondientes a 4 642 especies provenientes de los repositorios abiertos GBIF y OBIS.

La cobertura taxonómica se evaluó mediante curvas históricas de acumulación de especies y registros. Para la cobertura espacial y temporal calculamos la completitud de inventarios en celdas de 50 × 50 km, identificamos celdas bien muestreadas y estimamos la antigüedad de los registros con referencia a 2024. Posteriormente con esta información espacial elaboramos mapas bivariados para señalar las áreas prioritarias.

Los resultados muestran un aumento notable del conocimiento taxonómico y geográfico desde la década de 1930; no obstante, solo se dispone de información para menos del 35 % del área de estudio y menos del 1,5 % de las celdas puede considerarse bien muestreada. La acumulación de registros presenta sesgos marcados hacia zonas costeras y sistemas arrecifales, donde se concentra la información más reciente.

En consecuencia, aunque el conocimiento sobre la biodiversidad marina ha crecido, los estudios futuros deben enfocarse en los ecosistemas marino-costeros y de mar profundo poco explorados, así como en la actualización de áreas que llevan décadas sin muestreo, donde es probable documentar especies nuevas o nuevos registros para México.

Posters Session

7020594

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Room: Main Hall & Virtual

EN

Biological Characteristics and Maturity Sizes of Selected Commercial Fish Species from the Saudi Coast of the Arabian Gulf

Authors

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Abstract

The relationships between length and weight, condition factor, gonadosomatic index, and length at reproductive maturity of commercially important fish species were assessed in the Arabian Gulf. The research was based on 5,030 gutted specimens collected over three years from major landing sites along the coastline of Saudi Arabia. The b value for the length–weight relationship ranged from 2.72 to 3.20. All species exhibited a tendency toward allometric growth, except for the male populations of *Lethrinus lentjan*, *Epinephelus areolatus*, and *Siganus canaliculatus*, and the female populations of *Carangoides bajad* and *Rhabdosargus haffara*, which showed an isometric growth pattern at the 95% confidence level. The relative condition factor and monthly variations in the gonadosomatic index (GSI) were also calculated. The mean $Krel$ value ranged from 0.99 to 1.10, indicating satisfactory growth for all the studied species. The GSI values were generally high from February to June for most species, whereas *Rhabdosargus haffara* and *Argyrops spinifer* exhibited peak spawning activity from October to February, suggesting year-round spawning among these species. Length at first maturity ranged from 20.68 to

39.34 cm, while the length at 90% maturity varied between 26.02 and 72.86 cm.

Posters Session

7017781

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

BUSINESS RHYTHM SURVEY - SPECIAL BIOECONOMY AND SUSTAINABILITY

Authors

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Abstract

This study presents a comprehensive analysis of the relationship between business activities and biodiversity awareness within the Colombian economic landscape, based on survey data collected from over 6,500 companies affiliated with 22 Chambers of Commerce across 13 departments, including the prominent region of Valle del Cauca.

Our findings reveal a growing familiarity among Colombian companies with key sustainability concepts, particularly biodiversity, climate change, and the bioeconomy. Notably, companies in Cali demonstrate the highest levels of awareness of biodiversity-related issues nationwide, highlighting the regional leadership in integrating environmental concerns into business strategies.

A significant portion of the regional business fabric in Valle del Cauca shows high dependency on natural resources and biodiversity, with approximately 20% of companies indicating strong reliance on these environmental factors for their core operations. This dependence spans across sectors such as agriculture, mining, industry, commerce, and services, emphasizing biodiversity’s integral role in sustaining economic activities.

The data also indicates a positive trend toward environmental responsibility: nearly 60% of the surveyed companies in the Cámara de Comercio de Cali are actively considering implementing environmental sustainability practices in 2025. This readiness reflects an increasing corporate commitment to align with green economy principles and supports Colombia’s broader goals for decarbonization and circular economy.

This research underscores the vital importance of applying robust data analytics to monitor biodiversity-related business trends and to guide policy formulation. Leveraging these insights enables more effective promotion of sustainable business models that balance economic growth with ecological conservation. The study advocates for continued data-driven approaches to support biodiversity preservation as a cornerstone of Colombia’s sustainable development agenda.

Posters Session

7012082

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

A FAIR catalog for essential biodiversity variables: the EBV Data Portal

Authors

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Abstract

Essential Biodiversity Variables (EBVs) are used to monitor the status and trends in biodiversity at multiple spatiotemporal scales. These provide an abstraction level between raw biodiversity observations and indicators, enabling better access to policy-relevant biodiversity information. Furthermore, the EBV vision aims to support detection of critical change with easy to use tools and dashboards accessible to a variety of users and stakeholders.

We present the EBV Data Portal, a platform for sharing and visualizing EBV datasets. It contains a geographic cataloging system that supports a novel biodiversity-specific metadata standard called the “EBV Cube Standard”. This standard builds on metadata specifications of the Attribute Convention for Data Discovery (ACDD) and is interoperable with the Ecological Metadata Language (EML) vocabulary. The EBV Cube and Data Portal work together enabling discoverability and sharing of complex biodiversity data of different types, from remote-sensing derived ecosystems data to modelled spatiotemporal species distributions. Furthermore, the infrastructure offers a web-based interface and API resources to publish, explore and visualize EBV data.

Posters Session

7020814

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Growing global empowered locally: the importance of the iNaturalist network

Authors

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Abstract

iNaturalist hosts a global network of 21 national sites managed by local institutions such as government agencies, museums, universities, and non-profit organisations. These sites are distributed across all continents and reflect a rich diversity of people and communities. Nine are in Latin America (Mexico launched the first in 2013), and only four use English as their main language. The sites not only manage platforms, but also lead outreach, education, and curation efforts tailored to their cultural and ecological contexts. Although iNaturalist continues to grow globally, the contributions and progress of its local site network remain understudied. Here we show the collective progress of the network through numbers and reveal that countries with a local iNaturalist site differ from the global average. Specifically, we tested several explanatory variables (area, population, and GDP per capita) and found that the presence of a national iNaturalist hub was a highly significant positive factor in all three models: total number of iNaturalist records, number of records from iNaturalist in GBIF, and number of active users. Since users often engage beyond national borders, e.g., through identifications, taxon curation, and travel, our results suggest that the efforts of the network have contributed significantly to iNaturalist's global success beyond the United States. Our findings also highlight the value of localised strategies within global citizen science platforms.

Posters Session

7020704

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

How can a Biodiversity Network help understand the effects of climate change on biodiversity?

Authors

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Abstract

Quebec is one of Canada's largest provinces, with a remarkable latitudinal gradient and ten bioclimatic zones ranging from maple forests to arctic tundra. This great diversity of ecosystems is linked to a rich biodiversity that can be highly vulnerable to climate change. The Quebec Biodiversity Monitoring Network is an initiative of the Ministry of the Environment, Climate Change, Wildlife and Parks (MELCCFP) launched in 2016. This sub-national program aims to provide a comprehensive description of Quebec's biodiversity and monitor the impact of climate change on species, communities and ecosystems by sampling a series of bio-indicators in space and time. The data is collected using a standardised methodology with the participation of numerous local partners and managed through a portal developed by Biodiversité Québec. To date, 422 sites have been visited (25% of which were revisited) between 45 N and 62 N. The protocols were carried out in forests (23%), wetlands (peat bogs 28% & marshes 6%), aquatic environments (lakes 19% & rivers 17%) and tundra (6%), inventorying several terrestrial taxonomic groups (mammals, birds, insects, vegetation) and aquatic groups (fish and zooplankton). Our aim here is 1) to present the methodology and bio-indicators of the Biodiversity Network, 2) to detail preliminary analyses of the impact of temperature across the latitudinal gradient of sites on species richness, indicator species and community composition, using multi-variate analyses, and 3) to demonstrate the relevance and contribution of such a network as part of a global vision aimed at meeting society's needs in terms of environmental policy and decision-making.

Posters Session

7020999

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Collaborative Nature: documenting the flora of Maranhão's Restinga on iNaturalist with citizen science

Authors

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Abstract

Along the coast of biodiverse Maranhão — a state in the northeast region of Brazil — the coastal sedimentary dune vegetation called restinga holds significant ecological value but remains poorly understood. This unique ecosystem is increasingly threatened by urbanization, facing intense pressure from urban expansion and real estate speculation. However, human proximity also offers great potential for citizen science using iNaturalist, a platform that simplifies biodiversity data collection for observers. Engaging local communities through platforms like iNaturalist enhances biodiversity monitoring and provides critical data for conservation. iNaturalist's AI-assisted species suggestions further streamline species identification in the field, but relies on diverse and well-documented records — including photos and geolocation — and their accuracy in data-poor but species-diverse regions like restinga is unclear. iNaturalist hosts hundreds of millions of biodiversity records globally, and Brazil's Northeast contributes ~124,000 plant observations and 6,200 recorded species, but Maranhão's observation density is ~4X lower than this regional average, with only 6,428 observations and 1,272 species. The restinga of Maranhão is even less well represented, including Curupu Island, which covers 16 km², but only counts 24 observations for 16 species on iNaturalist, despite possessing over 120 known species. To test if these data gaps affect accessibility to accurate AI-powered species identifications for citizen scientists, we present a new observation dataset and species checklist for Curupu Island collected via workshops with citizen scientists to both train them how to take better botanical photos and increase the data availability of the region. This new restinga-focused dataset will further support accuracy evaluations of AI-powered plant identification models, improving the overall quality and quantity of restinga observations, and increasing the rate of correct identifications. This study highlights how community engagement can enhance biodiversity data and improve the performance of digital tools for environmental monitoring in underexplored ecosystems like restinga.

Posters Session

7021005

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Room: Main Hall & Virtual

ES

Fortaleciendo vínculos comunidad-naturaleza: uso de iNaturalist en procesos de monitoreo participativo en el marco de acuerdos de conservación en Bogotá

Authors

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Abstract

Los Acuerdos de Conservación son una herramienta eficaz para el fortalecimiento de medidas de preservación y conservación en zonas estratégicas de Bogotá que vienen siendo implementados por la Secretaría Distrital de Ambiente. Entre las diferentes estrategias desarrolladas en los Acuerdos de Conservación, el monitoreo comunitario de la biodiversidad ha sido clave para generar datos sobre fauna y flora en predios privados y, a su vez, enriquecer el conocimiento que las comunidades locales tienen sobre la diversidad biológica. La inclusión de comunidades locales ha fomentado el conocimiento, el cuidado y la apropiación del territorio.

Desde 2022 se han realizado alrededor de 138 jornadas sobre técnicas de monitoreo e identificación de biodiversidad con la participación de aproximadamente 1360 personas de las comunidades vinculadas. Estas jornadas han incluido charlas, talleres, caracterizaciones y monitoreos participativos que abarcan temas referentes a los grupos de avifauna, artropofauna, herpetofauna, mamíferos y flora. El uso de iNaturalist como plataforma de ciencia participativa ha sido fundamental ya que ha permitido registrar, sistematizar y socializar los resultados de cada jornada, facilitando así la construcción de bases de datos abiertos.

