BioMonWeek
2026
The European
Conference for
Biodiversity Monitoring

4-8 May 2026
Montpellier

Book of *abstracts*

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Plenary sessions

Keynote & panel : Bridging Research and Policy: the state of art and future of biodiversity monitoring

Tuesday 5 May 10h00-11h00, Auditorium Pasteur
Nathalie PETTORELLI, Institute of Zoology, Zoological Society of London, United Kingdom
Marialuisa TAMBORRA, European Commission, DG Environment
Gilles DOIGNON, European Commission, DG Research

Description: The keynote will introduce biodiversity monitoring within the long term, both historical and future expectations, with a dual perspective from research and public policy. It will place the role of biodiversity monitoring within different contexts, for instance societal and policy expectations. The session will explore the role of biodiversity monitoring alongside other key tools (e.g., Knowledge Centre for Biodiversity, Joint Research Centre, EEA) and how these can be better integrated to meet societal and policy expectations. This session will also position the respective roles of research, development and implementation for biodiversity monitoring. By the end, participants should have a clearer understanding of whether a unified strategy for biodiversity monitoring exists—and how research, policy, and implementation can align.

Keynote & panel : Building a Community: Human Dynamics in Biodiversity Monitoring

Tuesday 5 May 14h00-15h00, Auditorium Pasteur
Arne LANGLET, University of Vienna, Austria
Margarita HARTLIEB, University of Vienna, Austria
Nirmala SEON-MASSIN, Muséum national d'Histoire naturelle, France
Jenny WIK KARLSSON, Svenska Samernas Riksförbund, Sweden

Description: Biodiversity monitoring is often framed around data as the outcome—but it is fundamentally a human process, and we stand as a newborn community. We need to acknowledge that our system is based on humans, and that human behaviour has a strong impact on it. This session will explore how to foster collaboration, clarify individual roles, and strengthen our identity as a unified community. By the end, participants should recognise the importance of building a cohesive community to create a more harmonised and effective monitoring system.

Keynote & panel : Integrating Monitoring Tools: Insights from Australia’s TERN Programme

Wednesday 6 May 14h00-15h00, Auditorium Pasteur
Beryl MORRIS, Director of Australia’s Terrestrial Ecosystem Research Network (TERN), Australia
Allan SOUZA, Institute for Atmospheric and Earth System Research (INAR), University of Helsinki, Finland
Jan-Erik PETERSEN, European Environment Agency
Sandra LUQUE, Institut national de recherche pour l'agriculture, l'alimentation et l'environnement (INRAE) UMR TETIS, France

Description: This session will introduce three complementary approaches to biodiversity monitoring: satellite remote sensing, field-based monitoring, and research site networks: Australia’s Terrestrial Ecosystem Research Network (TERN) offers a model for integrating these tools—combining broad-scale data with local insights. The discussion will explore the specificity of each “tool”, and how they can benefit from each other, while drawing a parallel with Europe where remote sensing (Copernicus) and research site networks (eLTER) are already active, while field-based monitoring is not fully set up yet. The session will also reflect on the development of Copernicus and eLTER in Europe, and how cross-programme cooperation could be strengthened.

Keynote & Panel: From Local to European: Harmonising Biodiversity Monitoring at Different Scales

Thursday 7 May 14h00-15h00, Auditorium Pasteur
W. Daniel KISSLING, University of Amsterdam, the Netherlands
Klaudia KURAS, Carpathian Convention, UN Environment Programme, Austria
Aino LIPSANEN, Finnish Environment Institute (Syke), Finland

Description: This session will present the challenges of monitoring biodiversity with perspectives at different spatial scales. The former EuropaBON project will represent the largest scale (continental/global); , the Carpathian Convention will represent the regional/transnational scale and Finland will represent a national perspective together with the network of national centers developed in Biodiversa+, in order to structure monitoring governance. Harmonising protocols across scales is challenging, as it may disrupt long-term data continuity. This session will explore which scales are most effective for policy impact—and how to balance harmonisation with local needs.

Inspiring keynote: SCANS: A Model of European Cooperation for Marine Biodiversity Monitoring

Anita GILLES, University of Veterinary Medicine Hannover (TiHo), Germany
Matthieu AUTHIER, La Rochelle Université, France
Benjamin GUICHARD, PatriNat (OFB-MNHN-CNRS-IRD), France

The SCANS (Small Cetaceans in European Atlantic waters and the North Sea) survey programme is a landmark example of successful cross-border collaboration in Europe. This session will showcase how SCANS has achieved tangible results—and inspire confidence in our collective ability to deliver impactful monitoring programmes.

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Booths

Alliance for Nature

At Alliance for Nature, our mission is to ensure the protection and preservation of Nature now and for future generations while supporting the development of sustainable human activities. Our Alliance of like-minded companies achieve that by offering science-based, innovative services and research activities. During BioMonWeek, we will be happy to engage with all colleagues interested in biodiversity monitoring topics.

Association for Farmers Rights Defense (AFRD)

The Association for Farmers Rights Defense (AFRD) Georgia has been actively involved in terrestrial biodiversity monitoring, particularly in agricultural landscapes, rural ecosystems, and degraded land areas. AFRD integrates scientific research, community-based monitoring, and policy engagement to support biodiversity conservation, sustainable land management, and climate-resilient agriculture. The organization's work links biodiversity monitoring with food security, ecosystem restoration, and rural development, ensuring that conservation outcomes are aligned with farmers' livelihoods and national environmental priorities. AFRD conducts monitoring of agrobiodiversity and genetic resources, including traditional crop varieties and livestock breeds, to safeguard locally adapted genetic material and strengthen resilience to climate change. Through its work on seed systems, germplasm conservation, and GMO analysis, AFRD contributes to national evidence-based agricultural and environmental policy processes. The organization also integrates biodiversity indicators into ecosystem restoration and land degradation neutrality initiatives, particularly in arid and semi-arid landscapes, rangelands, and degraded agricultural areas. Monitoring focuses on vegetation dynamics, habitat quality, soil health proxies, and ecosystem recovery following restoration interventions. A key feature of AFRD's approach is participatory and farmer-led biodiversity monitoring. By engaging farmers, pastoralists, and rural youth, AFRD combines traditional ecological knowledge with scientific monitoring frameworks. This participatory approach strengthens local stewardship of ecosystems and supports adaptive management of agricultural landscapes, including pollinator protection, sustainable pasture management, and agroecological practices. AFRD contributes biodiversity monitoring data and expertise to national and international platforms, including collaboration with FAO, UN agencies, and research institutions.

BioAgora: Building the Science Service for Biodiversity and the Knowledge Exchange Network on Monitoring

BioAgora, a co-organiser of BioMonWeek2026, is a Horizon project working to build the Science Service for Biodiversity (SSBD), a platform for bridging policy needs to expert research at the European level. It has established a dedicated Knowledge Exchange Network (KEN) on biodiversity monitoring, mobilising existing institutions, initiatives and networks in the field. The monitoring KEN is thus positioning itself as a key collaborative network for experts that would aim to contribute to the Science Service. Occupying a prominent place in the science-policy interface landscape of Europe, BioAgora and the aforementioned KEN regularly and comprehensively engage with fellow research projects involved in biodiversity monitoring. BioMonWeek2026 has been identified as an opportunity to take this collaboration further via a joint showcase in a conference booth that introduces a broader audience to the knowledge transfer and outreach support the initiatives afford each other. In this way, the proposed display would showcase the objectives and achievements of BioAgora and its partners through a range of promotional materials, engaging videos and key outputs aimed at both researchers and policy-makers. The vision is to create an inviting space that supports communication and dissemination through direct and meaningful interaction with attendees. In addition to the furniture already foreseen by the organisers (poster board and high table with chairs), the booth could also benefit (if possible) from a larger lower table where the arrangement of project assets can be in full view.

BioDash Project - European Biodiversity monitoring scheme Dashboard

The BioDash project aims to provide the monitoring community a tool that facilitates access to information on monitoring schemes: · Inventory and description of all biodiversity monitoring schemes, ecosystemic services and the results they produce, based on the EBV approach. For centralize, harmonize and enhance the data from biodiversity. · Overview of the schemes, their ecosystems and their results. Networking of stakeholders involved in biodiversity monitoring. · Support public policies and European stakeholders in decision-making for the conservation and restoration of biodiversity. It will allow strategists, scheme leaders, researchers and funders to identify the most appropriate approach for implementing a program or monitoring scheme based on an analysis of existing programs and monitoring schemes at nationals and European levels. The project is part of the European Biodiversa+ partnership, contributing to the implementation of the European Biodiversity Strategy for 2030. The project will take place in 2 phases · Phase 1: design, development, and deployment of BioDash in its MVP (Minimum Viable Product) version on February 26, 2027. · Phase 2: corrective and evolutionary maintenance of the BioDash dashboard until the end of September 2030.

Biodiversa+, the European Biodiversity Partnership

Biodiversa+ is the European Biodiversity Partnership supporting excellent biodiversity research with an impact on policy and society, and a co-organiser of BioMonWeek. Advancing biodiversity monitoring is one of its core priorities. The partnership is building a long-term transnational network linking national and regional biodiversity monitoring schemes, and strengthening Europe-wide capacity to track trends. Biodiversa+ works across six areas: 1. defining shared priorities and indicators 2. harmonising protocols, methods, and data standards 3. promoting innovative technologies and citizen participation 4. enabling data use by policymakers and businesses 5. establishing governance and networks connecting national and regional schemes 6. running pilots to test common monitoring approaches. Hosting a booth at BioMonWeek would provide an opportunity to present our monitoring activities, and to engage with the wider monitoring community, stakeholders, and policymakers. The booth would serve as a space to exchange experiences, explore synergies and foster new collaborations across scales.

Biodiversity Information Management Systems (BIMS)

BIMS is an open-access platform for serving, hosting, analysing, visualising, and sharing biodiversity data. It is designed to support data-driven ecosystem management and conservation. Who is it for? BIMS is shaped by the needs of water resource managers, biodiversity planners, conservation agencies, researchers, and environmental consultants. The goal is simple: get high quality biodiversity evidence into real decision-making pipelines. What kind of data? Species occurrence and abundance, habitat and abiotic parameters, freshwater taxa (fish, invertebrates, algae, anurans, wetland plants), SASS biomonitoring, physico-chemical parameters, water temperature time series, and more. Why was it built? To make biodiversity data usable — not just stored. To improve long-term conservation outcomes and guide real-world freshwater management. Open source & collaboration BIMS is open source. The full platform codebase is developed in the open and maintained collaboratively. The project lives in kartoza/django-bims on GitHub

Carpathian Conservation in Practice: A Multi-Domain Monitoring Framework for Actionable Insights

Effective biodiversity monitoring is fundamental to understanding ecosystem dynamics, measuring conservation outcomes, and informing evidence-based policy decisions. As the biodiversity crisis intensifies, there is growing recognition that monitoring programmes must transcend disciplinary silos, integrate diverse methodologies, and engage multiple stakeholders to generate actionable insights at meaningful spatial and temporal scales. Foundation Conservation Carpathia operates in the Făgăraș Mountains of the Southern Carpathians having two major objectives: conserving biodiversity and restoring degraded habitats while fostering sustainable local development through nature-based economies. Over the past decade, we have developed and implemented a comprehensive monitoring programme that spans three interconnected domains: (1) terrestrial ecosystem monitoring (forest structure, habitat quality, and ecological restoration success), (2) wildlife population monitoring (targeting reintroduced and native flagship species including beaver, bison, brown bear, wolf and lynx, and their impacts on socio-ecological systems), and (3) socio-economic indicator monitoring (assessing community engagement, livelihood impacts, and stakeholder perceptions). Our biodiversity monitoring approach combines multiple non-invasive technologies: camera trapping, AI-powered species recognition systems, eDNA sampling, acoustic sensors, genetic monitoring, and remote sensing. At our booth, we wish to showcase the practical implementation, case studies, opportunities for collaborations, and lessons-learned. We are particularly interested in engaging with researchers, policymakers, and practitioners working on themes aligned with BioMonWeek's priorities. We believe that our experience can offer relevant insights for those developing monitoring programmes across institutional and geographic boundaries.

Data Terra : Integrated Observation of the Earth System and the Environment

As the thematic node EOSC for Environment, the French research infrastructure Data Terra will be happy to hold a booth at the BioMoonWeek. The booth will display flyers, posters and a portfolio of data and services proposed among Data Terra and its thematic hubs (atmosphere, land surfaces, ocean, solid earth, and biodiversity) and will be used as a meeting point to discuss projects and possible collaboration.

Exploring Biodiversity Monitoring from Space. Earth Observation applications and case studies across ecosystems

Satellite Earth Observation (EO) offers powerful opportunities for biodiversity monitoring by providing consistent, transparent and openly available data across large areas and long time periods. These datasets can complement field observations, support monitoring efforts and help track environmental change across ecosystems. Despite this potential, many organisations still find it challenging to navigate the growing landscape of EO data, tools and services, and the use of satellite information in biodiversity monitoring remains uneven. The ESA Stakeholder Engagement Facility (ESA SEF) booth at BioMonWeek will offer an opportunity to explore how satellite-based information can support biodiversity monitoring in practice. Visitors will be able to discover a range of EO-based applications across terrestrial, freshwater, coastal and marine ecosystems, illustrating how satellite data can contribute to monitoring habitats, environmental pressures and restoration activities. The booth will feature practical case studies, short demonstrations and opportunities for discussion with EO experts. In collaboration with the European Association of Remote Sensing Companies (EARSC), industry representatives will showcase examples of operational EO services already supporting biodiversity monitoring and environmental management. Participants are invited to share their monitoring challenges, explore relevant EO solutions and exchange ideas on how satellite data can better support biodiversity monitoring in the future.

From Sensors to Open Biodiversity Data: AI-enabled Monitoring at Scale

BMD, OneSTOP and MAMBO advance biodiversity monitoring through complementary field technologies and shared data workflows designed to scale across regions. This booth presents integrated approaches using CamAlien, camera traps, audio devices, AMI insect traps, eDNA sampling and Air-DNA collectors to detect species across habitats and seasons. We highlight how automated and AI-assisted pipelines support identification from images, sounds and molecular signals, while maintaining transparency, and data quality and FAIRness. A central theme is rapid and repeatable publication of biodiversity data:

standardised processing, clear provenance, and workflows that can be reused across sites, countries and years. Visitors will discover how these projects link field innovation with interoperable data outputs that can support near real-time biodiversity monitoring, research, conservation and policy, and strengthen connections to open biodiversity infrastructures like GBIF and OBIS.

GBIF

As a co-organizer of the conference, a GBIF booth should be available to provide additional information, resources, and support for conference attendees.

MARCO-BOLO

MARCO-BOLO will connect existing initiatives, optimising and improving methods, and further innovating technologies to structure and strengthen European marine, coastal and freshwater biodiversity observation capabilities, linking them to global efforts to understand and restore ocean health.

NextBON: From Methods to a Shared Blueprint for European Biodiversity Monitoring

Despite major EU policy frameworks, we still cannot assess in a consistent, cross-realm way whether biodiversity restoration and conservation measures, including those under the Nature Restoration Regulation, are working across terrestrial, freshwater and marine ecosystems. Monitoring remains fragmented across countries, realms and sectors, limiting comparable indicators for the Habitats and Birds Directives, the Water Framework Directive, the Marine Strategy Framework Directive and the EU Biodiversity Strategy 2030. NextBON creates and validates a harmonised three-tier biodiversity observation network as a blueprint for large-scale, policy-relevant monitoring. The architecture combines 50 Tier 3 sites, 350 Tier 2 field monitoring sites and 1,000 Tier 1 locations based on remote sensing and citizen science, using cross-tier calibration to link intensive reference measurements to broad spatial coverage and support robust Essential Biodiversity Variable (EBV) generation at scale. Core components include protocol harmonisation using Darwin Core-based schemas and multi-scale gap analyses, integration of environmental DNA, computer-assisted image and sound analysis, and satellite- and drone-based remote sensing with structured citizen science into interoperable EBV workflows, and a FAIR data backbone aligned with the European Open Science Cloud and connected to GBIF, DiSSCo and LifeWatch

ERIC. The presentation will introduce the three-tier design and cross-tier calibration, outline the EBV-to-indicator governance strand, and invite other initiatives to plug their sites, protocols and data flows into the three tiers to jointly refine the blueprint.