A mayo del 2025, se han elaborado aproximadamente veinte proyectos colaborativos en la aplicación, en los que se han recopilado alrededor de tres mil quinientas observaciones, correspondientes a un aproximado de cuatrocientos especies de fauna y flora, principalmente en la RFRP del Norte de Bogotá D.C. – Thomas Van Der Hammen y la RFP Bosque Oriental de Bogotá, zonas que hacen parte de la Estructura Ecológica Principal del Distrito. iNaturalist no solo ha sido una herramienta de registro, también, de afianzamiento del vínculo entre la comunidad, la naturaleza y el Distrito.

La experiencia de los Acuerdos de Conservación ha demostrado el valor de la participación ciudadana en la conservación de áreas privadas y la gestión de datos de biodiversidad en Bogotá.

Posters Session

7020995

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LA FLORA EN ÁREAS PROTEGIDAS DISTRITALES DE BOGOTÁ, D.C. - COLOMBIA

Authors

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Abstract

La ciudad de Bogotá D.C cuenta con ocho Parques Distritales Ecológicos de Montaña (PDEM) y diecisiete Reservas Distritales de Humedal (RDH) que forman parte de la Estructura Ecológica Principal, cuyo fin es conservar y recuperar los recursos naturales y la biodiversidad, a través de corredores que permitan el desarrollo de los procesos ecológicos.

La recopilación de datos desde el año 2016, basada en protocolos estandarizados de muestreo, ha permitido construir líneas de base confiables, facilitar la comparación entre áreas y años, y orientar decisiones de conservación fundamentadas en evidencia. Con el fin de avanzar en el conocimiento de la flora presente en estas áreas, el Grupo de Monitoreo de la Biodiversidad (GMB) de la Secretaría Distrital de Ambiente realizó el inventario de especies vegetales registradas en las diferentes áreas. Se realizaron registros fotográficos y recolecciones de muestras botánicas para su debida identificación, las cuales fueron depositadas en el Herbario del Jardín Botánico de Bogotá (JBB); asimismo, se consultaron diferentes bases de datos digitales, garantizando la calidad y trazabilidad de los datos.

A mayo del 2025, se registran 139 familias distribuidas en 464 géneros y 896 especies. Las familias más diversas son: Asteraceae (104 *sp.*), Fabaceae (44 *sp.*) y Solanaceae (36 *sp.*), mientras que para treinta y nueve (39) familias sólo se registra una especie. Además, según su origen se registran 45 especies endémicas, dos endémicas/cultivadas, 310 nativas, 32 nativas/cultivadas y 188 exóticas.

En cuanto a su estado de conservación, según la Lista Roja de la UICN, cinco especies se encuentran en la categoría “En Peligro” (EN), diez como “Vulnerables” (VU) y siete como “Casi Amenazadas” (NT). Adicionalmente, 15 especies están incluidas en el Apéndice II del convenio CITES, y de acuerdo con la Resolución 0126 de 2024 del MADS, cinco de estas se encuentran bajo la categoría de “Vulnerable”.

Posters Session

7020998

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BIODIVERSIDAD DE FAUNA DE LAS ÁREAS PROTEGIDAS: MONITOREO ESTANDARIZADO PARA LA CONSERVACIÓN DE FAUNA SILVESTRE URBANA EN BOGOTÁ, D. C.

Authors

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Abstract

Bogotá D. C. cuenta con 32 áreas protegidas que hacen parte de la estructura ecológica principal de la ciudad, entre las que se incluyen 17 Reservas Distritales de Humedal y 8 Parques Distritales Ecológicos de Montaña.

Desde el año 2021 y hasta la fecha el Grupo de Monitoreo de la Biodiversidad (GMB) de la Secretaría Distrital de Ambiente implementa un programa de monitoreo. A través de protocolos estandarizados, se recolecta información sobre distribución, abundancia y estado de artrópodos, aves, reptiles y anfibios, y mamíferos. Estos datos han permitido consolidar una línea base de la diversidad faunística en el territorio, identificar especies de importancia ecológica, evaluar amenazas y orientar acciones de conservación. Este esfuerzo posiciona a Bogotá como uno de los grandes centros urbanos que utiliza la evidencia científica en la toma de decisiones basada en datos para gestionar la conservación de la biodiversidad.

Entre los principales resultados, para la artropofauna se registran 818 especies y morfoespecies de 195 familias. Destacan algunas endémicas como *Agesander ruficornis*, *Deretrachys juvenicus*, *Ozodera callidioides*, *Tityus columbianus*, esta última clasificada como vulnerable. En la avifauna, con 207 especies registradas, destacan especies endémicas como el *Synallaxis subpudica* y *Rallus semiplumbeus*, esta última en categoría de amenaza.

Para reptiles y anfibios, se han registrado siete especies de reptiles (tres endémicas), incluida la lagartija de Bogotá (*Anadia bogotensis*), y cinco especies endémicas de anfibios como la rana de niebla (*Pristimantis elegans*), ambas clasificadas como vulnerables. En cuanto a la mastofauna, se cuenta con registro de 15 especies de mamíferos terrestres y 25 especies de murciélagos. Se destacan tres especies endémicas, el ratón de montaña (*Thomasomys niveipes*), la musaraña andina (*Cryptotis thomasi*) y la ardilla andina (*Leptosciurus*

pucheranii), y la presencia de especies sensibles y de importancia ecosistémica como el tigrillo lanudo (*Leopardus pardinoides*) y el cusumbo (*Nasua olivacea*).

Posters Session

7021000

23/10/25 | 17:00 & Virtual

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SEGUIMIENTO A LA CALIDAD DEL AGUA EN LAS RESERVAS DISTRITALES DE HUMEDAL (RDH) EN BOGOTÁ, D.C. - COLOMBIA

Authors

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Abstract

Los humedales de Bogotá D. C. cumplen funciones esenciales: regulan el clima y el recurso hídrico, mitigan inundaciones y sostienen una gran diversidad de fauna y flora. Estos ecosistemas, además, son nodos clave en la conectividad ecológica de la ciudad. Actualmente, la Secretaría Distrital de Ambiente administra diecisiete (17) Reservas Distritales de Humedal (RDH) las cuales están registradas como parte de la Estructura Ecológica Principal, y once (11) de ellas conforman el complejo de humedales urbanos reconocidos por la Convención Ramsar. Su relevancia exige un monitoreo constante y basado en datos confiables como insumos para la toma de decisiones, que permitan evaluar su estado ambiental de manera objetiva y oportuna.

Con este propósito, desde 2017 la Secretaría Distrital de Ambiente desarrolla campañas anuales y desde 2024 trimestrales de muestreo que integran variables fisicoquímicas, biológicas y ecológicas. La información recolectada incluye indicadores como índices de calidad del agua, índices de contaminación, y métricas de diversidad, lo que permite trazar un panorama detallado y dinámico del estado de estos cuerpos de agua a lo largo del año, bajo distintas condiciones climáticas.

Los humedales bogotanos, al ser sistemas lénticos, están fuertemente influenciados por el nivel freático y la precipitación, suelen presentar alta carga de materia orgánica y procesos de mineralización asociados a suelos de origen andisol. Estas condiciones determinan la presencia de organismos acuáticos adaptados, y, junto a variables como temperatura y oxígeno disuelto, moldean la estructura de las redes tróficas: desde fitoplancton y zooplancton hasta macroinvertebrados, peces y aves.

Los datos generados son esenciales para identificar amenazas, entender procesos ecológicos y diseñar estrategias eficaces de conservación y restauración del recurso hídrico, asegurando la resiliencia de los humedales frente al cambio climático y la presión urbana.

Posters Session

7020876

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Managing Ornithological Data within the PlutoF Common Data Space

Authors

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Abstract

PlutoF is a comprehensive biodiversity data management platform developed by the University of Tartu, Estonia. It is widely adopted by Estonian birdwatchers, with bird-related data constituting over two-thirds of its approximately 5.8 million stored observations.

PlutoF facilitates the entire data lifecycle, supporting seamless integration of diverse datasets through a modular and intuitive workspace. Researchers can integrate a variety of data types, including field observations, museum specimens, samples, and genetic sequences. The platform offers customizable data access controls, allowing datasets to remain private, shared within defined workgroups, or made publicly available.

Data entry into PlutoF is highly flexible and includes multiple user-friendly pathways. The official PlutoF GO mobile application offers extensive functionality comparable to the desktop interface, enabling efficient data collection by both researchers and citizen scientists during fieldwork. PlutoF's interactive CSV import tool simplifies the integration of GPS tracking data from external sources, such as Movebank and BirdMap.5dvision.ee.

Specialized applications are also being developed for bird observatories to streamline bird ringing (banding) data management, utilizing integration through Google Sheets and the PlutoF API. Additionally, historical monitoring data have been digitized using AI technologies, ensuring long-term data preservation and accessibility.

PlutoF supports extensive data dissemination through its API, enabling publication on external platforms such as GBIF using standardized Darwin Core formats, complete with DOI generation. Furthermore, PlutoF underpins Estonia's national eBiodiversity portal, which includes specialized thematic resources like the Plant Atlas and Breeding Bird Atlas, as well as customized web applications like NatureSound of Estonia.

Overall, PlutoF empowers researchers with advanced tools for effective data management, collaboration, and dissemination, thus enhancing biodiversity research and conservation efforts.

Posters Session

7020885

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Integrating biodiversity data and niche modeling to evaluate climate change impacts on rare plant species from Brazil's Iron Quadrangle

Authors

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Abstract

The Iron Quadrangle (Quadrilátero Ferrífero) in southeastern Brazil hosts a high number of rare and endemic plant species adapted to unique geological formations and microclimates. This study assessed the potential impacts of future climate change on the distribution of eight species: *Aiouea tetragona*, *Dyckia consimilis*, *D. rariflora*, *Hoplocryptanthus ferrarius*, *H. schwackeanus*, *Paepalanthus amoenus*, *P. magalhaesii*, and *Vriesea minarum*. Geographic coordinates were compiled through online herbarium searches using the R packages spocc and BIEN, which accessed GBIF records; direct queries on the speciesLink platform, a Brazilian initiative for biodiversity data; and field records provided by Vale S.A. Bioclimatic variables from WorldClim v2.1 were used to model current distributions, while future projections from regionally suitable climate models (EC-EARTH3-veg, INM-CM5-0, MRI-ESM2-0) supported predictions under optimistic (SSP126) and pessimistic (SSP585) scenarios for 2050 and 2090. Ecological niche models were generated in R using the ENMTML package, incorporating spatial rarefaction and four algorithms. Only models with high predictive performance, based on AUC (Area Under the Curve > 0.75) and TSS (True Skill Statistic > 0.5), were retained for ensemble forecasting. *A. tetragona*, *P. magalhaesii*, and *H. ferrarius* are projected to lose all suitable habitat under SSP585 by 2090, while *D. consimilis*, *H. schwackeanus*, and *V. minarum* are expected to maintain small persistent ranges. In contrast, *D. rariflora* and *P. amoenus* show range expansion under SSP126 by 2090. Based on these data and modeling outputs, priority areas for conservation and reintroduction were identified, including Serra do Caraça, Sinclinal Moeda, Serra do Gandarela, and Serra de Ouro Branco. This study is part of Rede Propagar, an initiative by Vale S.A. that aims to guide the conservation and reintroduction of native plant species in the Iron Quadrangle. The use of open data and predictive modeling provides a scientific foundation for long-term biodiversity management in this climate-vulnerable hotspot.