Pl@ntNet

Pl@ntNet is a citizen science platform launched in 2009 and supported by a consortium of French research centres (CIRAD, INRAE, Inria, IRD). Its aim is twofold: to make plant identification accessible to everyone worldwide and to generate high-quality data in large quantities for scientific research. Pl@ntNet relies on an AI model capable of identifying over 85,000 plant species from a single photo. This database continuously grows thanks to user contributions. Available on Android, iOS, and as a web version, the app encourages public participation by allowing users to validate or reject the AI's identification suggestions, thereby improving both the quality of the collected data and the AI's performance. Beyond its practical use for nature enthusiasts, Pl@ntNet plays a vital role in research. The data collected and shared with GBIF has already supported over 1,400 scientific publications. It also fuels a range of tools developed within the platform, such as plant community identification; GeoPl@ntNet, a mapping tool for predicting habitats and plant distributions across continental Europe with a 50x50m resolution; and a tool for identifying diseases and pests. Pl@ntNet is also involved in diverse projects, including the analysis of drone-captured images of tropical canopies and the monitoring of invasive species. With over one billion images collected and a community of more than 20 million users, Pl@ntNet is a key player in understanding, monitoring, and preserving plant biodiversity. Available in multiple languages and covering diverse regions—from tropical forests to temperate zones—the platform raises public awareness of environmental issues while documenting an ever-expanding range of plant diversity.

spcfy – Cloud Platform for Standardized DNA Metabarcoding Data in Biodiversity Monitoring

Scaling biodiversity monitoring across Europe demands not only more sequencing but also harmonized, reproducible, and accessible data workflows. DNA metabarcoding has become essential for surveying terrestrial, freshwater, and marine ecosystems, yet heterogeneous pipelines, reference databases, and reporting formats hinder cross-project comparability and data reuse. spcfy addresses this gap as a cloud-based, lab-agnostic platform for DNA metabarcoding data management and analysis. Sequencing laboratories upload Illumina FASTQ files and process them through standardized, no-code pipelines with curated reference and primer databases, integrated quality control, and transparent parameterization — ensuring reproducibility across labs, projects, and time points. The platform connects data producers and data users through a structured digital ecosystem. Labs manage and deliver results via spcfy, while customers — companies, agencies, research institutions, and public authorities — access interactive visualizations, cross-project comparisons, and exportable reports. The spcfyINSIGHT module lets users merge datasets across campaigns, explore taxonomic composition through OTU browsers and KRONA charts, and track biodiversity trends over time and space. All data is hosted on EU servers in compliance with GDPR, and an integrated marketplace facilitates collaboration between accredited labs and end users. A predictive analytics layer (spcfyPREDICT) is in development to enable risk scoring and scenario planning on top of monitoring data. At this booth, we invite the monitoring community to explore how standardized data infrastructures can support Europe's path towards mass biodiversity monitoring.

Taxonomy, the fundamental science for biodiversity monitoring and conservation

Without knowing what life forms exist and how to distinguish them, it is impossible to measure, manage, or conserve biodiversity effectively. Taxonomy provides the basic framework for knowing what species exist, where they are, and how they change over time. Without taxonomy, biodiversity monitoring would lack accuracy, consistency, and meaning. Taxonomy allows species to be correctly identified and thus ensures reliability in monitoring processes. Misidentification can lead to incorrect population estimates, overlooked extinctions, or ineffective conservation actions. A stable taxonomic system facilitates comparison and interoperability among the different sources and across the different collection mechanisms of biodiversity data. Additionally, taxonomy underpins biodiversity indicators and assessments. Conservation priorities, such as identifying threatened or endemic species, rely on taxonomic knowledge. Red Lists, protected area planning, and international agreements all depend on clearly defined species boundaries. Strong taxonomic references and resources support informed and evidence-based conservation decisions may protect the wrong targets or miss those most at risk. Moreover, taxonomy is essential for understanding ecosystem function and resilience. Different species play different ecological roles, even if they appear similar. Accurate classification helps reveal relationships among species, their evolutionary history, and their responses to environmental change, such as climate change or habitat loss. Finally, taxonomy supports long-term monitoring and policy-making. Biodiversity trends including declines but equally recoveries, or shifts in species distributions, can only be detected when species names and classifications remain consistent through time.

TEOSS: Training the European Orthoptera Sound System – Building Capacity and Innovation in Bioacoustic Monitoring

The TEOSS project (Training the European Orthoptera Sound System) addressed critical gaps in Orthoptera biodiversity monitoring across European biodiversity hotspots. Funded by the TETTRIs programme, this 20-month initiative (March 2024–October 2025) united researchers, taxonomists, and citizen scientists to advance bioacoustic methods for grasshopper, cricket, and bush-cricket identification. TEOSS organized four international workshops across the three Mediterranean peninsulas—Italy (Alpine region), Spain (Sierra de la Demanda and Andalusia), and Greece (Konitsa)—training over 55 taxonomists and 70 participants from 48 European institutions. Using an innovative "Wheel Learning Strategy" cycling between theory, fieldwork, and lab analysis, participants mastered sound recording protocols, species identification, and data management. The project's cornerstone achievement is the creation of the first continental-scale Orthoptera sound database, with over 30,000 recordings uploaded to Xeno-canto, including 545 high-quality recordings covering 83 species contributed directly through TEOSS activities. This open-access resource now covers nearly 80% of European Orthoptera species and enables, for the first time, comprehensive regional lists for Europe's primary biodiversity hotspots. By integrating taxonomy, bioacoustics, and machine learning, TEOSS directly supports the development of AI-driven sound recognition tools while fostering a self-sustaining pan-European research community. The project demonstrates that strategic investment in both human networks and technological infrastructure creates lasting capacity for biodiversity monitoring. TEOSS offers a replicable model for citizen science engagement, inclusive training methodologies, and open-data practices that strengthen Europe's capacity to monitor and conserve its threatened Orthoptera fauna.

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Theme: Terrestrial Monitoring — Land surveillance in focus

TR05 Biodiversity monitoring in terrestrial protected areas (including Natura2000)

Tuesday 5 May 11h30–12h30, Room Rondelet
Chair: Niels Raes

Description: Protected areas, and Natura 2000 sites in particular, are designated to ensure that habitats and species (including birds) are protected and maintained in a favourable conservation status (FCS) within Europe. Reporting on the status of conservation is often based on expert judgement and not always supported by FAIR data, meaning that the data is Findable-Accessible-Interoperable- Reusable. This session welcomes contributions on novel and high-throughput biodiversity monitoring techniques including Earth Observation data, camera trap, passive acoustic device and eDNA data in combination with AI species identifications (among others) that deliver FAIR data and support tracking the status and trends of terrestrial biodiversity across Europe.

High-throughput biodiversity monitoring and Biodiversity Analysis Tools in support of the EU Nature Directives

Niels RAES

Abstract: As early as 1979 the EU recognized the importance of protecting and conserving biodiversity with the adoption of the Birds Directive, extended with the Habitats Directive in 1992, that are implemented in the Natura 2000 conservation network. Regardless of the targets set by the EU Nature Directives, biodiversity in Europe is in decline. To halt the negative trend and mitigate the consequences, there is an urgent need for better biomonitoring, and improved understanding of the state of nature and the drivers of biodiversity loss. 'Biodiversity Meets Data - BMD' responds to these needs by capitalising on innovative tools and technologies developed through many EU projects and making these available to managers of Natura 2000 sites, policy makers, and governmental organisations. The tools include high-throughput biodiversity monitoring devices including camera-traps, audio recording, and eDNA sampling in combination with user-friendly AI species identification portals, and a suite of Biodiversity Analysis Tools (BATs) covering all three realms that are co-designed with relevant stakeholder communities. Access to this ecosystem of tools and BATs is provided through BMD's interactive Single Access Point (SAP). By integrating with the broader European data landscape, including LifeWatch ERIC, Green Deal Data Space (GDDS), ARISE Digital Species Identification platform and GBIF, BMD ensures sustained availability of developed tools, workflows and infrastructures. By utilizing a dedicated Biodiversity Data Space architecture aligned with FAIR and Common European Data Space (CEDS) principles, the project centralizes biodiversity and Earth Observation data within a

comprehensive data catalog, preserving long-term data integrity for future environmental decision-making. In this presentation, I introduce the BMD project, tools, BATs and SAP, and acknowledge the national and EU projects and research infrastructures that support biodiversity monitoring across Natura 2000 sites.

Monitoring of Annex I habitats in Denmark

Bettina NYGAARD

Abstract: This presentation provides a comprehensive overview of the national monitoring programme covering all 43 terrestrial habitat types currently appointed in Denmark. The monitoring has been systematically con-ducted in permanent plots since its establishment in 2004, and represents a reliable and scientifically robust data foundation for the assessment of conservation status under Article 17 of the EU Habitats Directive. The presentation walks through the monitoring methods employed across these habitat types, with particular attention to the key indicators used to evaluate the structure and function of the habitats. These indicators form the backbone of the assessment framework and allow for consistent, comparable evaluations over time. In addition, the presentation offers an overview of the conservation statuses reported as part of the 2025 reporting. This is complemented by a selection of concrete examples illustrating the trends that have been observed in Danish nature over the course of the monitoring period, offering insight into both the pressures habitats face and the progress — or lack thereof — made in their conservation.

Patterns of plant population trends in the NE of the Iberian Peninsula

Maria B GARCIA, A Múgica-Carnicero, H Miranda-Cebrián, C Díaz

Abstract: Long-term population trends, and how they are modulated by global change drivers, are essential for assessing species conservation status and setting conservation priorities. Here we analyzed two large plant datasets generated with the help of expert naturalists and participatory science programs in the NE Iberian Peninsula, a highly heterogeneous landscape ranging from semideserts to the highest calcareous summits in Europe. Our aim was to compare population fate and performance across habitats, and to estimate the influence of external stressors (vegetation or landcover change, climate change). We first estimated the persistence-to-extirpation ratio for more than 3,600 populations of rare species recorded before industrial development (mid 20th century) by matching historical and contemporary records. Plant persistence resulted to be nine times higher than extirpation over the past century, with wetlands showing the highest extirpation risk and rocky habitats the greatest persistence. We then assessed population growth rates for over 300 populations whose abundance of density was monitored during the last 15 years across multiple habitats and an altitudinal gradient of 2,800 m. Most of them displayed stable or uncertain trends, with the strongest stability again in rocky habitats and in the alpine belt. Overall, our results

indicate that plants in topographically complex areas may be more resistant to global change than previously assumed from simple climatic models or compared to patterns observed in animals. Effective biodiversity assessment requires robust, validated datasets combining extensive species inventories with long-term population monitoring. These efforts greatly benefit from integrating scientific infrastructures with the knowledge and involvement of citizens and expert naturalists. Such integration is especially critical in the Mediterranean Basin— a major global biodiversity hotspot—due to its high concentration of endemic and threatened species

Developing approaches to monitor subterranean biodiversity in karst

Maja ZAGMAJSTER, Gergely Balázs, Grega Benko, Anna Biró, Ruxandra Bucur, Claire Audrey Chauveau, Olivier Collard, Teo Delić, Cene Fišer, Jean-François Flot, Catalina Haidau, Sanda Iepure, Anja Kos, Stéphanie Lippert, Enrico Lunghi, Oana Teodora Moldovan, Orest Sambor, Cristian Sitar, Fabio Stoch, Valerija Zakšek, Dieter Weber, Hannah Weigand, Alexander Weigand

Abstract: Subterranean habitats and their associated fauna are among the most challenging to monitor. Subterranean species are difficult to sample, generally rare and often narrowly endemic. The diversity of subterranean species varies greatly across space and can reach very high numbers only in some regions. There are difficulties in accessing and sampling subterranean species. Caves represent rare, direct natural access points to subterranean habitat which extends also through the large fissure systems behind these voids. However, caves are protected as a habitat type under the EU Habitats Directive and require biological monitoring. Despite recently published EU guidelines, there is still no clearly defined approach for the biological monitoring of caves as habitats across Europe. This challenge is addressed in the EU Biodiversa+ funded project Sub-BioMon (https://www.sub-biomon.net/), with a focus on karst regions. The project involves six European countries, representing different geographic regions, with varying proportions of karst, different numbers of exclusive subterranean species, as well as different states of activities dedicated to national monitoring of subterranean habitats. We explored potential differences that could influence the implementation of subterranean biological monitoring by a questionnaire survey of different stakeholder groups. We tested different field sampling methods for terrestrial and aquatic fauna in up to three caves and springs per country. Based on the results, we aim to develop minimal standards for monitoring subterranean biodiversity. To ensure the accurate and rapid identification of samples, we apply DNA-based molecular approaches (DNA barcoding, eDNA metabarcoding) and test their efficiency for routine species identification and detection. The project activities involve different stakeholders, from governmental to nongovernmental organizations, including nature parks, show caves, as well as cavers and general public.

Drone-based monitoring of threatened plant species on inaccessible cliffs: from manual census to AI-assisted plant detection within the LIFE Seedforce project

Costantino BONOMI, Antonia Cristaudo, Mario Di Stefano, Valentino Casolo, Gianluigi Bacchetta, Jože Bavcon, Aaron Iemma

Abstract: Site accessibility is a frequent constraint that prevents an accurate estimate of the population size of threatened species, making traditional field surveys difficult, often dangerous, and inherently incomplete. To overcome this barrier the partners of the Life Seedforce project (LIFE20 NAT/IT/001468) adopted drone-based monitoring supplemented by image analysis and AI assisted assessment of population size of 5 Annex II species in 11 Natura2000 sites. This approach was successfully applied to plants growing on vertical cliffs such as *Saxifraga tombeanensis* in the Central Italian Alps, Eryngium alpinum in the Italian and Slovenian Eastern Alps, *Silene hicesiae* and *Cytisus aeolicus* in the Aeolian Islands in Sicily and *Centranthus amazonum* in Central Eastern Sardinia. The techniques adopted ranged from a basic manual counting to a more sophisticated automated AI-assisted census. Surveys were conducted using DJI platforms flying vertical strip patterns along cliff faces, to generate micro-topography-DEMs at metric resolution. After eliminating redundant frames, each image was processed using annotation software (Ksnip) to mark individual plants and link them to geographic coordinates. This dataset was used to train a convolutional neural network (CNN) for automated YOLOv8 object detection model. On held-out validation imagery, the model achieved a mean Average Precision (mAP@0.5) of 0.81 with a recall of 0.78 and a precision of 0.86, effectively distinguishing the target species from visually similar features (lichen patches, calcium deposits, other cliff vegetation). Automation reduced processing time by 70% and proved to be a valuable tool for repeatable, non-invasive long-term population trend assessment. The analysis led to the discovery new sub populations and returned higher sizes with respect to ground surveys, identifying donor populations and prioritising plant translocation actions under projected climate change scenarios.

TR08 Monitoring common species at the European scale

Wednesday 6 May, 9h00-10h00, Room Sully 3

Chair: Mathieu Basille

Description: Monitoring common species is important for awareness and management issues, by providing examples of successful recoveries, expansions or important highlights on biodiversity decline. Monitoring common species also benefits from statistical approaches at the national scale, and are good candidates for protocol harmonisation at the European scale. We welcome contributions about terrestrial common species describing national schemes and transnational or European cooperation.

MISSING

Testing the EMBAL Methodology for Grassland Biodiversity Monitoring in Slovenia

Irena BERTONCELJ, Azra Šabić, Mateja Grašič

Abstract: Effective biodiversity monitoring in agricultural landscapes remains a major challenge in Slovenia, where systematic Natura 2000 monitoring covers only a small proportion of target species. We evaluated the applicability of the European EMBAL (European Monitoring of Biodiversity in Agricultural Landscapes) methodology for assessing grassland biodiversity, with emphasis on vegetation-based indicators. Field surveys were conducted in May–June 2024 across six Slovenian regions (48 transects). We recorded standard EMBAL parameters, including grass and forb cover, flowering entomophilous plant abundance, flower colour diversity (max. 10), and the presence/cover of predefined “key taxa”. Soil physico-chemical properties and land-use intensity (mowing, grazing, fertilisation) were additionally assessed. Data were analysed using ANOVA, PCA ordination, and linear regression. Significant differences among regions were detected for flower colour number and flowering plant abundance. The intensively managed site (Suhadole) showed markedly lower values of both parameters, strongly associated with higher mowing frequency, fertilisation, and grass dominance. Fertilisation negatively correlated with the number of key taxa, particularly orchids, highlighting their bioindicative value. PCA analyses demonstrated clear separation of intensively and extensively managed grasslands, while differentiation among moderately extensive sites was less pronounced. Our results indicate that EMBAL provides a useful baseline for grassland biodiversity monitoring. However, predefined pan-European indicator groups and simplified flowering metrics are insufficient for fine-scale national assessments. We recommend complementing EMBAL surveys with species-level composition data and establishing long-term, systematic monitoring to improve evaluation of agri-environmental measures.

Monitoring Biodiversity in Intensive Farming Areas

Agasse C., Boutaud E., Gancedo I., Hance T., Herve M., Jacquemart A., Marrec R., Redlich S., Saska P., Skuhrovec J., Timm S., Tougeron K., Vašková H., Audusseau H., Burtchen L., Fricke U., Ganuza C., Geisendörfer P., Karpf C., Klimm F., König S., Korten H., Krügl A., Mahsberg D., Sauer N., Schrauth K., Schultes L., Stör J., Uhl B., Joan VAN BAAREN, Nicolai A.

Abstract: Biodiversity loss in conventional farmland is one of the most urgent challenges facing humanity today. Through the use of living labs—an approach that encourages citizen involvement in science—the ConservES Biodiversa+ project aims to collectively develop field-to-landscape management strategies, primarily through floral enrichment. In this project, we focused on cereal fields across a climatic gradient, ranging from the mild Atlantic climate of western France to the more continental climate of central Europe (western Czech Republic), encompassing five locations. Aligned with the concept of ecological intensification, our goal was to conserve biodiversity in ways that maximize ecosystem services. We employed two distinct approaches: First, we organized BioBlitzes—short, intensive biodiversity surveys—at all five locations, both before and after the sowing of flower strips. Our objective was to assess how BioBlitzes contribute to broader biodiversity knowledge documented on the GBIF platform, and to explore participants' expectations and outcomes. Our findings revealed that BioBlitzes significantly enhanced knowledge of under-sampled taxonomic groups, particularly among invertebrates. Participants primarily sought to gain biodiversity knowledge, but what they valued most was the convivial atmosphere of the events. They also reported learning about sampling methods and deepening their understanding of specific taxa. Overall, BioBlitzes in agroecosystems appear to be promising tools for supporting the agroecological transition, combining hands-on learning with biodiversity assessment. Second, we conducted classical biodiversity monitoring, led by the project's researchers. The unique aspect of this approach was our focus on sampling three undesirable taxa (weeds, slugs, and aphids), four taxa of natural enemies, and three taxa of pollinators. This allowed us to determine when and where ecosystem services were maximized.

Building structured transnational Odonata monitoring schemes across Europe

Martin JEANMOUGIN, Lisa Nicvert, Geert Deknijf, Roy van Grunsven, Colin Fontaine, Reto Schmucki

Abstract: Temporal monitoring schemes are among the most effective tools for estimating population trends and deriving indicators that assess the impacts of anthropogenic change and guide conservation policy. However, such standardized data remain scarce at the European scale outside a few well studied taxa such as birds or butterflies, and are particularly limited for terretrial small waterbodies that fall outside the scope of the EU Water Framework Directive. In this talk, I will outline several initiatives focused on a charismatic yet understudied taxon -Odonata- that aim to bring together existing structured monitoring schemes across Europe. I will first present the DRAGON project, which seeks to improve our understanding of the drivers of Odonata biodiversity change in Europe and to provide actionable recommendations to mitigate human impacts. Building on the experience of previous European butterfly monitoring initiatives (e.g., eBMS), DRAGON is developing a common European database for Odonata. I

will report preliminary results on continental scale species distribution trends and discuss how they can foster synergies with the recent establishment of Dragonfly Conservation Europe (DCE). Through DRAGON, DCE contributes by collating, mapping, and harmonising existing datasets and monitoring protocols available across Europe. Finally, I will highlight additional DCE initiatives and present the strengths and limitations of national monitoring programs in France and the Netherlands. These case studies help chart a path towards more structured common goals and indicators that can inform EU conservation policy in the coming years, while identifying priority needs for research and cooperation.

Towards transnational structured plant monitoring schemes in Europe?

Emmanuelle PORCHER, Solène Agnoux, Pierre Bonnet, Maxime Buron, Christian Damgaard, Pieter De Frenne, Nicolas Deguines, Lucien Desplanches, Bodil K. Ehlers, Jérôme Frei, María B García, Romain Goury, Clément Gros, Ute Jandt, Alexis Joly, Gabrielle Martin, Denis Michez, Oliver L. Pescott, Tobias Roth, Ania Schleicher, Clément Vallé, Jeanne Vallet, Donald Waller

Abstract: Whilst transnational collaborative efforts exist to structure animal monitoring schemes in Europe, such as the Pan-European Common Bird Monitoring Scheme or the European Butterfly Monitoring Scheme, research into the temporal dynamics of plants across Europe has relied primarily on the pooling of vegetation-plot observations (e.g., European Vegetation Archive), sometimes combined with unstructured resurveys (e.g., ReSurvey Europe). Structured monitoring schemes with regular plot resurveys increase the detectability of changes and reliability of forecasting, for example for detecting short-term trends and monitoring the effectiveness of conservation policies, but except for Switzerland and the UK, European countries are slow to support systematic programs to monitor plants and habitats. Here, I will outline the initial steps of an initiative to bring together existing structured plant monitoring schemes in European countries, which started with a workshop gathering those responsible for their management or for the scientific analysis of the data. They include six schemes launched between 2001 and 2017 that range from regional to national in scope, plus two international resurvey initiatives. I will review the existing schemes, their similarities and differences, particularly in terms of sampling strategy, characteristics of participants, as well as trends and indicators they produce. I will also report the first results of a joint analysis of the temporal trends in plant abundance across these schemes, revealing a strong signal for an impact of pollinator loss on plant dynamics across Europe, albeit with some heterogeneities, and outline future needs for research and policy.

The European Bird Census Council: 35 years monitoring changes in bird populations

Sara FRAIXEDAS, Petr Voříšek, Alena Klvaňová, Gabriel Gargallo, Jean-Yves Paquet, Sergi Herrando

Abstract: The European Bird Census Council (EBCC) was founded in 1992, emerging from the European Ornithological Atlas Committee and the International Bird Census Committee, as a partnership of national organisations aimed at producing the first European Breeding Bird Atlas (EBBA1) through the integration of information on breeding birds across Europe. Likewise, in 2002 the EBCC and BirdLife International initiated the Pan-European Common Bird Monitoring Scheme (PECBMS), integrating population trends from national monitoring schemes. In 2010 the General Meeting of the EBCC decided to start a second European atlas (EBBA2) following the same principles as EBBA1 and PECBMS. In 2014 the EuroBirdPortal (EBP) began integrating a vast amount of bird observations collected through online portals managed by national organisations to build a comprehensive European portal. Currently, the EBCC is developing the spatiotemporal dimension of change to regularly update bird distributions every few years. All these achievements have been possible thanks to the development of governance agreements, coordination units, data flows, databases and analytical tools. The outcomes of these projects have been extremely useful for determining population and distribution trends of birds in Europe and, in close cooperation with many other scientific institutions, for disentangling the drivers behind these changes. The EBCC partnership of ornithological organisations has a clear policy dimension across EU, national, and subnational levels. For example, the Farmland Bird Index and the Forest Bird Index have both been recognised as key tools for tracking progress in EU environmental policy. Based on the concept of citizen science, this international monitoring infrastructure has been capable of robustly tracking bird populations over decades, while constantly adapting to changes in society and technology.

TR02 Monitor connectivity & Spatial Planning

Wednesday 6 May, 10h00-11h00, Room Sully 3
Chair: Rozália Kapás

Description: Land-use change has been identified as one of the main direct drivers of biodiversity loss for terrestrial ecosystems. This session will address the use and change in use of land across Europe. Talks will highlight methods, guidance, tools, scenarios, models, data, knowledge and capacity-building for integrating biodiversity considerations into and promoting connectivity (both structural and functional) in spatial planning, across sectors and scales. We also encourage talks dealing with lessons learned and best practice for identifying, restoring and enhancing ecological connectivity, focusing on how ecological connectivity contributes to biodiversity conservation, restoration, sustainable use and management.

Effectiveness of dimensionality reduction in multi-species connectivity analysis

Lise LAYOTTE, Marie-Caroline Prima, Wilfried Thuiller

Abstract: Establishing ecological corridors adapted to a set of species is essential to preserve biodiversity and its ecological processes. However, landscape connectivity is inherently species-specific due to contrasting ecological and movement requirements. The most comprehensive method to model multi-species connectivity, the multifocal approach, combines individual connectivity models for each species. However this method remains both data- and computation-intensive. Consequently, several alternative approaches, generic, substitution, and agnostic, are used, though their ability to replicate the multifocal approach is poorly documented. In this study, we evaluated and compared landscape connectivity from the reference (multifocal approach) and these alternatives. Our results show that the substitution and generic approaches are valid alternatives to the multifocal approach, with a significant reduction of data and computational resources needed for the substitution method. The connectivity analysis was evaluated using independent movement datasets from three species. The approach was supported for the Alpine ibex and the golden eagle, but not for the common raven, indicating that the spatial scale at which connectivity was modeled may not match the movement scale of small populations. Moreover, the sensitivity analysis indicates that the choice of explanatory variables for the methodology strongly influences the connectivity maps generated using the generic and agnostic approaches, whereas it has little effect on maps produced with the substitution and multifocal approaches. Consequently, we recommend the substitution approach as an effective compromise between comprehensiveness and feasibility, if aligned with the study objectives.

Functional Habitat and Ecological Connectivity: Indicators and Decision Support for Spatial Planning under Cumulative Impacts

Bram VAN MOORTER

Abstract: Land-use change and infrastructure development are major drivers of biodiversity loss across European landscapes, largely through their cumulative effects on habitat suitability and ecological connectivity. Spatial planning therefore requires indicators that capture not only the amount of habitat available to species, but also how effectively landscapes remain connected. We present a framework for identifying and monitoring **functionally connected habitat**, linking habitat suitability with ecological connectivity across landscapes. By integrating species' environmental requirements with landscape structure, the

approach estimates how much habitat remains accessible to species under current conditions and how this changes under alternative land-use scenarios. The resulting indicators provide a landscape-scale measure of functional habitat that can support biodiversity monitoring and inform spatial planning. Applied to the impacts of hydropower development on wild reindeer in Norway, the framework revealed substantial reductions in connected habitat due to fragmentation. At the same time, the analysis highlights opportunities for restoration and mitigation. Through sensitivity analysis, the approach identifies locations where targeted interventions—such as wildlife overpasses or habitat restoration—could yield disproportionate gains in connected habitat. Implemented in the ConScape computational library, the framework enables high-resolution assessments of connectivity and cumulative impacts, making it possible to explore planning scenarios and prioritize actions at regional scales. By translating complex ecological processes into operational indicators and spatial priorities, the approach supports biodiversity-sensitive spatial planning and the restoration of ecological connectivity.

A national scale predictive model for the detection of high-conservation value forests from remote sensing data

Tobias ANDERMANN

Abstract: In this study, we implement a deep learning segmentation approach for detecting high-conservation-value forests using a nationwide inventory dataset and a set of remote sensing data products. Using this model, we produce a national data product showing remaining high-conservation value forests in Sweden, with a predictive accuracy of 91% and a high-detail spatial resolution of 10-meter pixel size. Sweden serves as a good test case for the 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 km^2 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.

Enhancing rule-based potential connectivity models for African savanna elephants (Loxodonta africana) using remote sensing in Binga district, Zimbabwe

Colas GUILLON, Lilian Blanc, Hadrien Vanthomme, Sébastien Le Bel, Jacques Baudry, Camille Deforceville, Hélène Dessard, Maxwell Phiri, Julie Betbeder

Abstract: The Kavango Zambezi Transfrontier Conservation Area hosts many protected areas and diverse fauna, including emblematic species. As animals move across landscapes shared with rural communities, maintaining connectivity is crucial for long-term conservation. Most studies in dry forests rely on expert knowledge and coarse global land use/land cover (LULC) data. Here, we use advances in remote sensing to improve connectivity models with more detailed and cost-effective LULC mapping. This study develops a framework to assess how remote sensing enhances rule-based resistance models, using the African savanna elephant (Loxodonta africana) as a focal species. Resistance maps were produced from two LULC classifications: a global dataset and a finer one distinguishing forest types and structure. Additional environmental variables influencing elephant movement were included. A graph-based connectivity index was modeled and qualitatively evaluated against corridors identified by stakeholders in a district of Zimbabwe. Results show that distinguishing forest type and structure improves connectivity precision. Adding environmental variables further strengthens contrasts between mapped corridors and surrounding areas. This study provides an efficient framework to test the impact of detailed LULC and environmental variables on connectivity models and corridor identification. It supports more informed, evidence-based conservation planning and management of elephant movement in fragmented landscapes.

TR01 Applied biodiversity monitoring in the terrestrial realm

Wednesday 6 May, 11h30-12h30, Room Sully 3
Chair: Guillermo Aguilera Núñez

Project InvazMap - Mapping and Monitoring of Invasive Species in Czechia

Zdenek RACANSKY

Abstract: The InvazMap project focuses on mapping and monitoring selected alien and invasive species in the Czech Republic. The project is implemented by the Nature Conservation Agency of the Czech Republic (AOPK ČR) and funded by the Operational Programme Environment 2021–2027. Running from 2023 to 2029, the project aims to establish a long-term system for collecting up-to-date data on the occurrence and distribution of invasive alien species. The project contributes to fulfilling obligations arising from EU Regulation No. 1143/2014 on invasive alien species and related national legislation. Field data are collected using standardized methodologies and mobile applications, and the records are stored in the Nature Conservation Occurrence Database (NDOP). The main outcome of the project will be detailed and regularly updated information on the distribution of selected invasive and non-native species across the Czech Republic. These data will support biodiversity conservation, improve management of invasive species, and provide a basis for national strategies and practical management measures.

A Successful Case Study on the Control of Invasive Alien Plant Species Along River Valleys in the Southern Făgăraș Mountains, Romania

Oliviu G. POP, Adrian Pătrulescu, Costin Enache

Abstract: The Făgăraș Mountains, located in the Southern Carpathians of Romania, host valuable riparian ecosystems that are increasingly threatened by the spread of invasive alien plant species (IAS). Between 2020 and 2024, the Foundation Conservation Carpathia conducted an IAS inventory, mapping, management, and monitoring program along the main valleys' tributary to two major river basins: the Dâmbovița and Argeș basins. Seven IAS were targeted: Erigeron strigosus, Erigeron canadensis, Reynoutria japonica, Impatiens parviflora, Impatiens glandulifera, Xanthium strumarium subsp. strumarium, and Hemerocallis fulva. Following identification and mapping, mechanical control methods (uprooting, selective cutting, mowing) were applied based on invasion intensity, site characteristics, and the presence of native species. Between 2021 and 2024, IAS were removed from over 150 km of riverbanks. Monitoring evaluated management effectiveness and improvements in habitat conservation status. Fifty-seven plots were established (39 in restored areas and 18 in IAS-free reference areas) and surveyed annually for at least three years post-intervention. Assessments included botanical surveys (IAS cover relative to native species and total vegetation cover) and fixed-point photography. Results indicated significant reductions in IAS cover within monitored plots (up to 98% for E. strigosus, 50% for I. parviflora, 54% for R. japonica, and 100% for I. glandulifera), accompanied by recovery of native vegetation. No IAS colonization was detected in reference monitoring plots. These findings demonstrate that mechanical control yields measurable conservation outcomes and supports scalable restoration strategies for mountain riparian ecosystems, while underscoring the importance of continuous monitoring for adaptive management.

Operationalising soil biodiversity monitoring: addressing detection–attribution trade-offs from the RMQS-Biodiversity network

Mickael HEDDE, Sophie Pouzenc, Claudy Jolivet, Apolline Auclerc , Antonio Bispo, Nolwenn Bougon, Camille Chauvin, Daniel Cluzeau, Jérôme Cortet, Jean-François David, Sarah Guillocheau, Antoine Lévêque, Gwenaël Magne, Nicolas Henon, Franck Noël, Guénola Pérès, Cyril Versavel, Cécile Villenave, Quentin Vincent

Abstract: The integration of soil biodiversity into European environmental policies—such as the Soil Monitoring Law (SML) and the Nature Restoration Regulation (NRR)—requires robust, scalable monitoring systems. However, a key challenge remains largely overlooked: the trade-off between detection capacity (i.e. the ability to reliably observe biodiversity patterns) and attribution (i.e. the ability to link these patterns to environmental drivers or management practices). Here, we present the RMQS-Biodiversity programme, a national-scale soil monitoring network in France designed to capture biodiversity patterns across a wide range of pedoclimatic conditions and land uses. The programme combines standardised field sampling of soil fauna with environmental DNA metabarcoding across multiple taxonomic groups, alongside environmental covariates. We argue that different monitoring approaches inherently position themselves along a detection–attribution continuum. High-throughput methods such as eDNA maximise detection breadth and taxonomic coverage but may limit direct ecological interpretation and attribution. Conversely, trait-based or morphologically resolved approaches provide stronger links to ecological processes and management, but often at the cost of reduced detection power and scalability. Using RMQS-Biodiversity as a case study, we explore how combining complementary methods can help reconcile this trade-off, and we discuss the implications for indicator development and policy implementation. We highlight that making soil biodiversity operational for policy does not only require standardisation, but also an explicit acknowledgment and management of this detection–attribution compromise. By reframing soil biodiversity monitoring through this lens, we provide a conceptual and practical basis for designing monitoring systems that are both scientifically robust and policy-relevant.

LIFE IP Natureman, the process of changing to Digital Mapping of Habitats in Denmark

Ida Maria PÉCSELI

Abstract: The project LIFE IP Natureman (2018–2027) aims to achieve a favourable conservation status for habitat types (especially petrifying springs, alkaline fens, and grasslands) by making nature management a viable branch of farming in 11 Natura 2000 sites in Jutland, Denmark. As part of the Danish national monitoring programme (NOVANA), a methodological shift is underway toward more automated identification of habitat types. The LIFE IP Natureman project area serves as a case study, where the output from the new method can be examined on a large scale. In Natureman's reporting, a comparison is therefore included between data from traditional field mapping of open habitat types and the new method, based on datasets from 2018 and 2025. The new method is based on a machine learning model that classifies habitat types at a resolution of 10 × 10 m using a large amount of information from LIDAR, satellite data, and aerial imagery, as well as data on soil conditions, hydrology, geographic location, and a large number of training points. In the development process, work is being done on how to post-process these model outputs and how to handle the dating of the predictions made by the model. The model is better at predicting some habitat types than others. Improving the condition of the habitat types petrifying springs and alkaline fens is a central objective of Natureman, and therefore part of the project involves contributing to the further development of the model with a focus on wet habitat types, including alkaline fens.