Posters Session

7019836

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

SeedPOD, the Seed Portal for Online Data

Authors

Sarah Cheseldine (United Kingdom)**Mike McCormick** (United Kingdom)**Teagan Hartenthaler** (United Kingdom)**Naomi Carvey** (United Kingdom)

Abstract

Ecological restoration initiatives are currently hampered by a widely acknowledged global bottleneck in native seed supply. Quantitative and qualitative analysis of this bottleneck is made difficult due to the lack of availability of high-quality, detailed data on collections of native seeds and the wild populations they derive from. In practise, restoration practitioners can struggle to find seed sources, especially sources of high-quality, genetically diverse, native seeds. Compounding these issues, means for knowledge exchange between researchers and restoration practitioners and native seed custodians is often fragmented.

To help address these issues, SeedPOD is an exciting new open data resource for restoration and research communities due for release in 2026. SeedPOD will unlock detailed field, processing, seed quantity and viability test data on wild plant species throughout their global distribution range and will link related seed collections stored at multiple locations for easy identification and comparison. SeedPOD will also disseminate germination and propagation protocols to assist the process of transforming native seed back into thriving plant communities, which will be complimented with links to informative digital resources.

Significantly, SeedPOD will include a point of request for seed samples from participating native seed custodians, who will have in SeedPOD a user-friendly, reliable platform to disseminate seed stock availability data. Researchers and restoration practitioners will be able to access high-quality data, and to identify appropriate seed sources available for use.

Posters Session

7018727

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Addressing Data Sparsity in Species Occurrence Cubes Using Predictive Modeling Approaches: a case study in Québec, Canada

Authors

Guillaume Larocque (QCBS|Biodiversité Québec|GEO BON • Canada)**Rousseu François** (Biodiversité Québec|Université de Sherbrooke • Canada)**Juhasz Claire-Cécile** (Biodiversité Québec|Université de Sherbrooke • Canada)**Beauregard Vincent** (Biodiversité Québec|Université de Sherbrooke • Canada)**Gravel Dominique** (Université de Sherbrooke|Biodiversité Québec • Canada)

Abstract

Species occurrence or abundance cubes are often presented as key inputs for biodiversity modelling pipelines within the framework of Essential Biodiversity Variables (EBVs) and for deriving biodiversity indicators. Generating these cubes can be very challenging when the available occurrence datasets – such as those dominated by citizen science data – are spatially, temporally, and taxonomically uneven and biased. In certain regions of the world, such as northern Canada, occurrence data are unavailable for large portions of the landmass and for entire taxonomic groups. As a result, raw occurrence cubes for these regions are very sparse and of limited value for reporting on biodiversity status and trends.

To address this problem, we assess various approaches to modeling species distributions prior to assembling the species occurrence cube for the province of Québec, Canada. We compare more classical species distribution modeling approaches to simpler methods based on nearest neighbors and more novel ones based on recommendation algorithms. We also assess the role of spatial and temporal resolution and summarize the cube along its three dimensions: taxonomic, to obtain measures of richness in space and time; spatial, to derive abundance time series for each species; and temporal, to generate spatial metrics of species prevalence over time. We then evaluate how the EBVs derived from different models compare to those from raw occurrence cubes, and how insights for biodiversity status and trend reporting vary depending on the model and cube dimension.

Overall, we emphasize that given the sparsity of biodiversity occurrence data, species distribution modeling should be integrated into every pipeline that relies on occurrence cubes for biodiversity reporting.

Posters Session

7019969

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Bridging Biodiversity Data Gaps: Mining Scientific Literature for Biodiversity Datasets Using Large Language Models

Authors

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Alexandre Alexandre Fuster-Calvo (Université de Sherbrooke • Canada)

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Abstract

Biodiversity monitoring relies on comprehensive datasets, but significant data gaps in taxonomic, spatial, and temporal coverage limit reliable trend analysis and evidence-based conservation strategies. Organizations like Biodiversité Québec, which operates as a sub-national Biodiversity Observation Network, exemplify this challenge as they depend on accurate, comprehensive data to monitor biodiversity trends and provide reliable indicators to researchers, decision-makers, and conservation organizations. While platforms like GBIF aggregate standardized biodiversity data, substantial valuable information remains trapped within unstructured scientific literature, as many researchers lack resources to format and share their data in discoverable formats.

Large Language Models (LLMs) like GPT-4 present an opportunity to extract this hidden data with greater ease than traditional Natural Language Processing approaches, which require extensive expertise and training datasets. This study explores using LLMs to identify and extract relevant biodiversity datasets from scientific literature to address data gaps in Quebec, Canada.

Our methodology employs GPT-4 to extract structured metadata from data abstracts, including studied species, spatial range, temporal range, and data type. We evaluate three key aspects: (1) precision and repeatability of LLM-driven extraction, (2) accuracy through comparison with manually annotated benchmark datasets, and (3) practical application by processing abstracts from repositories like Zenodo and Dryad, then comparing results with existing GBIF data to identify potential gaps.

The work will present preliminary results exploring LLMs ability to achieve reliable information retrieval of ecological dataset descriptions from literature. The proposed workflow successfully identifies potential datasets that could enhance structured biodiversity data coverage. Our findings contribute to identify and prioritize datasets that will help bridge biodiversity data gaps, facilitating improved monitoring and evidence-based conservation strategies through better integration of data currently hidden in scientific literature.

Posters Session

7020687

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Consolidating data on the vegetation of the northern Serranía de Los Yariguíes as a contribution to open science.

Authors

Silvia Fernanda Ardila Hurtado (Universidad Industrial de Santander • Colombia)**Björn Reu** (Universidad Industrial de Santander • Germany)

Abstract

This study aims to consolidate and publish data on the vegetation of the northern Serranía de Los Yariguíes through the Colombian Biodiversity Information System (SiB Colombia). Information from three research projects, each employing different methodologies, was integrated using cleaning, standardization, and validation processes in accordance with the Darwin Core standard. A total of 5,674 individuals across 140 plots and representing 309 species were analyzed, with 46.6% of the species previously unrecorded in GBIF for Serranía de Los Yariguíes. Among the projects, TRANSE excelled by recording the highest number of sampled individuals and achieving the greatest taxonomic resolution. Analyses of floristic diversity and composition helped identify methodological gaps, evaluate diversity patterns, and compare outputs from each project. Fagaceae and Myrtaceae emerged as the most ecologically significant families, while *Calycolpus moritzianus* was the species with the highest number of recorded individuals. The first of the databases has been published in SiB Colombia as part of this initiative, and the other two are in the publication process. This study is a valuable contribution to open science, providing standardized data that supports future research in an underrepresented and highly biodiverse region. Additionally, it underscores the importance of unifying sampling protocols, establishing consistent taxonomic standards, and increasing research efforts in poorly studied areas, thereby advancing the sustainable management and understanding of the region's vegetation.

Posters Session

7020530

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Cinco Años del Portal de Biodiversidad de Guatemala: Incrementando Capacidades de Movilización de Colecciones de Historia Natural con Symbiota

Authors

Samanta Orellana (University of Kansas • United States)**Zabdi López** (University of Bern • Switzerland)**Maura Quezada** (Centro de Estudios Conservacionistas, Universidad de San Carlos de Guatemala • Guatemala)**Jiichiro Yoshimoto** (Universidad del Valle de Guatemala • Guatemala)**Lucía Prado** (Museo de Historia Natural, Universidad de San Carlos de Guatemala • Guatemala)**Ana Luisa Ambrocio** (Museo de Historia Natural, Universidad de San Carlos de Guatemala • Guatemala)**Nico Franz** (University of Kansas • United States)**Edward Gilbert** (University of Kansas • United States)

Abstract

Symbiota es un software de código abierto para el manejo y movilización de información de biodiversidad. Los portales generados con Symbiota funcionan como sistemas de manejo de colecciones y agregadores a mediana escala, lo que facilita la digitalización y publicación de registros de biodiversidad de manera simultánea. Los más de 60 portales Symbiota activos actualmente tienen distintos enfoques geográficos o taxonómicos y son manejados por comunidades de investigadores alrededor del mundo, con apoyo técnico del equipo Symbiota de iDigBio. En 2020, fue generado el Portal de Biodiversidad de Guatemala (PBG) con el propósito de digitalizar y hacer accesibles los registros en colecciones biológicas del país. Con cinco años de funcionamiento, el PBG ha facilitado la digitalización y movilización de más de 56,000 registros de especímenes de animales, hongos, plantas y fósiles. Además, la conexión directa del PBG con la Instalación Global de Biodiversidad (GBIF) ha agilizado la movilización adicional de datos e imágenes a esa plataforma global. La presencia digital de las colecciones guatemaltecas ha permitido su utilización en al menos 500 publicaciones científicas, incluyendo trabajos de investigadores nacionales, y la incorporación de las instituciones locales al Registro Global de Colecciones Científicas (GRSciColl). Por su interfaz en español, el PBG ha servido como plataforma para la capacitación de cientos de usuarios en Guatemala y toda Latinoamérica, contribuyendo con el incremento de capacidades de movilización de datos de biodiversidad en la región.

Posters Session

7020198

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Digitization and Rapid Specimen Identification: a New Initiative at the Missouri Botanical Garden Herbarium

Authors

Matthew Austin (Missouri Botanical Garden • United States)**Jordan Teisher** (Missouri Botanical Garden • United States)**Mike Blomberg** (Missouri Botanical Garden • United States)**Gabrielle Rosa** (Missouri Botanical Garden • United States)**Jeddy Choi** (Missouri Botanical Garden • United States)**Meredith Woodward** (Missouri Botanical Garden • United States)**Gunter Fischer** (Missouri Botanical Garden • United States)

Abstract

Applications of artificial intelligence (AI) technology to the online mobilization of herbaria have the potential to expedite research and increase curatorial efficiency. This year, the Missouri Botanical Garden embarked on a major new initiative – coined the *Revolutionizing Species Identification* (RSI) project – that combines digitization and AI to create tools for rapid specimen identification. The RSI project will

(1) image and transcribe all 8 million specimens in the MO herbarium, (2) use digitized specimen data and hyperspectral scans to develop models that can automatically predict specimen taxonomy, and (3) establish a curatorial mentorship program to build taxonomic expertise in early career herbarium professionals. This 6-year project will provide MO specimen data and resulting identification tools as online resources for the botanical community. As biodiversity loss continues unabated across the globe, it is vital to expedite the digitization of herbaria, while building taxonomic expertise and tools to ensure these collections remain well curated into the future.