What disease ecology can bring to wildlife animal health monitoring : the case of long lived colonial species

Thierry BOULINIER, Jérémy Tornos, Mathilde Lejeune, Augustin Clessin, Tristan Bralet

Abstract: Wildlife animal health surveillance is often relying on passive surveillance using networks of professionals linked to the general public and field actors that are in contact with wildlife. Abnormal mortality cases are reported and subject to reactive investigations. We argue that monitoring wildlife diseases would gain from relying more on disease ecology approaches and population ecology monitoring. We illustrate this with the case of long lived colonial species affected by high pathogenicity avian influenza and avian cholera.

TR03 Scaling biodiversity monitoring: From ecosystem function to infrastructure impacts

Wednesday 6 May, 16h30-17h30, Room Sully 3
Chair: Mona Naeslund

CoForFunc- Toward a biome-scale monitoring of the Congo basin FORest FUNCtional composition

Gilles DAUBY, Ploton Pierre, Barbier Nicolas, Besson Ninon, Maréchaux Isabelle, Sonké Bonaventure, Fortunel Claire, Deveiller Grégory, Bastin Jean-François, Martinez Vilalta Jordi, Middleby Kali, Adet Lucette, Simo-Droissart Murielle, Oliver Binks, Tresson Paul, Heuret Patrick, Fayolle Adeline, Pélissier Raphaël

Abstract: Covering approximately 240 million hectares, the Congo Basin Forest (CBF) represents the second-largest unfragmented block of tropical forest on the planet. It hosts remarkable levels of biodiversity and carbon stocks and plays a critical role in the global carbon cycle and climate regulation. Yet, its internal functioning, phenology, and fine-scale dynamics remain poorly characterized. Through a unique European research partnership and transnational collaborations with experts from Central African countries, CoForFunc aims to develop an integrated approach for monitoring the tree functional diversity of the CBF, in order to support biome-scale assessments of its vulnerability to climate change and human-induced transformations. We address these challenges by establishing a multi-step workflow that should facilitate the monitoring of biome-scale Essential Biodiversity Variables, with the ultimate goal of providing indicators capable of detecting early warning signals of compositional and functional changes within the forests. In this talk, I will present an overview of the project's activities, with emphasis on: (1) the development of a transnational platform of primary biodiversity datasets for CBF tree species; (2) the deployment of a network of UAV-based forest observatories, enabling spatially continuous and temporally dense monitoring of canopy structure, forest functioning (phenology in particular), and biodiversity at resolutions inaccessible to satellites alone; and (3) in situ monitoring of tree functioning to better interpret the shifts in canopy functioning in terms of functional strategies (drought tolerance and photosynthetic capacity in particular).

Scaling tree species monitoring from drones using the Pl@ntNet model: opportunities for mass biodiversity monitoring

Vanessa HEQUET

Abstract: The growing need for large-scale biodiversity monitoring calls for new approaches capable of rapidly producing reliable species-level information across extensive areas. Recent advances in computer vision and remote sensing offer promising opportunities to complement traditional field inventories. In this study, we explore the potential of the Pl@ntNet model for the identification of tropical tree species from drone imagery. Using a dataset of drone images collected over forest plots in Cameroon, we evaluated the ability of the Pl@ntNet model—originally designed for plant identification from ground photographs—to recognize canopy trees from aerial perspectives. The dataset includes multiple images per tree crown and spans a diverse set of species representative of Central African tropical forests. Our results show encouraging performance for several species and genera, highlighting the potential of existing large-scale plant recognition models to contribute to automated biodiversity monitoring from aerial imagery. This work illustrates how combining drone imagery with AI-based plant identification can contribute to emerging mass monitoring approaches for forest biodiversity, while also identifying critical challenges that must be addressed to implement these methods at scale.

Leveraging data from Earth Observation, Administrative Agricultural Data, and Citizen Science in Germany's farmland biodiversity monitoring

Sophie OGAN, Andrea Ackermann, Stefan Erasmi, Damien Finn, Sebastian Klimek, Christian Levers, Demetra Rakosy, Norbert Röder, Marcel Schwieder, Wiebke Sickel, Diana Sietz & Jens Dauber

Abstract: In Germany, about 50% of land is used for agriculture. Hence, biodiversity conservation and restoration in agricultural landscapes is of crucial importance. Despite policy interventions such as agri-environmental measures, farmland biodiversity is still in decline. However, current farmland biodiversity monitoring schemes remain insufficient to robustly evaluate the effectiveness of agri-environmental measures and to identify key drivers of biodiversity trends. This limits evidence-based policy-making and underscores the need for a coherent, representative nationwide monitoring system. The German nationwide monitoring of biodiversity in agricultural landscapes (MonViA) addresses this gap.

It provides an adaptive framework that combines nationwide trend monitoring with targeted studies of agricultural land systems, capturing temporal dynamics, enabling policy recommendations, and providing robust indicators. Data collection integrates established and innovative approaches, including Earth Observation, data from the Integrated Control and Administration System (IACS), metabarcoding on environmental DNA (eDNA), and Citizen Science. Here, we present the overarching MonViA framework and insights from the MonViA Indicator Report 2024 , which comprises 41 indicators across three biodiversity levels: habitat-, species-, and genetic diversity (https://www.agrarmonitoring-monvia.de/fileadmin/SITE_MASTER/content/Dokumente/MonViA_Indikatorenbericht_2024.pdf). By linking science, policy, agriculture, and society, MonViA contributes to a comprehensive evidence-base for decision-making. Long-term monitoring ensures data reliability, while transparent communication and participatory approaches strengthen societal engagement with farmland biodiversity.

Large-scale in-situ survey and monitoring system design for habitat types

Aapo AHOLA, Topi Tanhuanpää, Vuokko Heikinheimo, Virpi Junttila, Linda Kartano, Tytti Kontula

Abstract: EU's Nature Restoration Regulation, alongside other policies, requires Member States to produce new extensive and accurate information about habitat type loci and their ecological quality parameters. To date and in the foreseeable future, most of such data can only be collected by field surveys. Even where remote sensing methods are suitable for monitoring, they depend on ground proofing data. Thus, reliable in situ sampling of habitat type information is paramount, but at the same time, however, it is a particularly demanding task. How do you plan a field monitoring campaign that covers nature's variance in habitat types and their qualities, but appears reasonably cost-efficient to your funders? We present a novel transect-based design for nationwide habitat type inventory and monitoring which will soon start operatively in Finland. We also discuss some general principles to follow when designing field sampling on different scales.

TR04 WORKSHOP Remote Sensing Application for Biodiversity

Thursday 7 May 9h–11h, Room Rondelet
Chairs: Therese Eriksson and Rozália Kapás
Contributors: Tobias Andermann, Topi Tanhuanpää, Arvid Sjöberg, Hans Gardfjell

Description: This workshop demonstrates use-cases on remote sensing applications for biodiversity monitoring and focuses on strengths, limitations and relevance for policy use. Through concrete examples and guided collaborative discussion, the participants will explore remote sensing-based modelling approaches, the integration of validation of field data, method selection based on spatial scale and data availability, and ways to improve predictive modelling of biodiversity metrics and overall modelling workflows.

PS01 Posters

Automating Manual Polen Monitoring Dataflows

Arturo H. ARIÑO, Berta Caballero-López, Irene Lobato-Vila, Mercedes París, Arturo H. Ariño, Francisco J. Cabrero-Sañudo, Sergio Montagud, David Galicia, Celia Santos Mazorra, Neus Brañas Valcárcel, Sergi Gago Carrión, Adrián Sánchez Albert, Sandra Grzechnik, Ana Amézcua, Piluca Álvarez Fidalgo, Angel Chaves, Manuel Sánchez Ruiz, Marina González Cristóbal, María Imas, Robert J. Wilson

Abstract: While nowadays transitioning to fully automated procedures, airborne pollen monitoring data are still required to be delivered through standardized protocols heavily reliant on cumbersome manual identification and counting of pollen grains sampled in impact traps. The dataflow, from sampling through to data publication, requires a significant workload that is prone to human error as multiple steps are involved. Tasked with providing daily reports and forecasts for the region of Navarra in Spain, we developed an automated dataflow, NApoleOn (v.26) to both ease the data handling burden and to reduce human handling to the bare minimum (i.e. identification). Technicians can just single-click confirm each identification in a button panel, and leave the system to handle mostly everything else down to the feed to regional, national, and European databases. The system was deliberately designed to work within common off-the-shelf software: Microsoft Office tools and the Google environment working in tandem. This approach ensures negligible maintenance costs, as updates are largely “outsourced” to the platforms, and code adjustments, if any, are limited to the improbable case of major changes in the platforms’ ingestion schemes. The reliance on ubiquitous platforms also facilitates migration to other sites by merely updating the regional pollen catalogue. NApoleOn fills on the cheap the gap between the widespread classical pollen monitoring protocol with manual reporting and the forthcoming fully-automated, AI-driven systems that, though vastly more expensive, are yet to reach human accuracy--but can more easily integrate into an automated dataflow than manual counting.

Citizen science as a tool for environmental compliance assurance under the EU Nature Restoration Regulation (NRR)

Maud BRUMMANS, S. Teurlincx, Z. van Helvoirt, F. van Haastrecht

Abstract: Citizens across Europe have collected data on bees and especially butterflies for decades. In countries like the Netherlands, long-term butterfly schemes are internationally recognised, and volunteer networks generate growing datasets on wild bees. The evidence is clear: many pollinator species are declining. Under the EU Nature Restoration Regulation (NRR), Member States must establish science-based methods to monitor pollinator diversity and populations and assess trends at least every six years (Article 10). While this strengthens monitoring, it does not in itself mandate restoration measures. Measuring decline does not automatically reverse it. This creates both a gap and an opportunity. In cities, healthy wild bee communities often coincide with structurally diverse, flower-rich and well-connected green spaces. Because bees respond sensitively to habitat quality, they can serve as bio-indicators of urban green space. Improvements in bee diversity often reflect improvements in green space design and management. Article 8 of the NRR requires Member States to show an increasing trend in urban green space from 2031 onwards. Here, citizen science can contribute directly to Environmental Compliance Assurance. Initiatives such as BeeGrateful demonstrate how structured monitoring with citizens can generate consistent, locally embedded bee data: using standardized nesting sites and species identification based on nesting preferences and entrance hole diameters. When using bees as an indicator of urban green space, this data can inform spatial planning, support reporting under Article 8 and guide habitat improvements. Strengthening urban green space benefits pollinators and indirectly supports Article 10 objectives. By positioning bees in the city as indicators of urban green space, citizen science becomes a governance tool linking community data to compliance and tangible restoration under the NRR.

PUBLIC ENGAGEMENT IN RESEARCH: MONITORING THE GREATER WHITE-TOOTHED SHREW IN THE CZECH REPUBLIC

Alena Fornůsková, Iva Holásková, Jan Matějů, Joëlle GOÜY DE BELLOCQ

Abstract: Public engagement in scientific research has become an important tool for collecting data across large spatial and temporal scales. In this study, we applied citizen science approaches to monitor the spread of the greater white-toothed shrew (Crocidura russula), a non-native synanthropic species that has begun expanding into the Czech Republic from Germany in recent years. The project was launched in autumn 2023 in the Karlovy Vary Region, where the species was first recorded in 2022. Members of the public were invited to submit photographs, video recordings, and in some cases biological samples of white-toothed shrews and other shrews, primarily from human settlements. Between December 2023 and January 2025, more than 200 records were collected across the Czech Republic. Species identification of selected individuals was verified using genetic analyses based on sequencing of the mitochondrial cytochrome b gene. By combining photographic records, video material, and genetic data, we confirmed the occurrence of the greater white-toothed shrew in the Cheb region, the Aš borderland, and the Kraslice area. We documented co-occurrence of the greater white-toothed shrew and the bicoloured white-toothed shrew (*Crocidura leucodon*) in Cheb and confirmed the absence of the lesser white-toothed shrew (*Crocidura gueldenstaedtii*) in the Cheb region. In addition, new photographic evidence revealed the presence of the bicoloured white-toothed shrew in northeastern Bohemia, where it had not previously been recorded. Our results demonstrate that citizen science is an effective, cost-efficient tool for monitoring synanthropic species. Collecting comparable data using standard scientific methods would require substantially more time and funding. The project also raises public awareness of biological invasions and the impacts of anthropogenization and climate change, with strong potential for future nature conservation. Funding: GACR 26-22322S; CAS regional project R200932601.

Ecological Monitoring in Agricultural Living Labs: Assessing the Long-Term Effects of Landscape Transformation

Susanne LACHMUTH, Bettina Matzdorf, Katharina Helming

Abstract: Agriculture faces critical challenges maintaining sustainability and food security amid climate change, biodiversity loss, environmental degradation, and supply disruptions, urging system transformation. The Innovation Center for Agricultural System Transformation (IAT), launched in March 2026, advances multiple socio-ecological transformation goals through participatory Living Labs in a landscape context. Research and innovations are co-designed with stakeholders to develop viable solutions along the agricultural value chain. We present the ongoing conceptualization of an integrated ecological monitoring concept - including biodiversity - that will assess the Living Labs' long-term activities and landscape-level impacts. Our approach integrates four system components: (1) performance regarding sustainability and resilience functions, (2) baseline states and dynamics, (3) activities specifying interventions, and (4) external driving forces. Thematic ecological components span abiotic conditions via biodiversity to ecosystem services. Indicators, measurements, and spatio-temporal design will be adopted iteratively and participatively per thematic component. We will leverage technological innovations for ethical and FAIR data workflows and governance, and interactive communication of results. We will link up with an associated IAT socio-economic monitoring scheme and existing monitoring frameworks, such as the European agro-ecology partnership.

The unseen third: Mineral soil layers account for ~30% of total fungal diversity

Monica GUILERA RECODER, Anna Rosling, Karina Clemmensen and Tobias Anderman

Abstract: Fungal biodiversity is essential for forest ecosystem functioning. High-throughput sequencing of environmental DNA (eDNA) has greatly expanded our knowledge of below-ground fungal communities, but methodological choices can strongly influence detection outcomes. Here, we investigate how sampling strategy affects fungal detection using eDNA from soil and deadwood in a 400 × 400 m forest area near Uppsala, Sweden, previously inventoried by citizen scientists. We assessed whether fungal communities vary across soil layers, how deep soil should be sampled to capture heterogeneity, and how well eDNA reflects known species occurrences. Soil cores (2 cm diameter, 45 cm length) were collected from 34 plots and divided into four layers: litter, organic, mineral 1, and mineral 2. Deadwood samples were taken from Picea abies logs at decay stages 2 and 4. DNA was extracted from 189 samples, amplified using ITS1ngs and LR5 primers, and sequenced with PacBio. Fungal richness and community composition varied markedly with depth. The litter layer showed the highest Observed and Shannon diversity, while the deepest mineral layer (mineral 2) showed the lowest. Genus-level analyses revealed clear vertical stratification of taxa across the soil profile. Sampling only the litter layer captured about 50% of total soil fungal diversity, whereas the two mineral layers together accounted for ~30% that would be missed by topsoil sampling alone. Comparison with fruitbody inventories showed that eDNA detected 58% of recorded genera, while fruitbody surveys captured only 15% of genera detected by eDNA. These results demonstrate that soil depth and survey method strongly shape estimates of fungal diversity, and that comprehensive assessments require multi-layer sampling and complementary approaches.

Designing a Pollinator Monitoring Program to Evaluate the Effects of the Common Agricultural Policy in Sweden

Guillermo AGUILERA NÚÑEZ, Ander Glimskär, Karin Ahrné, Erik Öckinger

Abstract: Pollinators are recognized as key indicators of biodiversity change. The development of a European Union pollinator monitoring scheme offers an opportunity to track biodiversity responses to major environmental policies, including the Nature Restoration Law. However, pollinators are not restricted to semi-natural habitats such as grasslands; they are also abundant in agricultural landscapes. In these systems, pollinator populations may be influenced more strongly by agricultural management than by habitat restoration alone. In parallel, the EU's reformed Common Agricultural Policy (CAP) introduces new sustainability and biodiversity commitments that are expected to reshape agricultural management across member states. This convergence creates an opportunity to design a monitoring program that simultaneously tracks pollinator trends and evaluates the biodiversity outcomes of CAP implementation. To explore this possibility, we conducted a pilot study in Sweden during 2021–2022. Landscapes containing agricultural land were selected within the existing 3×3 km monitoring grid already used for bird and butterfly surveys. Within each landscape we sampled pollinators across three habitat types representing a gradient of management intensity: permanent grasslands, cultivated grasslands, and crops. Three complementary methodologies were employed: transect walks, pan traps (deployed at different time intervals), and flower-insect timed counts. Using data from two years of sampling, we evaluated key design parameters for a potential long-term monitoring scheme, including the number of sites required, sampling frequency, and the feasibility of different survey approaches.

Open-source tools for monitoring the conservation status of habitats of Community interest at field level in the Occitanie region

Mario KLESCZEWSKI, Nathalie Hiessler & Mathieu Bossaert

Abstract: The conservation status of natural habitats of Community interest can be assessed and monitored at various scales: Europe, Member States, regions, Natura 2000 sites, and field plots (polygons with presence of the habitat to monitor). This last « field » level is the most relevant for natural area managers as it takes into account what is observable at each known location of the habitat in question. The data collected in this way can then be aggregated at any higher scale, in a bottom-up process. In Occitanie, assessment grids based on those proposed in other European countries (Germany, Austria, etc.) have been developed and adapted for each terrestrial habitat of Community interest. To facilitate field surveys and their analysis, a specific ODK (Open Data Kit) form has been developed by the geomatics specialists at CEN Occitanie. All the assessment grids are available there, and the data collected is fed directly into the CEN database. The data contained in this database may be regularly exported to national databases (SINP).