Posters Session

7020489

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Assessing post-fire mortality of paramo giant rosette plants using artificial intelligence on high resolution drone imagery

Authors

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Björn Reu (Universidad Industrial de Santander • Germany)

Abstract

Paramo ecosystems are vital for biodiversity and ecosystem services such as water provision and regulation, but face increasing threats from climate change, human activity, and wildfires. Giant rosette plants (*Espeletia* spp.) are keystone species in these ecosystems, but their response to fire has received little attention. Monitoring their recovery from wildfires and other disturbances is crucial for an effective ecosystem management. However, traditional field surveys are often limited by the remoteness and the challenging terrain of paramos. This study aims to assess the post-fire mortality of giant rosette plants after a wildfire in the Santurbán Páramo (Colombia). We use You-Only- Look-Once (YOLO) and Real Time Detection Transformers (RT-DETR) to detect giant rosette plants in high resolution multispectral drone imagery captured approximately one year after the wildfire. We then employ image segmentation using the Segment Anything Model (SAM) to extract and individualize the rosettes from the background soil. Finally, we use an NDVI threshold to evaluate each plant's health condition. A better understanding of post-fire mortality rates of giant rosette plants could support conservation efforts and guide restoration strategies for paramo ecosystems. This novel approach leverages artificial intelligence techniques and its computational power to enable high-resolution, individual-level assessment of plant health, offering unprecedented precision in studying these diverse and ecologically important ecosystems that are traditionally difficult to monitor.

Posters Session

7020414

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

The Role of Protected Areas in Conserving Lowland Grassland and Savannah Ecosystems in Latin America

Authors

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Adriana Martin (Leibniz Centre for Agricultural Landscape Research – ZALF • Germany)

Carla Baldivieso-Soruco (Leibniz Centre for Agricultural Landscape Research – ZALF • Germany)

Janika Haemmerle (Leibniz Centre for Agricultural Landscape Research – ZALF • Germany)

Luca Eufemia (WWF – Mediterranean Marine Initiative • Italy)

Stefan Sieber (Leibniz Centre for Agricultural Landscape Research – ZALF • Germany)

Abstract

Grasslands and savannas rank among the most threatened terrestrial ecosystems globally, undergoing accelerated rates of land-use transformation. Despite this, they constitute critical reservoirs of endemic biodiversity and support a wide array of ecosystem services. In Latin America, these biomes encompass approximately 13% of the terrestrial surface and are integral to agricultural productivity—particularly extensive cattle ranching—while also possessing socio-cultural significance. In regions such as Colombia's Llanos Orientales and Argentina's Pampas, Protected Areas (PAs) and Private Reserves (PRs) are pivotal for biodiversity conservation and biological data acquisition; however, they occupied a relatively small proportion of the landscape (3.7%–12.8%). Emerging initiatives, including Civil Society Reserves and Regenerative Ranching systems, are gaining prominence as mechanisms for sustainable land stewardship.

Nonetheless, their role in sustaining primary productivity and contributing to biodiversity data remains underexplored through integrative spatiotemporal analyses. This study evaluates the ecological contributions of PAs and PRs within Colombian and Argentine grasslands by integrating remote sensing and biodiversity occurrence data. We utilized MODIS MOD13Q1 (2000–2025) and MapBiomas time series to assess vegetation productivity (via NDVI and EVI) across conservation areas, buffer zones, and adjacent unprotected landscapes.

Additionally, we analyzed over 1200 avian and 4000 vascular plant species occurrences, and species data cubes from the Global Biodiversity Information Facility (GBIF). Results indicate a positive trajectory in vegetation productivity within PAs since 2010, contrasting with stability or decline in neighboring non-protected farms. Biodiversity metrics were significantly higher within and near PAs, with endemism levels exceeding regional baselines by over 20%. Notably, surges in species records align with targeted conservation projects led by NGOs and universities in partnership with PR networks. These findings underscore the critical role of private conservation strategies in increasing biodiversity knowledge and enhancing ecosystem resilience in grassland ecosystems which remain under pressure from afforestation, agro-industrial expansion, and extractive industries.

Posters Session

7015314

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

From biodiversity knowledge to action at the subnational level: the Catalan Biodiversity Observatory

Authors

Lluís Brotons (CREAF, CTFC, Catalan Biodiversity Observatory • Spain)

Maria Blasi (CREAF • Spain)

Gerard Bota (CTFC • Spain)

Sergi Herrando Vila (CREAF • Spain)

Helena Ramírez Cervera (Catalan Biodiversity Observatory • Spain)

Dani Villero (CREAF, CTFC, Catalan Biodiversity Observatory • Spain)

Pau Sainz de la Maza (Catalan Government • Spain)

Abstract

The Catalan Biodiversity Observatory (*Observatori del patrimoni natural i de la biodiversitat*) is a space for dialogue between research, management, and policy-making in the field of natural heritage and biodiversity. The objective is to enable decision-making based on scientific evidence and to promote the integration of different research areas to respond to society's knowledge needs regarding the management and conservation of nature.

The observatory is an example of a regional knowledge hub, where data, researchers, policymakers, and society meet. To achieve this, the Observatory is organized in a way where each member entity provides data, analysis, and knowledge based on its projects and participates in scientific and technical debates on the implications of research on the initiatives and functions of the Observatory.

In this poster, we will present the structure, governance of the data, and showcase successful examples of data integration, data application, and community engagement in the orchestration of in-depth assessments on pollinators, the state of nature and the impact of drought on biodiversity.

Posters Session

7014825

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Sonochiro, a powerful tool for studying bats using their ultrasound

Authors

Cédric Elleboode (Biotope • France)**Thierry Disca** (Biotope • France)**Julien Tranchard** (Biotope • France)

Abstract

The conservation status of bats is a global concern, with many species threatened with extinction. Developments such as wind farms and transport routes have a particular impact on bats because, in addition to causing habitat loss and fragmentation, they can lead to direct mortality of individuals through collisions.

Many bat species use echolocation to move and feed, and the ultrasound signals emitted are characteristic of each species. For these reasons, over the last few decades, the analysis of bat ultrasonic emissions has played a major role in the study of this biological group. At the same time, the development of automatic acoustic recorders has led to the collection of huge volumes of acoustic recordings to inventory bat species and assess their activity, particularly as part of impact assessment of wind farm projects.

To process these volumes of data quickly and reliably, Biotope has developed the Sonochiro software. Thanks to its AI algorithm based on the use of a random forest classifier, Sonochiro makes it possible to quickly sort recordings by detecting the ultrasonic emissions of bats. This algorithm also makes it possible to predict the species associated with each emission with a confidence index.

To enhance Sonochiro's performance, Biotope has developed geographical classifiers that are selected by the user according to the location of the study. These classifiers are built up from thousands of recordings of the ultrasonic emissions of bat species known in the region of the world where the survey is taking place.

Posters Session

7014717

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Development of Marine Bio-Resource Information System and OBIS Korea Node

Authors

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Young-Ik Yang (Korea, Republic of)

Yong-Rock An (Korea, Republic of)

Abstract

The National Marine Biodiversity Institute of Korea (MABIK) has developed and currently operates the Marine Bio-Resource Information System (MBRIS) to systematically manage and share marine biological resources of national and industrial value. MBRIS is a centralized platform that integrates species data, metadata, images, publications, and patents collected by MABIK and Marine Fishery Bio-resources Centers (MFBiCs). All data are stored in a cloud-based system and made accessible to the public via

As of May 2025, MBRIS manages approximately 600,000 records. Its core services include the National Marine Species List, metadata on biological resources and specimens, online distribution and rental services, and the Marine Biobank, which provides functional materials— such as whitening, anti-wrinkle, and antimicrobial agents—for research and industrial use.

To support marine biodiversity research, MABIK also provides spatial information services, including verified occurrence data for 11,254 species and real-time satellite tracking of 59 individuals from three sea turtle species: green, loggerhead, and hawksbill.

In 2023, MABIK joined the Ocean Biodiversity Information System (OBIS) as the official Korea Node and began developing a national coordination framework. OBIS is a global network of over 500 institutions in 56 countries, operating more than 20 regional and national nodes to share standardized marine biodiversity data.

To fulfill its role, MABIK conducted a pilot study and developed a prototype system that included the English MBRIS website and a dedicated OBIS Korea Node portal. MABIK adopted IPT, an open-source tool developed by GBIF, to publish over 300,000 occurrence records to OBIS.

Since January 2025, the English MBRIS site has been officially launched, advancing MABIK's mission to become a global hub for marine biodiversity data.

Posters Session

7015638

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

One data source, multiple perspectives - maintaining accurate, integrated and high-quality collections data

Authors

Richard Dodd (Royal Botanic Gardens, Kew • United Kingdom)

Reinis Rozkalns (Royal Botanic Gardens, Kew • United Kingdom)

Udayangani Liu (Royal Botanic Gardens, Kew • United Kingdom)

Evgeniy Meyke (EarthCape Oy • Finland)

Robert Turner (Royal Botanic Gardens, Kew • United Kingdom)

Abstract

Royal Botanic Gardens, Kew is home to the largest and most diverse botanical and mycological collections in the world. Alongside the physical collections we also hold their associated data, the value of which, in the face of threats to global biodiversity, cannot be understated. Over the last six years, Kew has undertaken two major projects both to secure and to maximise the value of its collections. First, the Digitisation project, with the aim of digitising Kew's approximately 8 million plant and fungal specimens, to create a complete catalogue of our collections, ultimately, making specimen records and images freely available online and accessible to researchers worldwide. Secondly, with the aim of integrating our collections and simultaneously moving our data to a single, supportable and compliant system, was the development of the Integrated Collections Management System (ICMS), using EarthCape Oy software. ICMS now holds data for 12 distinct collections, all managed in the one application and the benefits of more visible relationships between collections, are now being realised. However, integrating very different collections within a single system, has had its challenges. We present our experience, insights, and best practices on developing an integrated application, whilst still meeting the often very different, specific needs of the different collections. We outline how, whilst applying common data structures and principles across all collections, but employing the very flexible configurability of the application, we have been able to create collection-specific views, enabling the variations in functionality required to support all the collections. Additionally, we describe our development of a mobile application to work in conjunction with the desktop application, providing a further route for secure data capture, whilst still maintaining data centrally. Through these mechanisms we hope to show the benefits to collection data quality of providing multiple user options for accessing data.