Supporting evidence-based conservation through robust monitoring of infrastructure impacts and offset measures.

Julia DAYON, Soumaya Belghali

Abstract: The mitigation hierarchy is increasingly used worldwide as a conservation tool to limit the impact of anthropisation, yet empirical evidence of its effectiveness remains scarce. In this study, we evaluated one of the largest ecological offset programs implemented in France to date, associated with the High-Speed Railway Nîmes–Montpellier, which became operational in late 2017. We first quantified abundance losses in two patrimonial steppe bird species, the Little Bustard (Tetrax tetrax) and the Eurasian Stone-curlew (Burhinus oedicnemus), through large-scale monitoring conducted within the Natura 2000 area crossed by the infrastructure (around 500 counting points), ith surveys starting before construction and continuing after the line became operational (10 years of monitoring). We further assessed the effectiveness of offset measures using a Before–After–Control–Impact design on 1 100 hectares of mitigation land.

Our results show that certain management actions were more effective than others to increase local Little Bustard abundance. Conversely, monitoring revealed additional negative impacts of these measures on Eurasian Stone-curlew populations. This knowledge acquisition made possible by the ambition and robustness of the monitoring design can then be used to predict the effect of future infrastructures and mitigation measures allowing a more relevant spatial planning of offsetting measures and helping refine conservation recommendations for these species. this long-term evaluation has also generated new research questions and prompted a revision of management strategies to better reflect the ecology of these species, enabling us to consider developing an adaptive management plan for the improving effectiveness of offsetting measure in the region.

PS02 Posters

Advancing forest biodiversity and conservation monitoring in Europe: A Harmonised Indicator Framework; Authors: Iciar Alberdi, Nerea Oliveira et al.

Iciar ALBERDI

Abstract: In the frame of the Horizon MoniFun project a comprehensive and harmonised framework for monitoring forest biodiversity and conservation across Europe has been proposed. An approach combining scientific review, expert consultation, and data feasibility assessment has been developed to define a set of indicators. First, a comprehensive literature review and screening of existing forest monitoring frameworks were conducted. Second, targeted workshops and questionnaires were organised to refine definitions and clarify methodological requirements. Indicators were then prioritised according to scientific validity, relevance to stakeholder information needs, compatibility with European policy frameworks, and scalability for EU-level reporting. This process allowed the distinction between operational indicators and future-oriented indicators requiring further methodological development or improved data integration. For species-related indicators, the main challenge lies in harmonising reference species lists and ensuring sufficient detection probability, particularly for rare or threatened taxa. National monitoring schemes differ in taxonomic coverage, sampling intensity, and update frequency, limiting comparability across countries. Structural biodiversity indicators—addressing deadwood, microhabitats, age structure, and regeneration—are conceptually robust but face inconsistencies in field protocols, threshold definitions (e.g., diameter classes, decay stages). Indicators related to naturalness, old-growth forests, reveal deeper conceptual gaps while genetic diversity monitoring is not yet systematically integrated into large-scale forest inventories. Finally, connectivity indicators depend heavily on

spatial resolution, forest definitions, and modelling assumptions. The methodology enabled the identification of operational components and documenting gaps as the need to improve the integration between forest inventories and biodiversity monitoring systems.

Auchenorrhyncha (Hemiptera: Insecta) as a model group for biodiversity monitoring

Oleg BORODIN

Abstract: Auchenorrhyncha represent a highly diverse insect group, with more than 48,000 species described worldwide, occurring across almost all terrestrial ecosystems. They are associated with a wide range of host plants and exhibit different levels of trophic and ecological specialisation. Many species are abundant and form a typical component of local communities, including invasive species and agricultural pests. Due to their ecological diversity and sensitivity to environmental conditions, Auchenorrhyncha have strong potential as indicators in biodiversity monitoring. At the same time, their use is often limited by taxonomic complexity. However, the most abundant species, which are most relevant for monitoring purposes, are usually identifiable based on field characters. An important advantage of this group is that Auchenorrhyncha are consistently present in samples collected within existing monitoring schemes, especially those based on trapping methods. Our study, conducted in Estonia, Latvia and Lithuania since 2021, shows that Auchenorrhyncha are regularly recorded in light traps, pitfall traps, Malaise traps and other standardised sampling approaches. In total, more than 100,000 specimens were analysed, including material obtained from monitoring programmes targeting other taxa. Based on these data, we demonstrate the dynamics of several biodiversity metrics of Auchenorrhyncha communities, which can be applied in integrated environmental monitoring. We also discuss practical aspects of implementation, including the potential use of lower taxonomic resolution in monitoring schemes.

Use of bioacoustics to improve detection of micromammals in ecological impact assessments

Paul HURST, Maxime Bru

Abstract: Micromammals such as rodents and shrews are frequently under-represented in ecological impact assessments. Survey methods are often specialised, time-consuming, non-exhaustive or relatively costly, and some species require genetic confirmation for reliable identification. As a result, certain protected species in France, including Hazel Dormouse (Muscardinus avellanarius) and semi-aquatic species such as Water Shrew (Neomys fodiens), may be overlooked despite specific ecological requirements. Recent advances in passive acoustic monitoring (PAM) have highlighted its potential for detecting small terrestrial mammals. Publications such as Middleton, Newson & Pearce

(2024) demonstrate that several micromammal species can be identified through analysis of audible and ultrasonic vocalisations recorded in the field, opening new perspectives for ecological surveys. In most impact assessments, bat surveys using acoustic detectors are already mandatory, generating large volumes of acoustic data. Re-using these datasets to detect micromammals represents a cost-effective opportunity, as it does not require additional field protocols, a single acoustic deployment can therefore contribute to monitoring multiple taxa. Ecosphère has developed a species-specific acoustic detection model designed to identify micromammal vocalisations within bat survey recordings. The first operational module, specifically trained for Hazel Dormouse (Muscardinus avellanarius), is currently in use. Two additional species modules are under development and are expected to be operational by 2027. Applied to recordings from 11 sites representing over 3 000 hours of analysed acoustic data, the tool demonstrates the feasibility of detecting Hazel Dormouse and other species in suitable habitats and provides a first-level assessment of micromammal diversity. This approach can help prioritise complementary survey methods where necessary. Our results illustrate how integrating micromammal detection into existing

Designing a Long Term Terrestrial Monitoring Program for Denmark's Newly Designated Protected Areas

Ane Kirstine BRUNBJERG

Abstract: Denmark's new Nature National Parks (NNPs) offer a rare chance to follow how restored natural processes reshape terrestrial biodiversity and nature quality over decades. Our aim is a durable, future proof program that can detect change on an open ended timeline, while acknowledging three constraints: limited budgets, cost volatility as methods evolve, and partial methodological immaturity. The solution is a modular, scalable framework that safeguards comparability across parks yet allows scope to be adjusted as funds permit. It combines (i) automated imaging of nocturnal insects via standardized light trap systems (AMI), (ii) DNA based metabarcoding of Malaise trap samples to capture diverse flying insect guilds, (iii) high resolution remote sensing to quantify e.g. vegetation height, heterogeneity and structural dynamics, and (iv) targeted follow up of selected red listed species as indicators of recovering processes (e.g., natural hydrology and grazing). We store raw, re analyzable data (images, remote sensing point clouds, specimens, DNA extracts) to enable deferred, cost intensive analyses without losing time series value. Implementation rules include: start alongside restoration to secure baselines; adopt adaptive cadences (e.g., annual flights where feasible, or years 0–1–3 then triennially); consolidate analysis/reporting every 4–8 years across multiple parks to increase power and cost efficiency; and prioritize methods with high automation, standardization and reproducibility. Interfaces to national monitoring (e.g., NOVANA) and structured citizen science

schemes for birds and butterflies minimize overlap and fill taxonomic gaps. By enforcing transparent protocols, the program remains robust to budget and technology shifts, supporting trend detection, attribution of restoration effects and adaptive management in Denmark's NNPs under real world uncertainty.

ELEVATE - implementing new technologies into an alpine monitoring program

Arvid SJÖBERG, Anna Allard, Ruben Valbuena, Hans Gardfjell, Sven Adler

Abstract: Environmental monitoring creates a foundation for understanding our natural environment and making informed policy and management decisions (Allard et al 2023). In Sweden, monitoring of open landscapes and habitats is gathered under the NILS (National Inventories of Landscape in Sweden) program. One such habitat is the alpine areas in Northwestern Sweden. The NILS alpine inventory relies on a two-stage inventory design where wall-to-wall models based on satellite and field data predict which areas that should be visited by field personnel. Ensuring that the correct areas are visited is essential for a cost-effective inventory, underscoring the importance of accurate model predictions. New technical solutions could assist in creating even better models. In recent years drones have emerged as a mature and versatile tool for data collection. Paired with high-resolution cameras and advanced photogrammetry software, high-quality orthophotos and point clouds can be created. Those data sets can be used for a variety of tasks such as object detection and vegetation cover mapping. Drone imagery can also be used as a bridging solution between field inventories and relatively low-resolution satellite imagery, creating a "near ground truth" data set. Another emerging area of research is computer vision using DNNs (Deep Neural Networks). Such algorithms paired with drone and satellite data have been successfully used to classify vegetation cover in grasslands, however similar research on Scandinavian alpine vegetation types is lacking. ELEVATE seeks to address these issues by using drone data collected by NILS field personnel along with satellite scenes to develop robust DNN workflows to estimate vegetation cover, type and change. LiDAR, aerial and field data will also be used to fine tune models. The project started in July 2025 and is expected to finish mid-2028, with the goal to deliver a generalized and useable model for project stakeholders.

Connecting People, Experts and Satellites: An Integrated System for Invasive Species, Protected Plant Species and Remote Habitat Monitoring in Latvia

Jānis KOTĀNS, Anda ZAKENFELDE

Abstract: LatViaNature - LIFE Integrated Project implemented by the Nature Conservation Agency of Latvia - to strengthen terrestrial biodiversity monitoring and evidence-based conservation management. The project develops interoperable digital infrastructures integrating citizen science, standardized expert field surveys and Earth observation-based habitat assessment within the national nature data management system. Important component is the Invasive Species Manager (www.invazivs.lv), a national-scale platform enabling structured reporting of invasive alien species by citizens, municipalities and experts. Submitted records undergo expert validation and are incorporated into the national biodiversity database, supporting early detection of invasive species, coordinated management and improved spatial prioritization. A standardized digital survey module (Plant monitoring tool) has been implemented for protected vascular plant species, enabling experts to collect georeferenced, harmonized monitoring data within and beyond Natura 2000 sites. The system provides access to historical observations, permanent sample plots and previous survey data, facilitating spatially explicit sampling design and longitudinal monitoring. The information collected through the tool was essential for, for the first time in Latvia, defining site-specific conservation objectives and favourable reference values for plant species listed in Annexes II and IV of the Habitats Directive. It also served for preparation of the species conservation status report. In parallel, Earth observation and geospatial analytical workflows are applied to identify potential habitat distribution, detect temporal changes and assess habitat conditions. Satellite-based screening supports expert-based habitat delineation, verification and conservation status evaluation. Pilot applications also explore the integration of Earth observation data in invasive species distribution analysis.

Fungal diversity in European black pine forests: disentangling the multi-scale ecological drivers across native and non-native ranges

Lucas MALLET, Małgorzata Ruszkiewicz-Michalska; Georgios I. Zervakis; Armin Mešić; Antonela Blažević; Alfredo Vizzini; Giuseppe Bazan; Francesco Dovana; Irmgard Krisai-Greilhuber; Sergio de-Miguel; Franziska Richter; Glen Dierickx; Nadjat Mezaour; Saliha Kadi-Bennane; Franck Richard; Jean-Michel Bellanger; Flavien Frizot

Abstract: The European black pine (Pinus nigra J.F. Arnold) is a major component of landscapes in Southern Europe, and a cornerstone of European conservation strategy. This species displays extensive genetic diversity comprising five subspecies with non-overlapping native ranges, several of which are among the most emblematic priority natural habitats sensu Natura 2000, due to their restricted distribution and their sensitivity to global change. Owing to its broad ecological amplitude – including low soil specificity, drought-tolerance and relatively fast growth – P. nigra is an ideal candidate for forest management and restoration. Hence, its distribution even extends beyond its native range toward northern latitudes, covering approximately 9.5 million hectares in Europe. The European black pine depends on ectomycorrhizal fungi for nutrient and water acquisition, while decomposition is mainly carried out by saprotrophic fungi, making these two guilds crucial for forest functioning. Despite their key roles,

both guilds remain largely overlooked in studies of fungal diversity in P. nigra. To address this knowledge gap, we intensively sampled P. nigra forests across all subspecies and across a broad spatial extent, encompassing 55 sites from 15 different countries, including both native and non-native areas. We investigated fungal diversity using environmental DNA (eDNA) from more than 500 deadwood and soil samples collected at these sites. We aim to integrate local environmental data (e.g., forest management and stand structure, host identity inferred from P. nigra genetic diversity) alongside climatic data to disentangle the multi-scale ecological drivers structuring fungal communities in P. nigra forests. Such knowledge is essential to suggest effective conservation and management strategies for this ecologically critical species and its associated fungal diversity.

Detecting bat roosts using eDNA: a case in point

Peter ROEMERS, D. Ekkers, I. Janse, werkgroep eDNA Netwerk Groene Bureaus

Abstract: Surface-swab eDNA sampling at potential bat roost entry points is emerging as a promising tool for ecological assessments, which are legally required for renovation and insulation projects in the Netherlands. The method has been developed rapidly over the past two years, progressing from a promising approach to a technique that is now actively being applied in practice. Although eDNA detection of bat roost sites represents a significant opportunity — a scalable and potentially year-round assessment tool — it also poses a risk: if the technique is implemented prematurely or in the wrong manner, roost sites might be missed. In collaboration with other experts and organizations, Waardenburg Ecology performed a review of data from recently performed validation studies and a risk-of-bias assessment. In the review we outline which aspects of the technique have been validated and where uncertainties remain. For example: whether the method in its current form is equally suitable to detect all relevant bat species is not certain, as the technique was predominantly tested on roost sites of the Common Pipistrelle. Based on this review, a best practice guideline and survey protocol were developed; these set quality standards and operational safeguards to reduce the risk of false negatives. In the guideline we suggest core quality assurance requirements for laboratory workflows, and the protocol provides guidance on sampling windows, frequency, interpretation and reporting. But some risks and uncertainties remain; therefore we also address policy needs and propose data-sharing solutions to enable responsible adoption of this novel technique. Implementation of eDNA detection for bat surveys is a case in point of how both successful development and implementation of any survey method depend as much on politics and policy as on innovation and good science. If done well, it offers an opportunity for advancing eDNA-based biodiversity monitoring. Let's discuss what well means.

BioMonWeek
2026
The European
Conference for
Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Marine Monitoring — Observing Ocean Ecosystems

MR07 Monitoring and mapping of marine benthic habitats

Tuesday 5 May, 11h30-12h30, Room Barthez
Chairs: Louise Forsblom and Damianos Chatzievangelou

Description: This session is open for talks on topics covering the monitoring and mapping of marine benthic habitats. Recent technological advances have opened up new opportunities for monitoring and mapping these habitats, including the use of remote sensing technologies, underwater vehicles, and advanced sensor systems but capturing all facets of biodiversity still require conventional sampling methods. This session will explore the status and next steps for monitoring of benthic habitat extent and condition in the context of conservation and restoration. This session seeks to highlight cases where multiple approaches are used to offer a more holistic approach to biodiversity monitoring.

Monitoring of benthic habitats in Finland: from intense spatial mapping to temporal trends

Louise FORSBLOM

Abstract: Recent years have brought on alarming reports of decline in biodiversity, and admirable goals, such as the CBD Global Biodiversity Framework. To combat further loss and move towards restoration, we need to understand spatial patterns in biodiversity. To know where we stand now, and how mitigation efforts progress, schemes to monitor changes in biodiversity need to be implemented. The Finnish inventory programme for underwater marine diversity, Velmu, has conducted extensive mapping of the Finnish marine areas since 2004 and has to date collected over 200 000 unique observations of underwater biodiversity. Here we wish to share how we have used this extensive mapping data to support the development and piloting of monitoring aimed at supporting the monitoring of both extent and condition of the marine benthic habitats defined in annex II of the Nature Restoration Regulation. The suggested monitoring will include both the combination of novel technologies and model based selection of monitoring sites.