Posters Session

7016195

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Valorización de la Biodiversidad del Cerrado: Experiencia en el Desarrollo de Barra de Cereal con Aprovechamiento Integral del Baru

Authors

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Daniel Emanuel Cabral de Oliveira (Instituto Federal de Educação, Ciência e Tecnologia Goiano campus Rio Verde • Brazil)
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Paulo Alexandre Perdomo Salviano (Instituto Federal de Educação, Ciência e Tecnologia Goiano campus Iporá • Brazil)

Abstract

Este trabajo presenta un relato de experiencia sobre el desarrollo de una barra de cereal elaborada con el aprovechamiento integral del baru (*Dipteryx alata*), fruto típico del Cerrado brasileño, destinada a la comercialización por parte de la Cooperativa Mixta Agroindustrial de Diorama y Región (COOPERMIX). El proyecto fue ejecutado en asociación con el Instituto Federal Goiano – Campus Iporá, con apoyo de la Fundación Grupo Boticario y la FAPEG. La iniciativa busca agregar valor a un fruto tradicionalmente vendido en su forma natural, utilizando su almendra, pulpa y cáscara para crear un producto alimenticio sostenible y de alta densidad nutricional. La metodología empleada incluyó investigación participativa con los cooperados, análisis comparativo (benchmarking) en ferias agroecológicas y plataformas digitales, levantamiento de formulaciones existentes y experimentación en laboratorio para la composición del producto. Se llevaron a cabo etapas de sanitización, secado y molienda de la pulpa y cáscara, así como tostado de las almendras, que luego fueron incorporadas a la fórmula de la barra de cereal junto con avena, copos de cereales y frutas deshidratadas. El fundamento teórico se basa en la valorización de la sociobiodiversidad, el fortalecimiento del cooperativismo familiar y el potencial económico de los frutos nativos del Cerrado. Como resultados, se destaca la viabilidad técnica del uso integral del baru en la formulación de la barra, así como el potencial de retorno financiero con la comercialización de un producto con valor agregado, diferenciado y alineado con las tendencias de consumo saludable. La iniciativa contribuye al fortalecimiento de la cadena productiva del baru, promueve prácticas agroextractivistas sostenibles y amplía las oportunidades de ingresos e inclusión productiva de los cooperados. Se concluye que el proyecto posee alta relevancia social, económica y ambiental, y refuerza la importancia de estrategias que integren innovación tecnológica, conservación ambiental y desarrollo territorial.

Posters Session

7016216

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Valorización de la Biodiversidad del Cerrado: Estrategias Sostenibles de Ingreso y Conservación en Diorama-GO

Authors

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Paulo Alexandre Perdomo Salviano (Instituto Federal de Educação, Ciência e Tecnologia Goiano campus Iporá • Brazil)

Abstract

El proyecto "Sabores del Cerrado: valorizando el agroextractivismo" tiene como objetivo fortalecer la cadena de la sociobiodiversidad en el municipio de Diorama-GO, articulando conservación ambiental y generación de ingresos. La región ha sido impactada por los efectos negativos de la deforestación, marcada por la sustitución de la vegetación nativa por la ganadería extensiva y, más recientemente, por el monocultivo de soya. Este cambio en el uso del suelo ha provocado un aumento de la temperatura, reducción de las precipitaciones y escasez hídrica, afectando los ecosistemas locales. Ante este escenario, y considerando que la mayoría de los propietarios de tierras son pequeños productores, es fundamental adoptar estrategias basadas en el uso sostenible de especies nativas del Cerrado como fuente alternativa de ingresos y medio para preservar los recursos naturales. La iniciativa, desarrollada mediante una alianza entre el IF Goiano - Campus Iporá, COOPERMIX, la Municipalidad de Diorama, Emater, FAPEG y la Fundación Grupo Boticário, incluye la identificación de árboles semilleros, recolección de semillas, producción de plántulas y el cultivo de especies como pequi, baru, mangaba, jatobá del Cerrado y anacardo silvestre en un área de 8,659 ha. Paralelamente, se está estructurando una propuesta para el aprovechamiento integral de los frutos nativos del Cerrado, con enfoque en la diversificación del portafolio de productos alimentarios y el acceso a nuevos mercados mediante la agricultura familiar organizada. La propuesta está alineada con los Objetivos de Desarrollo Sostenible, especialmente el ODS 15 (vida de ecosistemas terrestres), al promover la restauración de áreas degradadas, la conservación de recursos naturales y la valorización de productos de la sociobiodiversidad. Con la participación activa de los cooperados, la acción fortalece el protagonismo comunitario y demuestra cómo la biodiversidad puede convertirse en un activo estratégico frente a los desafíos socioambientales de los territorios rurales vulnerables.

Posters Session

7016232

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Identidad Visual y Diseño Centrado en el Cliente: Estrategia de Marketing para Producto a Base de Baru de COOPERMIX

Authors

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Abstract

Este trabajo describe el proceso de desarrollo de la identidad visual de un producto alimenticio — barra de cereal elaborada a partir del aprovechamiento integral de la cáscara y la pulpa del baru (*Dipteryx alata*), fruto nativo del Cerrado brasileño. La iniciativa forma parte del proyecto “Sabores del Cerrado: valorizando el agroextractivismo”, que busca promover la generación de ingresos y la valorización de la sociobiodiversidad en Diorama-GO, mediante el fortalecimiento de las acciones de la Cooperativa Mixta Agroindustrial de Diorama y Región – COOPERMIX. En esta etapa, las acciones están enfocadas en el diseño de estrategias de comunicación visual y posicionamiento de mercado del producto, basadas en los principios del diseño centrado en el cliente. En este contexto, la figura del cliente es representada por los propios gestores de COOPERMIX, quienes participan activamente en la construcción de la propuesta estética, conceptual y simbólica del producto. El enfoque busca comprender sus percepciones, expectativas y valores, para garantizar que el resultado refleje la identidad colectiva de la cooperativa y dialogue con el público consumidor. El proceso incluye la creación del nombre del producto, logotipo, paleta de colores, tipografía y etiquetado, integrando elementos culturales y ecológicos asociados al Cerrado y al modo de vida agroextractivista. Complementariamente, se está desarrollando el sistema de identidad visual de la propia cooperativa, fortaleciendo su presencia institucional y contribuyendo a la coherencia en las acciones de marketing y comercialización. La estrategia adoptada promueve no solo la valorización del producto, sino también amplía el reconocimiento de COOPERMIX como agente de transformación socioambiental. La propuesta está alineada con los Objetivos de Desarrollo Sostenible (ODS), especialmente los ODS 12 y 15, al fomentar el consumo responsable y la conservación de la biodiversidad mediante prácticas sostenibles de producción y comunicación.

Posters Session

7016294

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Conservation gaps and priorities of range-restricted birds in the Northern Andes

Authors

Wilderson Medina (Tropical Mountains Research Foundation • Colombia)**Stuart Pimm** (Duke University • United States)**Ryan Huang** (University of Pretoria • United States)

Abstract

The ongoing destruction of habitats in the tropics accelerates the current rate of species extinction. Range-restricted species are exceptionally vulnerable, yet we have insufficient knowledge about their protection. A species' current distribution, range size, and protection gaps are crucial in determining conservation priorities. Here, we identified priority range-restricted bird species and their conservation hotspots in the Northern Andes. We employed maps of the Area of Habitat (AOH), that better reflect their current distributions than existing maps. AOH provides unprecedented resolution and maps a species in the detail essential for practical conservation actions. We estimated protection within each species' AOH and for the cumulative distribution of all 335 forest-dependent range-restricted birds across the Northern Andes. For the latter, we also calculated protection across the elevational gradient. We estimated the additional protection that community lands (including Indigenous and Afro-Latin American lands) would provide if they were managed for conservation. AOHs ranged from 8 to 141,000 km². We identified four conservation priorities based on cumulative species richness, which is the number of AOHs stacked per unit area. These priorities are high-resolution mapped representations of Endemic Bird Areas for the Tropical Andes that we consider critically important. Protected areas cover only 31% of the cumulative AOH, but community lands could add 19% more protection. Sixty-two per cent of the 335 species have ranges smaller than their published estimates, yet IUCN designates only 23% of these as Threatened. We identified 50 species as top conservation priorities. Most of these concentrate in areas of low protection near community lands and at middle elevations where, on average, only 34% of the land is protected. We highlight the importance of collaborative efforts among stakeholders: governments should support private and community-based conservation practices to protect the region with the most range-restricted birds worldwide.

Posters Session

7017617

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Designing a mobile application to capture on-the-spot data for living plant collections in botanic gardens.

Authors

Reinis Rozkalns (Royal Botanic Gardens, Kew • United Kingdom)

Richard Dodd (United Kingdom)

Udayangani Liu (United Kingdom)

Robert Turner (United Kingdom)

Abstract

Alongside the 8 million botanical and mycological items of the Science Collections, the Royal Botanic Gardens, Kew has an extraordinary wealth in its living plant collections across two sites in the United Kingdom, Kew Gardens and Wakehurst. A key feature of botanic gardens is that the living plant collections contain accurately identified, documented, and labelled collections of plants for one or more of the purposes of conservation, reference, research, interpretation, education, and pleasure. To fulfil this role effectively and to support cutting-edge research at RBG Kew and beyond, a significant milestone was achieved recently by integrating previously isolated living collection data with other science collections, by migrating them to RBG Kew's new Integrated Collections Management System (ICMS) supported by EarthCape software. The system holds data for 12 distinct collections, all managed in one system, centralizing data and enabling linkages between collections to be explored more easily. However, using the desktop version of ICMS posed challenges, as curating living plants mostly involves outdoor activities. With mobile technologies becoming an increasingly integral part of recording biodiversity data, we present our experience, insights, best practices, and knowledge on developing an interactive mobile application, running on Android tablets, that works alongside the desktop version of ICMS, so that horticulturalists can capture data and images in real-time whilst engaging in their outdoor tasks. We discuss how functional requirements were gathered, hardware and software challenges were addressed, limitations were identified, and the user-interface was designed to capture current location data when georeferencing plant locations, taking and uploading images, updating the status of plants as dead or alive, recording evidence of pests or disease, documenting phenology, taking stock checks, and making requests for plant identification and printing labels, with this information all then being synchronised with the main application.

Posters Session

7009427

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

PLANNING AND MONITORING-EVALUATION SYSTEM (SPSE) OF THE MINISTRY OF THE ENVIRONMENT AND SUSTAINABLE DEVELOPMENT IN MADAGASCAR

Authors

Rabevazaha Felanirina (GBF Implementation - GIZ • Madagascar)

Ralivelo Lynah Fenohasambarana (Ministry of Environment and Sustainable Development • Madagascar)

Abstract

The island of Madagascar is renowned for its unique biodiversity, the conservation of which is one of the greatest challenges facing the Ministry of the Environment and Sustainable Development. To ensure continuous monitoring of conservation actions by stakeholders, the Planning and Monitoring-Evaluation System (SPSE) has been designed, set up and updated three times, then operationalized as a decision-making tool. This system currently integrates priority themes, including biodiversity, with the consideration of indicators aligned with the Kunming-Montreal global framework for biodiversity following COP 15. Its relativity at international level is consistent with the objectives of multilateral environmental agreements, whose indicators are specific, measurable, quantified and spatially explicit. It plays a crucial role in achieving objectives and impacts. Technically, the mechanism of this system is based on the process of data collection, validation, consolidation and analysis, which seems to be well established and adapted to users at all levels, as well as the use of the information. The usefulness of the SPSE enables in-depth analysis of existing data, harmonization of activity planning and geolocation of achievements at national and regional level, monitoring and measurement of the results and impacts of the implementation of legal and strategic frameworks, as well as tracking the achievements of environmental actions in terms of projects and programs. It's excel-format template can be downloaded online, is easy to read and fill in, and could provide achievements on various themes at any given time, since the data is already stored on a server.