Computational methods for monitoring Nephrops norvegicus populations

Damianos CHATZIEVANGELOU

Abstract: The Norway Lobster (Nephrops norvegicus L.) is a top European demersal fishery resource and an important food web component of intermediate trophic level. Its burrowing behavior makes it a major agent of sediment bioturbation in muddy habitats of European continental margins, where it digs complex burrow systems of interconnected tunnels and emerges to the seabed regularly to feed or protect its territory. For decades, trawling-based stock assessment surveys led by the ICES WGNEPS Working Group only partially accounted for diel emergence patterns of Nephrops on a populational level. Gradually, they were replaced by UnderWater TeleVision (UWTV) surveys, counting burrow systems in towed sledge footage. However, the exact relationship of visible burrow systems to adult Nephrops abundances in an area remains uncertain. The Horizon-MSCA project CINNEPHILIA (GA-101104596) aims to bridge this gap by combining multiple optical and acoustic datasets. In particular, probabilistic computational approaches are developed to accurately estimate both Nephrops abundances and the overall biodiversity in Nephrops fields. Detections of acoustic signals of a small (~ 30 ind.) population of tagged Nephrops individuals (released within an array of 4 hydrophones in a No-Fishery Take Zone in Catalonia for a total period of ~100 days in 2019) were used to build a preliminary survival model. Based on that, the proportion of Nephrops individuals on the seabed (i.e., not in a burrow, so available to be recorded by any camera scanning the area) was estimated for each hour of the 24h cycle, and the detected diurnal (i.e., peak at noon) pattern was validated against both ROV and trawling data. A bigger dataset of more individuals over a broader area is currently being analyzed. Successful execution of the project will establish a reliable correction factor for Nephrops densities based on individuals counted in footage, as well as a finer tuned relationship for visible individuals and burrows.

New observation systems using computer vision for dynamic assessments of marine biodiversity

Louis FIORINA, Matthias Obst, Tuomas Rossi, Tomáš Martinovič, Ghaith Chaabane

Abstract: Biological monitoring needs to improve radically to serve our understanding of marine ecosystems and biodiversity under long-term global change and multiple stressors. Over the last decade, many new monitoring technologies, including genomics and image-based surveillance, have become available to marine biologists. However, the transformation to such new, high-throughput methods is not trivial as they produce enormous volumes of data. The MarcoBolo and DTO-Bioflow project collaborated to address this challenge and developed automated surveillance methods for marine biodiversity based on computer vision. This talk will introduce one popular application from this collaboration: the Swedish platform for subsea image analysis (SUBSIM). SUBSIM provides essential functions to conduct research and automated monitoring with image and video surveys, including data management, machine learning, digital collaboration, citizen science, and high-performance computing. The platform uses object detection and segmentation models to track changes in species richness, abundance, and the distribution of key ecological groups in coastal habitats. The digital services are now part of the Swedish Biodiversity Data Infrastructure (SBDI) and the Digital Twin of the Ocean (DTO) and are currently used in the management of marine protected areas, offshore wind test sites, aquaculture, and for tracking marine invasive species. We will present examples of

novel applications of these monitoring services and discuss their potential for the management and protection of marine biodiversity in the ocean.

Monitoring and mapping marine benthic habitat mosaics through multidimensional biodiversity in the Madeira Archipelago

Pedro NEVES, Cláudia Ribeiro, Rodrigo Riera

Abstract: Effective marine benthic monitoring is often constrained by an over-reliance on species richness, which can underestimate the ecological importance of habitats that support fewer species but distinct functional and evolutionary assemblages. This is particularly relevant in oceanic islands, where coastal biodiversity is distributed across heterogeneous habitat mosaics. Here, I present a coverage-standardized, multidimensional framework to support the monitoring of marine benthic habitats in the Madeira Archipelago. The study is based on standardized underwater visual census data collected between 2016 and 2024 across 19 coastal locations, spanning rocky reefs, ripraps, wrecks, sand, and rhodolith beds, and includes reef-associated fishes and mobile macro-invertebrates. Biodiversity was assessed across taxonomic, functional, and phylogenetic dimensions using Hill-number inference standardized by sampling completeness, allowing robust comparisons among habitats with unequal detectability and sampling effort. Results show that habitat complementarity, more than island identity, is the main driver of regional biodiversity patterns. Structurally complex hard substrates supported high local diversity and numerical stability, while soft and biogenic habitats, particularly rhodolith beds, contributed disproportionately to regional functional and phylogenetic diversity through high turnover, habitat specialization, and unique taxa. Rare species also accounted for a disproportionate share of functional and evolutionary breadth, indicating that apparent stability in richness may mask deeper biodiversity reorganization. These findings highlight the need to move beyond hotspot-based approaches and toward habitat-mosaic monitoring frameworks that represent the full range of benthic habitats. The approach is transferable to other island and coastal systems and offers a practical basis for conservation planning and long-term marine biodiversity monitoring.

MR02 WORKSHOP Understanding EBVs and EOVs

Tuesday 5 May 16h30–17h30, Room Barthez

Chairs: Lina MTWANA NORDLUND, Guillaume BODY, Lisa BENEDETTI

Description: This interactive session introduces Essential Ocean Variables (EOVs) and Essential Biodiversity Variables (EBVs) as key frameworks for monitoring ocean and biodiversity change. We will briefly present what EOVs and EBVs are, how they are used, and why they matter for observation, assessment, and decision-making. The session will then explore where these frameworks potentially overlap, how they complement and reinforce each other, and how closer alignment can strengthen biodiversity monitoring across marine systems. The session concludes with facilitated discussions to exchange perspectives, experiences, and ideas for improved integration.

MR10 Monitoring in Marine Protected Areas

Wednesday 6 May, 9h00-10h00, Room Joffre G
Chair: Hannah TRUTER

Description: Marine protected areas (MPAs) are increasing globally with the drive towards international conservation goals. Monitoring plays a key role in ensuring effective management in a changing environment as anthropogenic pressures and climate change reshape underwater ecosystems, we must evolve our methodologies to ensure all relevant data are included in assessments. This session invites contributions that explore innovative monitoring of MPAs to inform more adaptive management for long term success. We welcome abstracts that explore themes such as monitoring design and methodology, technological innovation, socio-ecological monitoring and effectiveness assessments in Europe. We look forward to showcasing diverse perspectives and practical insights that can help shape the future of MPA monitoring and ocean stewardship.

Developing indicators to assess anthropogenic impacts on naturalness of marine biodiversity.

Hannah TRUTER

Abstract: Marine ecosystems worldwide are undergoing rapid change due to increasing anthropogenic pressures, yet effective indicators for assessing the loss of naturalness remain limited. This research aims to evaluate maximum fish body size as a potential indicator of ecosystem health and anthropogenic impact, with a particular focus on its applicability in temperate marine systems. Grounded in size spectrum theory, life history theory, and broader concepts of ecosystem integrity, the project examines how body size distributions respond to human pressures such as fishing, habitat alteration, and protection status. The work follows a three part approach. First, a systematic literature review synthesizes existing evidence on the relationship between maximum fish size and ecosystem degradation, integrating ecological and anthropogenic theories that explain size based responses. Second, species specific models are developed to estimate expected maximum body sizes for fish observed in baited remote underwater video (BRUV) surveys, with particular attention to methodological challenges and latitudinal variation in growth potential. Finally, these modelled expectations are compared with empirical BRUV data collected inside and outside marine

protected areas (MPAs) in Norway to assess whether deviations in maximum size reflect differences in protection effectiveness. Together, these components aim to determine whether maximum fish body size can serve as a robust, sensitive, and operational indicator of marine ecosystem naturalness, supporting improved monitoring and management of human impacts.

Bridging Fisheries Data and Ecological Surveys for Biodiversity Monitoring in Mediterranean Marine Protected Areas

M. Tunca OLGUNER, Zafer Ali Kızılkaya

Abstract: Understanding how marine ecosystems change over time requires combining ecological observations with knowledge from local fisheries. In Gökova Bay (SE Türkiye), long-term biodiversity monitoring brings together underwater fish surveys and landing data collected in collaboration with small-scale fisheries cooperatives. Annual visual census surveys were conducted along standardized transects (50 × 10 m; 500 m^2) both inside no-fishing zones (NFZs) and in nearby non-protected areas to estimate fish biomass and community composition. Results from 2025 show a clear difference between protected and non-protected areas. Average fish biomass reached 33.29 g/m^2, with substantially higher values inside NFZs (44.66 g/m^2) compared to non-protected areas (21.92 g/m^2). The biomass of large predatory fish such as Epinephelus marginatus reached 12.11 g/m^2 within NFZs, indicating positive effects of long-term protection. Alongside ecological monitoring, landing data shared by local fishers provide valuable insights into catch composition, fishing effort, and changes in commercially important species around the protected areas. This cooperation helps link underwater biodiversity trends with fisheries activity and supports a more comprehensive understanding of ecosystem dynamics. Biomass assessments also highlight the growing presence of invasive alien species, including Parupeneus forsskalli, Sargocentron rubrum, and Siganus spp., which together account for approximately 27% of total fish biomass, with higher proportions in non-protected areas. Rabbitfish (Siganus spp.), in particular, show increasing dominance outside NFZs (3.89 g/m^2; 17.7% of total biomass). Overall, combining cooperative fisheries data with ecological surveys provides a practical and participatory approach to long-term biodiversity monitoring. This integrated framework strengthens the scientific basis for adaptive management in Mediterranean MPAs while reinforcing collaboration with local fishing communities.

Linking Long-Term Monitoring and Movement Ecology to Evaluate Marine Protected Area Effectiveness for Fish Populations on the Catalan Coast

Skye BROWN, Lucas Hayes, Iraida Argullós, Bernat Martí, Ángela Palomino,Martí Vilanova, Graciel·la Rovira, Bernat Hereu

Abstract: Marine Protected Areas (MPAs) are an important management tool for conserving marine ecosystems and addressing increasing anthropogenic pressures. They can be particularly effective in rebuilding fish populations following historic overexploitation. On the Catalan coast, long-term ecological monitoring and movement ecology studies provide complementary approaches to understanding how fish populations respond to spatial protection. Long-term monitoring using underwater visual census conducted in two Catalan MPAs has produced multi-decadal datasets on fish abundance and biomass. While several species show clear recovery after protection, surveys indicate that protection is not equally effective for all monitored species. These results suggest that population recovery depends on species-specific movement ecology and habitat use. To better understand these differences, acoustic telemetry is used to characterize the movement ecology and habitat use of several commercially and ecologically important species across the Catalan MPA network. Tracking individual fish movements between habitats, reserves, and fished areas provides fine-scale insights into habitat connectivity and the extent to which individuals remain within protected boundaries. Combined evidence indicates that protection is particularly effective for sedentary and benthic species, which exhibit stable or increasing biomass within no-take areas. In contrast, highly mobile species show weaker recovery signals, likely due to their broader spatial ranges. Movements between different MPAs also provide evidence of ecological connectivity across the Catalan coast. Together, these findings highlight the importance of incorporating species movement ecology into MPA design and management, emphasizing the need to consider MPAs as interconnected ecological networks rather than isolated spatial units.

Long-term monitoring supports adaptive management of recreational diving in a highly visited Mediterranean MPA.

Lucas HAYES, Graciel·la Rovira, Bernat Martí, Yanis Zentner, Iraida Argullós, Martí Vilanova, Bernat Hereu, Cristina Linares

Abstract: Marine Protected Areas (MPAs) are key tools for preserving marine biodiversity in the face of global change. However, their effectiveness relies on ecological monitoring to assess the status of populations and ecosystems, and support adaptive management. Within this framework, a long-term monitoring program in the Medes Islands MPA (northern Catalonia) evaluates the status and trends of sensitive benthic communities to inform adaptive management of recreational SCUBA diving. This MPA is host to a high number of recreational divers (over 50,000 a year), especially in the summer months, concentrated in only a few dive sites. To assess potential impacts of this activity on marine biodiversity in the MPA, populations of the red gorgonian Paramuricea clavata, the red coral Corallium rubrum, and submarine cave communities are monitored annually. Marine cave communities show signs of degradation in highly visited caves, including broken organisms and air accumulation on cave ceilings, likely linked to diving. In red gorgonian populations, impacts from diving interact with mass mortality events from recurrent marine heatwaves, which have driven an overall decline in biomass compared to initial monitoring years, despite relatively high recruitment. Red coral populations show little to no impact from diving, however they remain far from conservation targets due to historical overfishing. These results inform annual adaptive regulation of diving in the MPA, aiming to limit this activity to an appropriate carrying capacity and promote sustainable diving practices. Importantly, they also highlight the synergistic effects of local pressures and climate-driven disturbances, underscoring the importance of long-term monitoring for adaptive management in highly visited Mediterranean MPAs.

From seabed knowledge to management action: habitat mapping as a policy tool for Cabo Girão Marine Park (Madeira Island)

Cláudia RIBEIRO, Pedro Neves, Carolina Santos, Dília Menezes, Paulo Oliveira

Abstract: Marine protected areas (MPAs) are often created without detailed ecological baselines, which weakens zoning, surveillance, licensing, and long-term monitoring. This was the case for Cabo Girão Marine Park, the first marine park in the Madeira archipelago: a small multiple-use MPA designed to balance conservation with fishing, anchoring, diving, and tourism, but established without a dedicated baseline survey of habitats and biological communities. To fill this gap, we combined existing bathymetric and substratum data with underwater surveys to map benthic habitats and describe the park's main biological communities. This produced the first spatially explicit habitat baseline for Cabo Girão, making it the first MPA in Madeira with a habitat map, and generated practical information to support implementation of the park's management plan. The results were also used for institutional communication and knowledge sharing. Beyond its scientific value, this habitat mapping is directly relevant to marine governance. The data supported protective measures for sensitive habitats and species, including rhodolith beds, Cymodocea nodosa, and Avrainvillea canariensis; helped define multiple-use zones; improved monitoring of habitat cover; and strengthened decisions on compatible uses. By reducing uncertainty, these maps also support ecosystem-based management and marine spatial planning where conservation must be balanced with socio-economic activities. This case study shows how habitat mapping can help shift MPAs from broad conservation goals to operational management. In oceanic islands such as Madeira, where data gaps have long limited effective planning and progress toward good environmental status, habitat baselines are essential for turning biodiversity knowledge into actionable policy, management priorities, and stronger precautionary decisions.

MR06 Marine mammal monitoring programmes

Wednesday 6 May, 10h00-11h00, Room Joffre G
Chairs: Anita GILLES and Ana CORREIA

Description: Marine mammals are sentinels of ocean health. It is imperative that early warning triggers (or tipping points) are identified for the implementation of effective management measures. In the Anthropocene, with the rapid pace of environmental change and increasing anthropogenic pressures, regional coordinated monitoring of marine mammals is essential to detect population distribution shifts and declines. This session invites a) case studies of marine mammal monitoring that deliver internationally agreed Essential Variables (EBVs and/or EOVs) and demonstrate how these contribute to EU policy needs (e.g. MSFD, HD, NRR...) and b) contributions on how EBVs/EOVs can feed into cumulative effects assessment frameworks.

From Marine Mammal Monitoring Data to Biodiversity Assessment

Anita GILLES

Abstract: Marine mammals, as top predators and sensitive species that integrate environmental changes across broad spatial and temporal scales, are often used as ecological indicators of overall ecosystem health. Marine mammals have been and are subject to significant pressure from both natural impacts and human activity, which results in many populations and species not being in good status. Many pressures still occur on a wide scale today, such as incidental by-catch, or are even increasing, such as noise and hazardous substances, habitat loss or degradation of habitat. However, marine mammals characteristically exhibit wide distributional ranges, with certain species being extremely rare. This poses significant challenges to the monitoring of marine mammals and regionally cooperated large-scale surveys are needed to align data collection with relevant ecological and spatial scales. This contribution will showcase the assessment of marine mammals, using ecological indicators and tailored integration rules, for the recent OSPAR Quality Status Report with the goal for achieving a comprehensive assessment on the conservation status of the population of marine mammals. Starting with a synopsis of the available data, followed by an examination of the outcomes of four common indicators for 15 species, I will conclude with an assessment of the integrated status of marine mammal species grouped into four functional groups, across three OSPAR Regions in the OSPAR Maritime Area.

The EMPHATIC project: advancing non-invasive cetacean monitoring to support marine biodiversity conservation

Ana CORREIA, Afonso L, Álvarez-González M, Busch H, Costa J, Costas B, Gambardella N, Gil Á, Oliveira-Rodrigues C, Peixoto D, Petitguyot M, Ramos-Pinto

L, Rodriguez-Mendoza R, Rotllant J, Saura M, Sechi A, Sousa-Pinto I, Suarez-Bregua P, Tomasino MP, Valente R, Magalhães C, Matias J, Mendez-Fernandez P, Rosso M, Saavedra C, Pierce G

Abstract: Marine mammals are sentinels of ocean health, yet effective monitoring of their populations remains challenging due to their wide-ranging distribution and the logistical constraints of traditional survey approaches. Addressing existing knowledge gaps is therefore essential to support ecosystem-based management. With the Biodiversa+ project EMPHATIC (eDNA, Microbiomes, Photogrammetry and Hormones – Assessment Techniques In Cetaceans), we aim at developing innovative, non-invasive monitoring tools to improve cetacean population assessments and contribute to relevant European environmental policy. Environmental DNA (eDNA) is being used to monitor cetacean diversity and distribution. Analyses of the exhaled breath condensate, both of the respiratory tract microbiome and hormonal content, are providing insight into potential disease indicators and stress levels. Finally, drone-based photogrammetry and stranding data are enabling the evaluation of body condition metrics. Besides addressing key knowledge gaps, we intend to deliver practical solutions for policy actors and regional stakeholders. Towards that goal, we are developing a monitoring toolbox designed to support environmental assessments at national and European scales, including contributions to biodiversity monitoring frameworks and policy needs such as those of the MSFD. We further promote citizen science by preparing tailored protocols for sampling, thereby increasing the spatial and temporal coverage of data while fostering public engagement with marine conservation. Now at the project midpoint, we achieved significant progress in the optimisation of at-sea and laboratory techniques, and citizen science protocols have been successfully finalised and tested. With this presentation, we will showcase the early outcomes of the project, visually highlighting how these complementary approaches can inform indicators of cetacean distribution and health and support adaptive management of marine ecosystems.