Posters Session

7009647

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

Future-proofing Chocolate: the environmental resilience of cacao wild relatives

Authors

Emily Symington (Trinity College Dublin • Ireland)

Abstract

Chocolate is a billion-dollar industry that relies upon cultivation of *Theobroma cacao*, the chocolate tree. The global chocolate industry faces an existential threat from climate change, particularly increased drought. The genus *Theobroma* contains 42 other species, which can be described as crop wild relatives (CWRs) of *T. cacao*. It is highly likely that some CWRs are adapted to drought and may provide valuable genetic material suitable for “future proofing” chocolate production against climatic change. My research aims to advance this goal by (i) assessing CWRs for their drought tolerance and (ii) determining their conservation status. Species distribution models (SDMs) based on herbarium occurrence records and climate data will be used to map the current distribution of this genus. This dataset combines a processed, published dataset sourced from the Global Biodiversity Information Facility, as well as additional data from smaller in-country herbaria across Central and South America, the native range of this genus. The resulting SDMs will provide insight into each species’ environmental tolerance, highlighting which CWRs are most likely to have genes and traits associated with drought resistance. Assessing the conservation of CWRs is crucial as they are a natural bank of potentially useful genetic resources. Therefore, the SDMs will be projected into future IPCC climate scenarios to predict the fate of each species under global change. These results will be used to provide conservation status estimates of CWRs under IUCN criteria.

Posters Session

7009992

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

ES

Datos abiertos y cambio de uso de suelo para la priorización de áreas de conservación en el centro de México

Authors

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Tania Escalante (Universidad Nacional Autónoma de México, Facultad de Ciencias, Grupo de Biogeografía de la Conservación, Circuito Exterior s/n, • Mexico)

Abstract

Los datos abiertos son una fuente indispensable para informar decisiones de conservación y diseñar políticas públicas basadas en evidencia. En este trabajo, utilizamos datos abiertos para identificar áreas prioritarias para la conservación de especies endémicas de la Subprovincia Este de la Faja Volcánica Transmexicana (SEFVT) en México, bajo escenarios futuros de transformación del paisaje. Los registros de ocurrencia de GBIF, junto con variables climáticas de CHELSA y variables topográficas de la USGS fueron utilizados para elaborar modelos de distribución de especies (MDE) para mamíferos y anfibios endémicos. Por otro lado, calculamos el porcentaje histórico de hábitat degradado por cambio de uso de suelo (CUS) y proyectamos impactos futuros para el año 2050 bajo tres escenarios: optimista, tendencia actual (BAU) y pesimista. Posteriormente, priorizamos áreas para la conservación integrando los MDE con variables socioeconómicas y ambientales provenientes de plataformas abiertas como Co\$ting Nature, Copernicus y RAN. Actualmente, el patrón de riqueza endémica abarca el 68% de la SEFVT. Sin embargo, podría reducirse al 45% bajo un escenario optimista, al 17% en el escenario BAU y hasta un 2% en un escenario pesimista. Detectamos zonas críticas cuya conservación es clave para evitar la desaparición de especies de distribución restringidas, como en Iztaccíhuatl-Popocatepetl, la Malinche, Cofre de Perote, el Tepozteco y el Nevado de Toluca. Aunque existen 28 Áreas Naturales Protegidas (ANP) en la SEFVT, solo nueve coinciden con las áreas prioritarias identificadas y solo una protege completamente a una especie críticamente restringida. Este trabajo evidencia que los datos abiertos son herramientas de gran utilidad para fortalecer la toma de decisiones en conservación y proponer acciones concretas para la resiliencia de la biodiversidad ante escenarios de cambio global.

Posters Session

7013809

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

NatureDB: An Open-Source Database System for Managing and Customizing Natural History Collection Data Across Institutions

Authors

Szu-Hsien Lee (Taiwan Biodiversity Information Facility • Taiwan)

Abstract

NatureDB is an open-source database system for managing natural history and biodiversity collection data across institutions. Built with Python and PostgreSQL, it offers a lightweight, extensible backend for researchers, curators, and organizations seeking an alternative to commercial software.

The system supports core data types such as specimen records, taxonomy, collection events, identifications, geospatial coordinates, and multimedia. It also accommodates complex relationships, and offers features like tagging, controlled vocabularies, and GIS-compatible fields. NatureDB is designed for multi-institution use within a single deployment. Each institution can manage data independently while sharing the same infrastructure.

To promote interoperability, NatureDB supports ARK (Archival Resource Key) identifier assignment. It also allows data export in standardized formats such as Darwin Core (DwC). This enables integration with platforms like GBIF and institutional repositories.

Its minimalist schema is designed for easy customization and scalability. This makes NatureDB suitable for both small teaching collections and large digitization projects. It can be deployed on local machines, VPS, or cloud environments with minimal setup.

This poster will present NatureDB's architecture, use cases, and deployment scenarios. We will highlight its flexibility and alignment with community data standards. Our goal is to lower the barrier for institutions managing biodiversity data and to encourage collaboration among developers, data managers, and researchers interested in practical and extensible collection management solutions.

Posters Session

7023673

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

When Birds Speak: visualising Traditional Ecological Knowledge in Ghana's Upper West Region

Authors

Claire Bracegirdle (United Kingdom)

Abstract

Community-based biodiversity monitoring initiatives provide important opportunities to meaningfully engage with local peoples' environmental knowledge. However, they are often implemented in top-down ways, with insufficient attention given to how people already conceptualise 'monitoring' within their own contexts, and how this information informs local-level decision-making.

Additionally, community-based monitoring initiatives are predicated on collaborations between external experts and local people, who often hold considerable environmental expertise, learnt discursively and experientially. Although often unacknowledged, monitoring initiatives are sites of epistemological tension between abstracted and standardised indicators, and local peoples' more embodied and relational approaches to tracking change.

Based on research conducted in Ghana's Upper West Region by a team of two local community researchers, one Ghanaian academic researcher and one external academic researcher, this poster creatively presents our findings about how Birifor and Waale people living on the edge of the Black Volta River anticipate and observe change in the environment through interpreting the vocalisations, behaviour and migration patterns of birds. Participants in the research – recognising that economic and social changes are affecting the transmission of Traditional Ecological Knowledge to younger generations – requested that we document and share this information. Working with a Ghanaian illustrator, Muzeyi Yelyen, we have created a series of illustrations that record and share this knowledge.

The illustrations will be exhibited locally and printed as a deck of cards available to members of the communities that contributed to the research, as a way to encourage ongoing conversation and the sharing of knowledge. Exhibiting the work beyond these communities – which is the aim with this proposed poster – is also crucial as a way to raise awareness of the importance of engaging with local peoples' own conceptions of monitoring.

Posters Session

7021019

23/10/25 | 17:00 & Virtual

Room: Main Hall & Virtual

EN

A Visualization of TaxonWorks Data Model

Authors

Matthew Yoder (United States)

José Luis Pereira (Argentina)

Abstract

TaxonWorks, now in development for over decade, has one of the richest data models with well defined semantics within the biodiversity informatics application realm. A high-level visualization of the semantics behind its models, including degree of use, related standards, and anticipated extensions is provided in a light-weight visual format. The visualization is annotated with short notes on the philosophy behind its sttructure.

Posters Session

7020986

Virtual

Room: Virtual

EN

A nature-positive world is more than the sum of its parts

Authors

Simon Ferrier (Australia)

Abstract

Adoption of the Kunming-Montreal Global Biodiversity Framework (KM-GBF) has led to further growth in attention being directed to the challenge of halting and reversing biodiversity loss to achieve a nature-positive world. However, concerns have been raised that, unless progress towards achieving net gain in biodiversity can be measured effectively at a whole-system level, the term 'nature positive' risks becoming no more than a convenient label for any action intended to benefit nature. Biodiversity is complex, and initiatives promoting and informing the measurement of biodiversity change usually address this complexity by employing separate metrics to assess different biodiversity levels and entities (e.g. individual species or ecosystem types) and different causal-framework components (e.g. responses, pressures, state, benefits). As a consequence, assessing achievement of nature positive at a whole-system level is challenged by the reality that these various components do not exist or function in isolation from one another, but are instead connected and interact in a myriad of ways. By endeavouring to account for these interrelationships, more integrative biodiversity indicators can complement, and add significant value to, the use of simpler metrics focused on individual system components. Integrative indicators incorporating a predictive capability also offer considerable potential to more strongly couple monitoring of actions implemented under the KM-GBF targets to monitoring of outcomes achieved under that framework's goals. In addition, these same indicators can more effectively link monitoring to planning of further actions which can most effectively and efficiently advance progress towards achieving nature positive, across both public and private sectors.

Posters Session

7020925

Virtual

Room: Virtual

EN

Evaluating Deep Learning Architectures for 3D Point Cloud Classification of Mammalian Bones

Authors

Zakaria DOUBABI (Morocco)

hanane ARIOUAT (France)

Eric CHENIN (France)

christophe DENIS (France)

Jihad ZAHIR (Morocco)

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Abstract

3D point clouds provide rich geometric and structural information valuable for shape and object classification tasks, but the absence of an inherent ordering of points in 3D space poses a fundamental challenge for their direct use with conventional deep learning models. To effectively process this unordered data, a range of state-of-the-art architectures has been developed, covering different uses of multilayer perceptrons (MLPs), attention mechanisms, and transformers. In this study, we evaluate and compare the performance of these architectures on a custom dataset created by merging multiple datasets from different museums, containing various bone types from diverse mammalian species. Due to the limited amount of available training data, our experimental results reveal that these models consistently struggle to classify bones accurately by type. This outcome underscores both the limitations of current deep learning methods when applied to complex biological structures and the broader challenges inherent in leveraging deep learning for the analysis of biological diversity data.

Posters Session

7019926

Virtual

Room: Virtual

EN

Landscaping results and recommendations for improving eDNA-based data published in biodiversity archives

Authors

Katrina Exter (Flanders Marine Institute (VLIZ) • Belgium)

Emilie Boulanger (OBIS • France)

Peter Woollard (EMBL-EBI • United Kingdom)

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Antonio Camacho (Spain)

Christina Pavloudi (EMBRIC • Belgium)

Frederic Rimet (INRAE • France)

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Abstract

eDNA data in the form of occurrences (taxonomic identifications) are increasingly being included in biodiversity data archives (e.g. GBIF, OBIS); more types of eDNA-derived results will inevitably follow (e.g. functional annotations). This process makes data readily available to be used for biodiversity research – studies of ecosystems, biodiversity, invasive species, monitoring, etc. The biodiversity data publishing community has been addressing issues related to integrating eDNA-based data into their archives, thus making them understandable and (re-)usable by interested scientists who may not have any background in genomics.

eDNAqua-Plan is an EU Horizon-funded project that is investigating the eDNA “data ecosystem” in Europe. With a focus on the aquatic, we are analysing the (meta)data standards, (meta)data interoperability and reusability, and the harmonisation and interconnectivity of eDNA reference libraries, DNA and biodiversity data portals, and biobanks: by landscaping this ecosystem we will identify the gaps in the smooth flow of (meta)data, and make recommendations for improvements. Our focus is on making it easier for the different types of audience – researchers, policy makers, monitoring scientists and agencies, analysts etc – to find, access, and use these data.