Coastal Monitoring Reveals Fishery-Driven Distribution Shifts of Mediterranean Bottlenose Dolphins

Maria Silvia LABRIOLA, PARISI Antonio, MARINCHEL Nadia, RINALDUZZI Sofia, TURCHI Alice, GIACOMINI Giancarlo, PACE Daniela Silvia, RUSSO Tommaso

Abstract: Marine mammals are widely recognized as sentinel species, and at-sea monitoring programmes are essential to detect ecological responses to anthropogenic pressures. Fisheries are among the most pervasive drivers of change in coastal ecosystems, influencing the behaviour and spatial ecology of marine predators. Quantifying these interactions is critical for biodiversity monitoring and for informing marine conservation planning. This study investigates the relationship between bottlenose dolphin (Tursiops truncatus)

occurrence and bottom-trawl fisheries in the Tiber River estuary area (Tyrrhenian Sea, Western Mediterranean). Five years (2019–2023) of boat-based survey data from an ongoing monitoring programme of the local "Capitoline Dolphins" population were combined with fishing effort derived from the Vessel Monitoring System (VMS). The influence of fishing activity on dolphin distribution was analysed using spatial overlap metrics and generalized linear mixed-effects models (GLMMs) with environmental and vessel-level fishing predictors. Results show a strong spatio-temporal association between dolphins and trawling activity. During trawling days, dolphins shifted their distribution farther offshore and overlapped with fishing grounds, suggesting a behavioural response to increased prey accessibility around trawlers. Interaction patterns varied among vessels, indicating heterogeneous responses to fishing activity. Catch analyses revealed that vessels with higher dolphin co-occurrence landed greater quantities of key prey species such as European hake (Merluccius merluccius) and common octopus (Octopus vulgaris). These findings highlight the value of integrated monitoring programmes combining ecological surveys and fisheries data to deliver Essential Biodiversity Variables (EBVs) on species distribution and ecosystem disturbance, supporting cumulative impact assessments and management under EU frameworks such as the Marine Strategy Framework Directive.

Turning data chaos into conservation insight : Integrating heterogeneous cetacean sightings for robust biomonitoring

Marion PILLET, GIDOIN Cindy, AUTHIER Matthieu, CHERO Guillaume, PLARD Floriane, LE BRAS Yves

Abstract: Marine mammals are under significant and varied pressure from human activities at sea, such as fishing, renewable energy production and shipping. In the north-east Atlantic, recent assessments by the OSPAR Convention have revealed the poor state of marine mammal populations and have called for improved, integrated biomonitoring approaches. Monitoring of cetaceans is currently conducted through a variety of surveys operating at different spatial and temporal scales, ranging from large-scale scientific campaigns that cover vast ocean regions, to more frequent, localised monitoring associated with offshore wind farms. However, due to their heterogeneity, these datasets are challenging to analyse in tandem, and their collective potential for understanding species distribution and informing management is limited. The MODELCET ATL project aims to address this issue by compiling available datasets from the Bay of Biscay and the English Channel and developing robust statistical methods to generate reliable density surface models. To date, over 62 survey datasets and approximately 39,000 sightings from aerial and ship-based line-transect surveys have been incorporated into a fully reproducible workflow (R package Pelascope and a Shiny application). Preliminary results demonstrate a

substantial increase in spatial and temporal coverage compared to individual surveys. However, integrating heterogeneous protocols remains a key challenge, particularly for simulation and modelling steps. The intention of this contribution is to stimulate discussion within the scientific community on methodological approaches for integrating multi-source data, with the ultimate goal of enhancing cetacean distribution and density modelling, and providing more robust support for marine management decisions with respect to spatial planning.

MR05 Advances in marine biodiversity monitoring

Wednesday 6 May, 11h30-12h30, Room Joffre G

Monitoring of rocky reef fish communities: A case study at the Euro-Mediterranean level.

Gaëlle LEGRAS

Abstract: Marine policies (eg. MSFD, OSPAR, HELCOM) and biodiversity management frameworks require monitoring and assessment of the ecological status of rocky reef fish. However, observational methods used throughout Europe are heterogeneous and some traditional approaches (e.g., nets and pots) are invasive, causing fish mortality and impacting sensitive habitats. This has led to an increasing demand for non-invasive and interoperable methods for fish monitoring and ecological status assessments. To address these needs, the Biodiversa+ EuRockFish pilot study aimed to test and assess the complementarity between two visual methods (visual census by scuba diving and video) and environmental DNA (eDNA) in different environmental conditions at the Euro-Mediterranean level. First, we will present the implementation of the EuRockFish project, including its sampling design and the protocols that have been tested in various countries in the Euro-Mediterranean region. In a second time, we will present the first results of this study, which demonstrate that each method detects partially distinct subsets of the fish community. We will show that integrating multiple approaches provides a more comprehensive understanding and complete picture of biodiversity patterns. These preliminary findings emphasize that no single method can fully characterize rocky reef fish communities, underlining the importance using integrative monitoring strategies. Ultimately, this study supports the development of standardized, multi-method monitoring strategies for rocky reef fish communities, offering robust tools to detect biodiversity changes, assess ecosystem status, and inform management decisions in the context of global environmental change.

High-Frequency Monitoring Reveals Persistent and Emerging Low-pH Extremes in a Coralline Algae Reef

Heidi BURDETT, Jinhua Mao, Gavin L. Foster, Nicholas A. Kamenos

Abstract: Effective marine monitoring must resolve environmental variability at timescales relevant to natural variability, particularly in coastal habitats vulnerable to climate change. Coralline algae reefs are globally-distributed biodiversity hotspots, but are expected to be highly sensitive to future ocean acidification. However, high-frequency carbonate chemistry observations from these habitats remain rare, limiting our ability to place experimentally-based predictions in context. Here, we present the value of sustained high-resolution environmental records in addressing this, identifying how biological-physicochemical interactions drive exposure to extreme environmental conditions. Continuous sensor data show that the coralline algae community already experience pH conditions at or below those projected for 2100 for 63% of the year, including most of autumn and all of winter. Annual pH variability was 0.46 units and displayed clear structure across diel, tidal, and seasonal timescales – driven by interacting biological and physical processes. Coupled variability in dissolved oxygen and pH indicates strong biological control of local carbonate chemistry at multiple periodicities, while wintertime temperature-pH coupling reflects seasonal physical forcing. Monthly tidal cycles further modulated biological signals, enhancing intra-seasonal variability and generating episodic low-pH extremes. Forward projection of this observed variability suggests that future minimum pH conditions may go far beyond those represented in current IPCC emission scenarios. Our findings show that point measurements, or seasonal / annual averages can severely underestimate acidification stress exposure in high-variability environments – limiting the value of baselines and the power of predictions. Sustained, multi-parameter, high-frequency observations are therefore essential for detecting emerging extremes and in assessing vulnerability and resilience in climate-sensitive benthic habitats.

From marine biodiversity data to action

Cristina Huertas-Olivares, Christos ARVANITIDIS

Abstract: Transforming marine biodiversity observations into actionable knowledge remains a major challenge for effective ecosystem monitoring and management. Within the Horizon Europe project MARCO-BOLO, LifeWatch ERIC has developed a set of interoperable and reproducible analytical workflows designed to bridge this gap. These workflows, implemented within the LifeWatch ERIC e-Science Infrastructure, leveraging the Virtual Research Environment (VRE), Workflow Management System and distributed computational services, operationalize key analytical processes across multiple biodiversity use cases, including time-series analysis, habitat suitability modelling, blue carbon estimation, and metabarcoding-based assessments. By integrating heterogeneous data sources (e.g. in situ observations, remote sensing data, genomic data and environmental variables), analytical models (e.g. species distribution models, statistical time-series models and machine learning approaches) and computational services into modular and reusable components (e.g. Docker-based), the workflows enable transparent, scalable and FAIR-compliant analyses based on standardized metadata schemas, semantic annotations and persistent identifiers (PIDs). A core innovation lies in the transformation of domain-specific scientific scripts (e.g. R, Python) into standardized containerized and parameterized workflow components orchestrated through the LifeWatch Workflow Management System, , allowing end users to run both interactive and automated execution modes without requiring advanced programming skills. This approach enhances interoperability, reproducibility and long-term reuse, while facilitating the composition and chaining of workflows through standardized interfaces and APIs across different scientific and policy contexts. The resulting workflows support both researchers and environmental managers by providing accessible tools to assess biodiversity trends, model ecosystem dynamics and inform evidence-based decision-making. Their deployment within a persistent European research infrastructure ensures ensures technical and operational sustainability beyond the project lifetime through integration with persistent infrastructure services, versioning mechanisms and long-term data and workflow preservation strategies, contributing to long-term marine biodiversity observation and monitoring efforts. The workflows are published with persistent identifiers and documented following reproducibility best practices, enabling their discovery, reuse and integration within the European Open Science Cloud (EOSC). Overall, this work demonstrates how research infrastructures can turn complex biodiversity data into operational, policy-relevant and reproducible insights, supporting more effective monitoring and management of marine and coastal ecosystems.

Monitoring marine biodiversity: a new ecosystem modelling framework

Stefano CIAVATTA, and the NECCTON consortium

Abstract: Understanding and monitoring changes in marine biodiversity is a major scientific and societal challenge in the context of accelerating climate change and growing human pressures on the ocean. While global and regional observing systems have improved our capacity to monitor ocean conditions, the representation of marine biodiversity and ecosystem dynamics in operational ecosystem models remains limited. The NECCTON (New Copernicus Capability for Trophic Ocean Networks) project addresses this challenge by developing a new marine ecosystem modelling framework aimed at improving the prediction, accessibility, and practical use of marine biodiversity information. NECCTON advances ecosystem modelling by integrating multiple trophic levels, habitats, and human pressures within a framework coupled to physical ocean models. The approach spans ecosystem components from benthic flora and fauna to plankton communities and fish, while accounting for climate-driven variability and

anthropogenic stressors. By improving the representation of trophic interactions, functional diversity, and ecosystem structure, the framework enables more realistic simulations of marine ecosystem dynamics and energy transfer across marine food webs. The project integrates diverse observational data streams—including hyperspectral satellite observations, biogeochemical Argo floats, plankton imaging systems, and fisheries surveys—combined with artificial intelligence approaches to support model evaluation and parameterisation. We present an overview of the NECCTON framework and key results demonstrating its ability to reproduce marine ecosystem structure and biodiversity patterns from regional to global scales. These developments contribute to emerging digital ocean infrastructures and support applications for marine conservation and ecosystem-based management.

MR03 WORKSHOP Biodiversity mapping with advanced technologies

Thursday 7 May, 9h00-10h30, Room Barthez
Chairs: Julie ROBIDART, Javier ALONSO FERNANDEZ, Gloria CASABELLA HERRERO

MR03 SPECIAL FEATURE Advancing integrated marine biodiversity monitoring through knowledge transfer.

Thursday 7 May, 10h30-11h00, Room Barthez
Chair: Kara MCKEE

MR12 Mobilizing marine biodiversity monitoring data

Thursday 7 May, 11h30-12h30, Room Barthez
Chair: Dan Lear

Description: We invite researchers, practitioners, data managers, and policymakers to submit talks that showcase innovative approaches to mobilising marine biodiversity monitoring data. As part of BioMonWeek 2026, this session seeks contributions highlighting how data can be better collected, integrated, standardised, shared, and reused to inform conservation, policy, and sustainable management of marine ecosystems. Share your experiences, tools, frameworks, and case studies that help turn marine monitoring data into accessible, actionable knowledge with real-world impact.

From fragmentation to integration: Building MBON Europe for Operational Marine Biodiversity Monitoring

Isabel SOUSA PINTO, Mark Costello, Eirini Apazoglou , Christos Arvanitides

Abstract: Marine biodiversity is undergoing rapid change under the combined pressures of climate change and human activities, yet Europe still lacks a coordinated system to observe, understand, and respond to these dynamics at scale. The Marine Biodiversity Observation Network (MBON) Europe addresses this gap by building a distributed, long-term framework for harmonised biodiversity monitoring across marine ecosystems. Established within the EuroMarine network and endorsed as the European component of the global MBON initiative, MBON Europe brings together organisations committed to sustained monitoring, methodological standardisation, and open data sharing. Participating institutions sign a Memorandum of Understanding to support long-term time-series observations and ensure the publication of biodiversity data in European and global repositories such as EMODNE, OBIS and GBIF. To date 24 organisations with ongoing monitoring programs have signed this MoU. The initiative responds to a critical need: despite decades of research efforts, there is still limited knowledge of what biodiversity is monitored, where, and how consistently across Europe. MBON Europe contributes by mapping existing monitoring efforts, improving data interoperability, and enabling the synthesis of biodiversity trends and ecosystem change. LifeWatch ERIC supports MBON Europe by providing the e-infrastructure needed to integrate, harmonise and analyse heterogeneous biodiversity data, enabling reproducible workflows, FAIR data access, and cross-domain interoperability across research infrastructures and global data systems. Aligned with GEO BON, GOOS and the UN Ocean Decade, MBON Europe is building the foundations of a coordinated European observing system. By strengthening the link between observation, data integration and policy, it enables more effective, evidence-based marine biodiversity management.

Implementation of MSFD monitoring in France: challenges and perspectives

Laure CABASSE

Abstract: The EU Marine Strategy Framework Directive (MSFD) aims to protect marine ecosystems and biodiversity, upon which our health and marine-related economic and social activities depend. To support EU Member States in achieving Good Environmental Status (GES), the directive defines 11 qualitative descriptors that must be assessed every six years. Given the ambition of the directive and the vast extent of the exclusive economic zone (EEZ) to be monitored, France has had to integrate numerous monitoring frameworks into the MSFD implementation process, including systems that were not initially designed for public policy purposes. This integration raises several challenges depending on the descriptor considered, such as bridging the gap between local monitoring initiatives and national-scale assessments, developing new monitoring networks for non-indigenous species, and mobilising heterogeneous data sources, including administrative data. In addition, several monitoring programmes currently under development rely on innovative technologies such as acoustic monitoring and environmental DNA (eDNA). The broad scope of the MSFD and the diversity of monitoring tools involved make its implementation in France a valuable case study for analysing how marine biodiversity monitoring data can be mobilised to inform and guide public policy.

Seasonal variability of micronekton: a comparative analysis of acoustic observations and ecosystem models

Sarah ALBERNHE

Abstract: Micronekton, comprising marine organisms ranging from 2 to 20 cm, plays a pivotal role in oceanic food webs as the primary prey of large marine predators. By performing diel vertical migrations, these organisms also contribute to the ocean's biological carbon pump. Despite their ecological importance, knowledge of micronekton seasonal dynamics remains limited due to sparse temporal coverage and methodological constraints. To our knowledge, no open-ocean observational climatology capturing micronekton seasonal variability has yet been published. This study addresses this gap by reconstructing backscatter-derived climatologies from ship-based acoustic measurements at 38 kHz at two sites: the Subpolar Indian and Subtropical Pacific regions. These climatologies provide seasonally resolved estimates of acoustic backscatter as a proxy for micronekton biomass and were used to evaluate two versions of the SEAPODYM-LMTL ecosystem model: the original and a new version incorporating more realistic trophic interactions. The new model version showed improved alignment with observed seasonality, demonstrating that refining trophic interactions enhances the ability to reproduce seasonal patterns. A key finding is that deep mesopelagic seasonal variability is remarkably low, and that micronekton seasonal dynamics are primarily driven by epipelagic and vertically migrating groups. This result has direct implications for monitoring strategies, as these groups are more accessible to standard net-sampling methods. This work illustrates the synergy between observational datasets and ecosystem models: sparse monitoring data can anchor and validate numerical frameworks, which in turn provide continuous estimates in time and space. This study also underscores the urgent need for greater temporal resolution in mid trophic levels communities monitoring.

STAMM: an active movement model mobilising ocean data to reveal juvenile sea turtle dispersal

Tony CANDELA

Abstract: Marine biodiversity monitoring data are essential to understand and protect highly mobile and vulnerable species such as sea turtles, yet major gaps remain for early life stages. Juvenile sea turtles, which spend several years in poorly observed pelagic habitats, are particularly underrepresented in observational datasets, limiting their integration into conservation and policy frameworks. To address this challenge, we present STAMM (Sea Turtle Active Movement Model), an innovative modelling framework that mobilises heterogeneous oceanographic and ecological data to reconstruct the dispersal of juvenile sea turtles from their natal beaches. By integrating ocean current data with habitat-driven behavioural rules, STAMM moves beyond the traditional assumption of passive drift and enables the generation of spatially explicit, ecologically realistic movement trajectories. We apply this framework to multiple populations, including leatherback turtles (Dermochelys coriacea) in the Pacific and Atlantic Oceans, and loggerhead turtles (Caretta caretta) in the Indian Ocean. Our results demonstrate that combining physical and biological data substantially improves the representation of juvenile dispersal. Habitat-driven movements structure spatial distributions, drive seasonal migrations that reduce cold-induced mortality, and lead individuals towards productive habitats not reachable through passive drift alone. This work highlights how integrating and reusing diverse marine datasets through modelling approaches can fill critical observation gaps and generate actionable knowledge on otherwise inaccessible life stages.