In this poster we will present the landscaping results and recommendations for the eDNA-based data published in biodiversity archives and eDNA material and metadata held in biobanks: how well-connected are the various stakeholders, what standards for data and metadata are used, how consistently and commonly are they used by the various stakeholders, how is eDNA-based data included in the different repositories, and what recommendations could improve the smooth flow of widely-understandable eDNA-derived data to all possible users?

Posters Session

7020635

Virtual

Room: Virtual

EN

Spatial Analysis of Blue Carbon Potential in the Mangrove Ecosystem at Muara Gembong Beach-Indonesia, as a Climate Change Mitigation Effort

Authors

Nazli Raudhati (IPB UNIVERSITY • Indonesia)

Syamsul Bahri Agus (IPB UNIVERSITY • Indonesia)

Rinny Rahmania (National Agency of Research and Innovation (BRIN) • Indonesia)

Abstract

Blue carbon ecosystems—such as mangroves, seagrass beds, and coastal marshes—play a crucial role in naturally absorbing and storing carbon. Among them, mangroves are particularly effective due to their high carbon storage capacity, making their conservation vital in efforts to mitigate atmospheric carbon emissions. Muara Gembong, located in the northern part of Bekasi Regency and bordering Jakarta Bay, Indonesia, supports a mangrove ecosystem currently used by the local community for fisheries (ponds) and ecotourism. This study aims to evaluate the blue carbon storage potential of mangroves in the Muara Gembong coastal area. Using Sentinel-2 satellite imagery and the Mangrove Vegetation Index (MVI) algorithm (threshold range: 2.0 to 20), the assessment was conducted through ENVI and QGIS software. The analysis estimated a mangrove area of 776.40 hectares, with a total carbon stock of approximately 93,089 MgC (megagrams of carbon). These findings highlight the significant potential of Muara Gembong's mangrove ecosystem as a blue carbon sink and underscore the need to integrate its conservation into sustainable climate change mitigation strategies.

Posters Session

7020422

Virtual

Room: Virtual

EN

Moving from data silos to data streams -- together: the Freshwater Data Publishing Guide

Authors

Astrid Schmidt-Kloiber (BOKU University • Austria)

Jennifer Lento (Canadian Rivers Institute, University of New Brunswick • Canada)

Abstract

Freshwater ecosystems are among the most biodiverse and threatened systems on Earth – yet they remain vastly underrepresented in global open-access biodiversity databases. To help bridge this gap, we developed the *Freshwater Data Publishing Guide*.

This practical guide, published through GBIF, empowers researchers, monitoring agencies, and conservationists to publish high-quality freshwater biodiversity data in ways that are both FAIR (Findable, Accessible, Interoperable, Reusable) and scientifically robust. It provides targeted recommendations for preparing and standardising species occurrence data, stemming from sources such as biomonitoring datasets, national monitoring programs or museum collections.

Publishing freshwater biodiversity data is not just a technical task, it is an act of stewardship. It enhances data visibility, improves reproducibility, supports policy and conservation planning, and enables large-scale analyses across regions and time periods. We emphasise that even small datasets, when well documented, can make a big difference – especially for taxa or regions where data are sparse.

Our poster will introduce the guide's structure and highlight common challenges and solutions in freshwater data publication. We aim to inspire and support the freshwater community in unlocking the hidden value of their datasets, because every record counts, and the world needs more (and better) freshwater data.

If you've ever hesitated to publish your freshwater data, this guide is for you. Let's move from data silos to data streams – together.

Posters Session

7015294

Virtual

Room: Virtual

EN

Assessment of local chimpanzee populations with camera traps and AI

Authors

Yves Le Bras (Biotope • France)

Noémie Cappelle (Biotope • France)

Abstract

Chimpanzees, as highly charismatic and protected species, face global threats to their populations. Accurate assessments of their spatial distribution and population size are crucial in environmental impact assessments (EIA) and effective conservation planning. Such information, however, requires intensive data collection. Camera traps have emerged as a valuable method, enabling data collection at scale (across hundreds of sites over months of monitoring), even in remote and densely forested areas. While camera traps are effective for species inventories, mapping distributions and estimating population sizes present significant challenges.

To address these, Camera Trap Distance Sampling (CTDS) alongside spatial modeling techniques like Density Surface Modeling (DSM) to map chimpanzee densities is a promising method. Processing extensive datasets from thousands of camera trap days in ecosystems with dense mammalian communities is labor-intensive. Additionally, CTDS requires precise measurement of distances between animals and camera locations, a demanding task when done manually.

We evaluated Zamba, an AI-based tool, to automate both classification and distance measurement tasks. Zamba's automated species classification was compared against manually reviewed footage to assess accuracy, while distance measurements from Zamba were validated against traditional methods (manual inspection and comparison with reference footage). Initial findings indicate that Zamba significantly reduces processing time while maintaining classification accuracy and reliable distance estimates for chimpanzee

detections. Integrating Zamba with CTDS and DSM shows promise for scalable, efficient data processing in EIA, advancing the quantitative and spatial analysis methods necessary for informed conservation of threatened species like the chimpanzee.

Posters Session

7009845

Virtual

Room: Virtual

EN

Enhancing Biodiversity Data Quality through Automated Taxonomic Name Validation

Authors

Marco Proença (Museu Paraense Emílio Goeldi • Brazil)**Nelson Pinheiro** (Museu Paraense Emílio Goeldi • Brazil)**Marcos De Sousa** (Museu Paraense Emílio Goeldi • Brazil)

Abstract

Biodiversity databases suffer from erroneous taxonomic names, leading to ineffective ecological evaluations and conservation efforts rendering global biodiversity databases reliability tenuous. Here we present pytaxon, an open-source Python package that facilitates the automatic validation and correction of taxonomic names in any spreadsheet format to foster standardized and interoperable data.

pytaxon validates and corrects both exact and fuzzy matches using the Global Names Verifier (GNV) API (<https://verifier.globalnames.org>) to cross-reference multiple taxonomic resources including Global Biodiversity Information Facility (GBIF), Catalog of Life, iNaturalist, and National Center for Biotechnology Information (NCBI). It has a command line interface (CLI) for seamless incorporation into extensive automated pipelines and a graphic user interface (GUI) to allow use by those with little coding experience.

We assessed its effectiveness by adding taxonomic inconsistencies to a gold standard dataset, Modified Uropygi Collection, found here <https://doi.org/10.5281/zenodo.14472861>. The application was able to identify and notify me of greater than 30 inconsistencies, including typographical errors, invalid scientific names, through casing errors for family, order, class, phylum and kingdom. It exported a suggestions spreadsheet with potential corrections and a validated collection for downstream use.

The validated collections exported by pytaxon provide standardized naming conventions across various datasets in various file types, resulting in more reliable assembly of biodiversity data from multiple collections, improving the integrity of publicly accessible biodiversity repositories while also reducing the manual workload for independent researchers and larger curatorial efforts.

Ultimately, pytaxon improves data integrity and interoperability, which improves effective conservation and assessment capabilities. The application is open access at <https://github.com/pytaxon/pytaxon-cli> for use and collaborative improvement potential within the global research community.

Posters Session

7021011

Virtual

Room: Virtual

EN

Taxonomy for all: getting consistent taxonomic names for inter-agency stakeholders

Authors

Cassia Piper (Biodiversity Information Office • Australia)

Trisha Moriarty (Biodiversity Information Office • Australia)

Abstract

The Biodiversity Information Office (BIO) developed Dandjoo, a state-wide biodiversity data repository for Western Australia (WA), as part of initiatives by the WA State and Australian Commonwealth governments to mobilize data and make it more accessible, discoverable, and usable. A key requirement for Dandjoo was the management of taxonomic names to ensure standardization in reports and assessments.

While the Western Australian Museum and Western Australian Herbarium are the regulatory authorities for taxonomic names in WA, many users rely on taxonomy. Conservation codes for threatened and priority species are linked to taxonomic names for regulatory reporting and protection, as well as for the nomination, assessment, listing, and implementation of recovery plans for those species. Consultants need taxonomic identifications to submit data for environmental impact assessments, and scientists in the Department and external agencies use taxonomic names in their research. BIO positioned itself among these stakeholders to create a taxonomic names management system called Nomos, which was essential for informing names in Dandjoo and ensuring effective name standardization among stakeholders. A key requirement for Nomos was to streamline the process to maintain currency of the taxonomic data being sourced from the authorities.

The challenges of strict deadlines, limited awareness of data standards coupled with disparate and aging source databases managed by the project partners meant Nomos was initially implemented with the basic functions prioritised to directly support the launch of Dandjoo. Further working with stakeholders help align Nomos with the legislative obligations of the Department, ensuring that taxonomic name and conservation code changes were updated in Nomos to ensure changes to conservation listings were managed.

Streamlining these processes helps capture requirements for future development, and application of data standards within the Nomos system will assist with making taxonomic names consistent for all inter-agency stakeholders, contributing to better reporting and protection.

Posters Session

7009735

Virtual

Room: Virtual

EN

HexaWorld: A Simulation Framework for Explainable Reinforcement Learning in Marine Biodiversity Monitoring

Authors

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Luigi Amedeo Bianchi (University of Trento • Italy)

Abstract

Reliable marine biodiversity monitoring is essential to guide climate adaptation, spatial planning, and marine conservation policies. However, operational constraints, limited resources, and the spatial complexity of marine environments make large-scale data collection a persistent challenge. Reinforcement Learning (RL) combined with Autonomous Underwater Vehicles offers new opportunities to optimize sampling strategies, but the lack of transparency in learned behaviors limits their adoption in real-world decision-making processes. To address this gap, we present HexaWorld, a simulation framework that integrates biodiversity data with explainable RL-based navigation in spatially structured marine environments. The framework accepts biodiversity maps as input, enabling realistic scenario modeling. It supports two spatial discretizations—square and hexagonal grids—allowing users to analyze how spatial structure affects exploration efficiency and observability. A key feature of HexaWorld is its customizable reward function, designed to explicitly separate ecological objectives (e.g., maximizing biodiversity coverage) from operational ones (e.g., avoiding redundant paths or ensuring safe and timely return). This separation enhances explainability, making agent behaviors traceable and aligned with mission goals. We tested HexaWorld on three simulated marine habitats representing temperate, tropical, and deep-sea ecosystems. Results show that hexagonal grids improve navigation in complex environments, particularly in deep-sea scenarios where obstacles and limited maneuverability challenge exploration. Across all habitats, the modular reward design enabled clear analysis of trade-offs between exploration efficiency and operational safety.

These findings demonstrate that HexaWorld supports a complete pipeline from data-driven scenario definition to the design of interpretable and goal-oriented navigation strategies. By making AI decisions understandable and connected to ecological and operational priorities, HexaWorld contributes to advancing explainable, cost-effective, and stakeholder-relevant marine biodiversity monitoring solutions.

Posters Session

7020521

Virtual

Room: Virtual

EN

Use what you've got: Leveraging existing data to transform our understanding and management of biodiversity

Authors

Kelsey Huelsman (NASA | GESTAR-II | Earth Resources Technology • United States)

Stephen Formel (Formel Data Services • United States)

Shawn Serbin (NASA Goddard Space Flight Center • United States)

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Abstract

The potential to develop biodiversity products from existing biological data remains largely underrealized. Using plot-level vegetation surveys from the U.S. NSF-funded National Ecological Observatory Network (NEON) and vegetation occurrences from the Global Biodiversity Information Facility (GBIF), we developed novel methods to generate local biodiversity maps using these two publicly available datasets in concert. Our methods account for their different spatial, temporal, and taxonomic completeness and coverage, utilizing the vegetation surveys as a standard for comparison to assess the completeness and quality of available GBIF plant occurrence data and therefore the certainty of biodiversity estimates derived from those data. We also demonstrated the capacity to utilize complete, planned surveys to complement and augment incomplete GBIF data probabilistically. Our methods can be applied to taxa outside of plants to build a more holistic and probabilistic understanding of biodiversity via co-occurrences. Other data sources can be aggregated following our workflows, which will help to highlight critical data gaps in on-the-ground collection. Our work highlights the importance of best practices in biological data standards, which facilitate interoperability and reuse. We conclude with methods to pair these data products with existing satellite and other aerial imagery to assess relationships and predict biodiversity in areas that lack on-the-ground data, a crucial step in anticipation of NASA's Surface Biology and Geology satellite mission, which will further our understanding of global biodiversity and its trends.

Posters Session

7020752

Virtual

Room: Virtual

EN

Empowering experts: FADAtims for the future of freshwaters

Authors

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Abstract

Accurate and accessible taxonomy is the foundation of biodiversity data, but for many freshwater organism groups, maintaining reliable species lists is a major challenge. Names change, new species are described, and regional differences complicate standardisation. To support taxonomic experts in managing these dynamics, we are developing FADAtims: an online database and editing platform that enables collaborative curation of taxonomic species lists for freshwater biodiversity.

FADAtims is part of the Belspo-funded infraFADA project (see separate presentation), which brings together experts to consolidate and update global taxonomic information for freshwater groups. Coordinated by BOKU University and developed using open-source tools by Kartoza and the Freshwater Research Centre, South Africa, the platform allows registered members of the FADA taxonomic expert consortium to add, edit, or revise taxonomic names, synonyms, status information, and environmental data. Its aim is not to replace existing taxonomic databases, but to provide a flexible, expert-driven workspace that supports harmonisation and list-building for ecological assessments, biodiversity reporting, and data integration.

FADAtims is being developed as a taxonomic backbone system for Catalogue of Life and GBIF, ensuring that expert-validated freshwater taxonomy is integrated into global biodiversity infrastructures. Interoperability and data exchange are key priorities: species data are being aligned and synchronised with other major taxonomic systems, including WoRMS (World Register of Marine Species) and TaxonWorks, to support consistency and long-term sustainability.

The platform is designed with transparency, traceability, and usability in mind, and follows the FAIR principles. Each taxonomic change is logged, contributors are acknowledged, and data can be exported in standard formats. This poster introduces the FADAtims system, highlights its current applications, and invites feedback and participation from the Living Data community.

Posters Session

7020536

Virtual

Room: Virtual

EN

eHerbarium: AI-Enhanced Plant Identification and Global Sharing

Authors

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Abstract

eHerbarium is a mobile app that enables users to identify, document, and share plants with a global community. Since the publication of *"eHerbarium: A Global Platform for Exploring and Sharing Herbarium and Live Plant Images"* (BISSa 2023), the app has incorporated a high-precision AI-based identification system, significantly improving accuracy and usability.

Users can capture or upload plant images, receive identification suggestion, and annotate entries with location and ecological details— building a personal digital herbarium. eHerbarium also provides access to real herbarium collections, including specimens from the Royal Botanic Gardens, Kew.

By sharing observations across continents, users contribute to a global plant database that supports biodiversity research, education, and conservation. With an intuitive interface and community-driven content, eHerbarium connects everyday explorers with scientific resources, promoting global awareness and collaboration in plant knowledge.

Posters Session

7020465

Virtual

Room: Virtual

EN

Integrating genome annotations, occurrences, and environmental data to explore genome structure and function across the tree of life

Authors

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Abstract

The volume and diversity of digitally accessible biological data—from genes to ecosystems—is greater than ever, fuelling calls for more integrative approaches in biology. Despite this, much of the data remains siloed due to disciplinary traditions that have evolved independently. While several initiatives have focused on linking primary data, such as DNA sequences and species occurrences, less attention has been paid to integrating the secondary data generated by biological analyses.

A key type of secondary data is genome annotation: the interpretation of DNA sequences to identify gene structures and infer function. Genome annotations add a crucial layer of information that enables biological understanding of genome sequences and highlights another dimension of biodiversity: the diversity of gene structures and functional elements across species.

With the accelerating pace of genome sequencing across the tree of life, there is now an opportunity to explore genome structure and function in both phylogenetic and ecological contexts. To support this, we are developing a cloud-based data warehouse and analytics platform built on Google BigQuery, with interactive dashboards developed in Dash (Plotly) and integrated into custom web plugins. Our platform integrates genome annotations from Ensembl, species occurrence records from GBIF, and environmental context defined by CHELSA climatologies and biogeographic classifications.

This system is currently designed to enhance the EMBL-EBI Biodiversity Portal and support the goals of the Earth BioGenome Project. By connecting genomic structure with environmental and distribution data, we aim to support question-driven research into how genome structure and function vary across clades and environments. All data can be traced back to their original sources to ensure transparency and reproducibility.

We present this ongoing work, including biodiversity pipelines and dashboards, which will enable researchers to explore genome annotation data across species, identify broad-scale patterns, and develop new hypotheses in comparative and environmental genomics.

Posters Session

7014799

Virtual

Room: Virtual

EN

Earth Observation-based tools and methods co-designed with CSOs/NGOs to monitor and plan ecosystems conservation actions

Authors

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Abstract

Effective ecosystem conservation and restoration are crucial to halt global biodiversity loss and to mitigate the effects of global climate change. Stakeholders require a range of tools to support ecosystems conservation: from monitoring progress to global targets to planning of local actions. In a consultation process led by the European Space Agency (ESA), Civil Society Organizations (CSOs) and Non- Governmental Organizations (NGOs), key stakeholders identified the need to develop tools to monitor ecosystems under conservation and restoration actions as well as to identify high-priority sites for conservation or restoration interventions. Earth Observation (EO) can play an indispensable role, serving as the basis for such tools.

In the ESA-funded PEOPLE-ECCO project (Enhancing Ecosystems Conservation through Earth Observation Solutions, Capacity Development and Co-design, we co-developed EO-based tools and methods with conservation CSOs/NGOs to support their actions. This poster presents the preliminary results of these tools and methods. Developed applications include mapping of shifting agriculture extent, mapping submerged aquatic vegetation and coral reef habitat types, detecting vegetation condition trends, mapping habitat intactness, and before-after-control-impact assessment of conservation action effectiveness. We also present a user interface that allows non-EO experts to interact with large volumes of EO data through the openEO standard.

Posters Session

7019923

Virtual

Room: Virtual

EN

CIIMAR WATCH: A Coordinated Marine Biodiversity Monitoring Framework for Northern Portugal's Marine Ecosystems

Authors

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Abstract

CIIMAR WATCH is a novel institutional platform designed to coordinate and standardize long-term marine biodiversity monitoring across coastal and estuarine ecosystems in northern Portugal. Launched in 2024 by the Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), the initiative responds to national and global priorities for biodiversity observation by integrating interdisciplinary efforts from ten research groups and over 40 researchers. The program aligns with MBON and GEO BON principles by promoting harmonized protocols, FAIR data management, and open data sharing through platforms such as OBIS and PANGAEA.

Currently operating 14 strategically located monitoring stations under two regional observatories (PORTO WATCH and VIANA WATCH), CIIMAR WATCH captures essential biodiversity and ocean variables (EBVs and EOVs) including eDNA, macro- and microbenthos, cetaceans, plankton, and contaminants, alongside acoustic and oceanographic data. A multi-layered data structure, from field to visualization, supports real-time integration, long-term trend analysis, and policy relevant reporting. The initiative incorporates community- building, advanced training, and education, engaging MSc and PhD students in practical monitoring activities.

CIIMAR WATCH is designed to evolve into a scalable and replicable framework aligned with the goals of the UN Ocean Decade, SDGs, and the Convention on Biological Diversity. Ongoing developments include the implementation of real-time oceanographic buoys, aerial drone surveys, and a web-based GIS platform for open access visualization. As a national model for coordinated marine biodiversity observation, CIIMAR WATCH offers a transferable blueprint to support regional and global marine biodiversity networks and assessments such as IPBES and the Global Ocean Assessment.

This poster outlines the organizational model, data architecture, and interdisciplinary coordination that position CIIMAR WATCH as a valuable contributor to the global community of practice for biodiversity monitoring.

Posters Session

7020327

Virtual

Room: Virtual

EN

AI-assisted Image Annotation for Biodiversity Heritage Library Images

Authors

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Abstract

The Biodiversity Heritage Library (BHL) community has hand-curated nearly 320,000 scientific images and illustrations, many of which are available on Flickr and Wikimedia Commons. Despite their research value, these images lack granular, structured, searchable metadata at the page or component level—an obstacle to native image search and downstream reuse. Many more illustrations remain buried in BHL's 63 million-page corpus due to historic cataloging practices focused at the book level, with little page-level metadata to support image segmentation, captioning, or tagging.

This poster presents a pilot introducing AI-assisted image annotation for BHL images using Glycerine Workbench, a suite of IIIF-compatible tools that provide end-to-end workflows for researchers, curators, and students.

Key Pilot Features

- IIIF-based interoperability: facilitates platform-agnostic sharing and reuse of annotated images.
- Collaborative tools: support researchers, curators, and students in creating structured, multilingual image annotations.
- AI-assisted workflows: automate image segmentation, captioning, and tagging using scholarly vocabularies.
- Research-ready outputs: can be shared as visual, semantically enriched scholarly products.
- Iterative human validation: integration into BHL's InvenioRDM annotation repository ensures accurate, ethical training data for biodiversity-focused machine learning models.

Piloting this image annotation data pipeline, from Glycerine Workbench to InvenioRDM generates AI-assisted draft annotations that can be refined through collaborative human validation within BHL's InvenioRDM pilot repository. The result is high-quality, structured image data enriched with domain-specific vocabularies—paving the way for scientific trait extraction, image segmentation, ethical AI training, improved user discovery, and scientific reuse. By leveraging IIIF, a widely adopted image sharing standard, the pipeline allows for fluid interoperability between platforms and helps operationalize FAIR data principles by enabling scalable image annotation workflows across diverse and distributed infrastructures.

This poster will share early findings, technical strategies, and future directions—highlighting how long-dormant image collections can inform modern biodiversity research and find new applications.