Consolidating the Operational Marine Biology Network. The ANERIS project

Jaume PIERA, and the ANERIS Consortium

Abstract: The marine environment is constantly changing. Obtaining systematic and long-term routing measurements is a huge challenge which can be tackled with appropriate technologies and methodologies. In the European project ANERIS (Operational Technologies for Detecting Life in Marine Ecosystems), we are addressing these observational challenges by developing cutting-edge technologies for detecting marine life. The project proposes the concept of Operational Marine Biology (OMB), understood (by analogy with Operational Oceanography) as routine, systematic, and long-term measurements of oceanic and coastal life, as well as their rapid interpretation and dissemination. ANERIS has improved and integrated different acquisition technologies based on genomics, imaging, and participatory systems to encompass the wide range of body sizes of the different organisms that inhabit the ocean. Establishing the OMB Network will enable the creation of an operational biological information base related to Essential Biodiversity Variables (EBVs) and Essential Ocean Variables (EOVs). It will also provide crucial data for marine policy descriptors,

particularly the Marine Strategy Framework Directive (MSFD). Overall, the project aims to benefit all stakeholders within the framework of the quintuple helix of innovation, promoting innovation and knowledge sharing among them: (1) academia with new life detection technologies for use in research; (2) industry with new technologies and methods for exploitation; (3) governments with improved observation systems and data products for use in environmental management policies; (4) civil society, empowered through the proposed participatory technologies and large collaborative networks and (5) the marine research infrastructures involved in ANERIS, integrating a new generation of detection instruments and methods. The ANERIS technologies have been tested through four case studies and here we present the preliminary results obtained.

PS01 Posters

Integrating DNA Barcoding and BRUV Systems for Monitoring Marine Biodiversity in the Black Sea

Ayşe CEBECİ, Melike ALEMDAĞ, Şirin FİRİDİN, Rafet Çağrı ÖZTÜRK

Abstract: National genebanks play a critical role in preserving the genetic diversity of plants, animals, and microorganisms and ensuring their sustainable use. These institutions store genetic materials such as tissues, and DNA for long-term conservation, thereby preventing the loss of biological diversity and safeguarding resources for future generations. In Türkiye, the National Aquatic Genetic Resource Bank was established in 2021, and its sustainability has been supported through the development of the National Aquatic Genetic Database. Within the scope of this project, fish samples have been collected annually from the Black Sea coasts. Species identification was initially performed through morphometric analyses, followed by the collection of tail tissue samples preserved in 99% ethanol for genetic analyses. DNA extracted from these tissues was analyzed through sequencing of the mitochondrial DNA cytochrome c oxidase I (COI) gene region for genetic species identification. To date, tissue and DNA samples from 26 fish specimens collected along the Black Sea coast have been preserved in the National Gene Bank. In addition to these approaches, the Black Sea coast was monitored in 2025 using BRUV (Baited Remote Underwater Video) systems, through which 24 species were recorded. Comparison of BRUV-derived data with survey-based records revealed certain gaps in the current National Gene Bank dataset. The results demonstrate that non-destructive monitoring methods such as BRUV systems can effectively support marine biodiversity assessments and complement DNA barcoding approaches. The data generated in this study may help address existing data gaps in reporting processes under the European Union Marine Strategy Framework Directive (EU 2008/56/EC) and initiatives of the Food and Agriculture Organization. Furthermore, standardized

and continuous monitoring approaches could contribute to marine environmental management under the EU Biodiversity Strategy for 2030.

Diving into the unknown marine bacteria living under hydrothermal stressors in the Hellenic Volcanic Arc.

Alexandra ZACHARIADOU

Abstract: Comprising several active volcanic edifices in the South Aegean, the Hellenic Volcanic Arc serves as a natural laboratory for studying how microbes respond to concurrent stressors, since the marine environment of the area is simultaneously influenced by hydrothermal fluxes and several anthropogenic activities. This study aimed to characterize the functional and taxonomic diversity of these complex coastal ecosystems by applying shotgun metagenomic sequencing to 11 water and 5 sediment samples, with a focus on reconstructing metagenome-assembled genomes (MAGs). Through bioinformatic analysis of the samples collected from radon-rich and hydrothermal sites, we recovered 181 medium- to high-quality MAGs. Notably, 66 of these were of high quality, satisfying the thresholds of ≥95% completeness and ≤5% contamination. Taxonomic profiling of these high-quality MAGs highlighted novel and previously uncharacterized microbial diversity with several MAGs lacking valid taxonomic classification or being only partially assigned across taxonomic ranks. We identified a broad spectrum of bacterial phyla such as Pseudomonadota (primarily Gammaproteobacteria-related), Bacteroidota, Thermodesulfobacteriota, and Campylobacterota, in addition to four candidate or provisional phyla recognized by the Genome Taxonomy Database (GTDB). These recovered lineages comprise metabolically versatile organisms well-adapted to hydrothermal conditions. For instance, Thermodesulfobacteriota and Zetaproteobacteria (within the Pseudomonadota) are frequently linked to thermophily, resilience to redox fluctuations, and sulfur or hydrogen metabolism. Functional annotation further confirmed these diverse metabolic capabilities, underscoring their environmental adaptation. Pathways governing carbon fixation, sulfur oxidation, and nitrogen and methane metabolism connect these microbes to critical biogeochemical cycles within the hydrothermal system.

Black-legged Kittiwake (Rissa tridactyla) Diet in the Picardy Estuaries and Opal Sea Marine Nature Park: Implications for Fragile Ecosystem Management

Baptiste FAURE; Poisblaud S.; Avril C.; Vergondy A.; Williams G.; Andrialovanirina N.; Bled-Defruit G.; Cavalier F.; Petit-Berghem E.; Legroux N.; Mahé K.; Poisson E.; De Grissac S.; Jiguet F.; Luczak C.

Abstract: This study demonstrates the value of biomonitoring in understanding fragile marine ecosystems facing resource competition between a protected bird species, the Black-legged Kittiwake (Rissa tridactyla), and industrial fishing targeting small pelagic fish for fishmeal production in aquaculture. While the global Black-legged Kittiwake population has declined sharply since 1975, France's breeding population is steadily increasing, particularly in Pas-de-Calais, which harbors over 75% of the national population. The Boulogne-sur-Mer colony, located in France's leading fishing port, provides a unique case study. We tested whether this population increase relates to exploitation of fishing discards. Droppings from a subcolony of 125 breeding pairs were collected throughout the breeding season and analyzed using two complementary approaches: otolith identification and environmental DNA metabarcoding. eDNA analysis provides qualitative data and a comprehensive prey list (fish, invertebrates), while otolith analysis quantifies fish population dynamics (abundance, size classes, biomass). Results contradict the initial hypothesis: although discard species are consumed, directly caught sand-eels (Ammodytes sp.) constitute the majority of prey. This species is not commercially exploited in the English Channel–North Sea, indicating resource abundance. These findings highlight the importance of protecting prey species habitats from industrial fishing, particularly within marine protected areas, which are preferred kittiwake feeding grounds. Seasonal variations in prey composition and differences related to laboratories and primers used in metabarcoding analyses were also observed. This study demonstrates the potential of standardized, reproducible monitoring combining complementary techniques to track marine ecosystem dynamics. Only rigorous biomonitoring will enable detailed assessment of anthropogenic pressures on marine environments and associated species.

Succession dynamics of artificial reefs

Joel HJÄRNE KOKK, Matthias Obst

Abstract: Autonomous reef monitoring structures (ARMS) are increasingly being deployed to monitor hard-bottom marine biodiversity. They are used both as a means to standardise sessile sampling and biodiversity metrics, and tracking invasive species introduction routes. As the use of artificial reef structures is increasing both for monitoring and restoration purposes, the incentives grow to understand how sessile communities develop. This study aims to contribute to this knowledge. Combining a nine-month field experiment on the Swedish west coast with data from a standardised European monitoring programme (EMOBON), this study uses DNA metabarcoding to identify temporal ecological patterns. Results suggest alpha diversity grows quickly, then stabilizes after about half a year, including the summer. Beta diversity seems to be higher early on, affected by local differences in the intensity of initial larval settling waves, and then wear off as the communities adapt to the local conditions after about half a year. Possibly, in the more long-term perspective, after 2-3 years, beta diversity starts increasing again as a result of community build-up generating new differing structures and microhabitats that favour different successive communities. This study highlights the importance of standardised and

coordinated monitoring networks for discerning complex ecological trends that include the cryptobiome, with potential implications for management and interpretation of future monitoring efforts.

Monitoring reef fish using eDNA metabarcoding: how and where is it best to filter water?

Nina PRASIL-DELAVAL

Abstract: Coastal reef fish assemblages provide multiple key contributions to nature and people worldwide. Hence, they are primary conservation target and are included in several European Marine Policies, including the Marine Strategy Framework Directive but also in MPA monitoring, which promote the use of non-destructive sampling methods. Among non-invasive methods, eDNA metabarcoding has emerged as a powerful tool for assessing rocky reef fish communities. However, the methods used to collect eDNA samples are highly heterogeneous at the European level, even sometimes at the national level. Nowadays, few studies have investigated the influence of the sampling methods thus making data interoperability and results comparison difficult. To address this issue, we investigated the influence of the sampling depth, the pumping method used (mobile pumping vs static pumping) and the stratification level of the waters on reef fish detection. To test these hypotheses and investigate the necessity to combine sampling methods to maximize reef fish detection for observation and monitoring purposes, water was sampled along two kilometers long surface transects with a boat, statically at three different depths and while diving along the reef, in the Atlantic Ocean and the Mediterranean Sea. Then, for each locality we identified the sample(s) that 1) maximize alpha diversity but also 2) identified the unique samples that maximize beta diversity. Finally, we investigated the differences in community composition with an ecological perspective. By analyzing the data collected, we showcase the complementarity of these different sampling protocols to maximize fish detection in four contrasted locations.

PS02 Posters

Harnessing Environmental DNA Metabarcoding for the Detection and Mapping of Vulnerable Marine Ecosystems in the Mediterranean Sea

Simone GALLI, Giulia Maiello, Nadia Marinchel, Paolo Carpentieri, Archontia Chatzispyrou, Dimitrios Damalas, Konstantinos Charalampous, Caterina Stamouli, Stefano Mariani, Tommaso Russo, Alice Sbrana

Abstract: Marine resource overexploitation by commercial fisheries threatens biodiversity and ecosystem stability. Vulnerable Marine Ecosystems (VMEs) require urgent protection, particularly from deep-sea bottom trawling. Traditional methods for identifying VMEs rely on direct observations using ROVs,

experimental fishing campaigns, and incidental collection during commercial fishing operations. However, these approaches are often limited by logistical challenges, high costs, and potential sampling biases. We evaluated the effectiveness of environmental DNA (eDNA) metabarcoding as an innovative tool to detect and map VMEs in the Mediterranean Sea. A bespoke 3D-printed sampler ("metaprobe") was integrated into bottom trawling gear to collect eDNA during the 2023 International Bottom Trawl Survey in the Mediterranean (MEDITS) across 18 sites in the Eastern Ionian Sea (GSA 20). Through the amplification of the COI region of the mitochondrial genome, we were able to identify a total of 182 unique taxonomic units from the study area. Seven VME Indicator (VMEI) taxa were detected. We applied a Joint Species Distribution Model (JSDM) using Hierarchical Modelling of Species Communities (HMSC) to explore the distribution patterns of VMEI taxa and to examine relationships between VMEI taxa and environmental covariates. Results revealed taxon-specific responses: slope and temperature were key predictors for some species, while trawling effort significantly influenced others. A richness-weighted VME index highlighted areas of high VMEI concentration, underscoring zones of increased ecological vulnerability. Our results demonstrate that eDNA metabarcoding can effectively map VMEI distributions, identify environmental drivers influencing their occurrence, and assess ecosystem vulnerability. We argue that integrating eDNA with fisheries surveys may strengthen biodiversity monitoring and conservation planning in data-limited marine systems.

Southern Baltic Sea nematode monitoring: morphotaxonomy vs multiplex barcoding and metabarcoding

Matylda GAJDA, Jan Pawłowski, Lech Kotwicki, Katarzyna Grzelak, Justyna Falkowska, Ngoc-Loi Nguyen, Hedvig Csapó

Abstract: Marine ecosystems are undergoing drastic changes due to the climate change and various anthropogenic impacts. Monitoring these changes is essential for assessing ecosystem health and informing marine management. However, current biomonitoring programmes rely mainly on morphological identification of macrofaunal indicator species, which represent only a small fraction of biodiversity and require time-consuming taxonomic expertise. In contrast, most marine biodiversity consists of micro- and meiofaunal organisms that remain largely overlooked. Recent advances in high-throughput sequencing technologies offer new opportunities for DNA-based biodiversity assessment. In particular, environmental DNA (eDNA) metabarcoding can complement traditional monitoring methods and expand the range of detectable bioindicators. Meiofaunal organisms represent promising candidates for such approaches due to their abundance, diversity, and sensitivity to environmental stressors. In this study, we integrate molecular methods with traditional morphotaxonomic approaches to improve monitoring of benthic biodiversity in coastal

environments. We analyse meiofaunal diversity in sediments from the Southern Baltic Sea, a region exposed to anthropogenic pressures. As a first step toward establishing an optimal methodological workflow, we focus on one key meiofaunal group - nematodes. Diversity patterns obtained through nanopore-based multiplex barcoding and Illumina sediment DNA metabarcoding are compared with reference to traditional morphotaxonomic identification. Taxonomic composition, relative abundance, and correlations between methods are evaluated to assess the accuracy and applicability of molecular approaches. This study demonstrates how integrating emerging sequencing technologies with traditional monitoring can improve benthic biodiversity detection and support the development of rapid, cost-effective DNA-based marine monitoring.

Translating marine phytoplankton biodiversity data into essential variables for ocean governance and monitoring

Gladys VENTRE, Haesung Jee, Marco-Bolo WP2 consortium, Chris Bowler, Pedro C. Junger

Abstract: Information on ocean health and the state of marine biodiversity are increasingly critical to address the threats of climate change, food security and the global biodiversity crisis. Yet oceans, which cover 70% of Earth's surface, remain largely understudied and underrepresented in policy frameworks. Until the recent adoption of the BBNJ agreement, 64% of oceans fell outside legal jurisdiction. Initiatives and expeditions such as Tara Oceans play an important role in understanding the oceans better. The use of new technologies, such as eDNA alongside high-throughput imaging, also allows for unprecedented insights into marine microbial and planktonic communities at a global scale. Nevertheless these data are not always readily accessible to policy-makers and there remains much heterogeneity in definitions, uses, and interpretations of eDNA data. In this context, essential variables have the potential to provide a standardized framework that can then be translated into indicators adjusted to the relevant regional directives and monitoring programs. Here we used metabarcoding and imaging data from Tara Oceans to derive and compare phytoplankton diversity metrics, assessing methodological consistency, marker-specific biases, and taxon-level divergencies. These outputs were then mapped onto the GOOS BioEco Essential Ocean Variables (EOVs) and the GEO BON Essential Biodiversity Variables (EBVs) frameworks, which aim to standardize biodiversity monitoring and provide structured, comparable variables for better and more informed ocean governance. Finally, we also deposited the DNA-based EOVs following the Darwin Core Format into OBIS and the GOOS BioEco EOV metadata portal, bridging the gap between scientific knowledge and ocean governance. This case study demonstrates how a reproducible workflow, from one type of raw eDNA data to EOVs and EBVs, can deliver policy-relevant biodiversity indicators needed for efficient marine monitoring and conservation.

Global distribution and diversity of harmful algal bloom species revealed by eDNA metabarcoding

Laura KHIM, Chris Bowler, Pedro C. Junger

Abstract: Harmful algal blooms (HABs) are a growing concern for ocean health, coastal economies, and food security. While HABs are often important components of marine monitoring programs, their distribution patterns and environmental drivers remain poorly understood at the global scale. Here we address this gap using the size-fractionated Tara Oceans eDNA metabarcoding data, particularly targeting the 18S rRNA V4 and V9 regions. We found a significant correlation between the percentage of HAB species in V4 and in V9 datasets (rho=0.6, p-value < 0.01). HAB species represented 4.5% (n = 454) and 6.4% (n = 380) of phytoplankton ASVs, and 5.8% (n = 4,650,058) and 10% (n = 25,946,365) of the phytoplankton reads in the V4 and V9 datasets, respectively. HABs were significantly more abundant in surface waters than in the DCM, and in the nano- (3-20 µm) and microplankton (20-180 µm) size-fractions (p-value < 0.01 for V4 and V9). The predominant genera in V4 were the dinophyceae Alexandrium (25.6%), Prorocentrum (10.4%), Margalefidinium (13.9%) and Karlodinium (15%), and the haptophyte Phaeocystis (10.2%), which was particularly abundant in the largest size-fraction. For V9, the predominant genera were the diatom Pseudo-nitzschia (14.3%), the dictyochophyceae Pseudochattonella (12.7%), the haptophyte Phaeocystis (17.3%), and the dinophyceae Alexandrium (16.9%) and Karlodinium (22.4%), with variations across size-fractions. This work demonstrates the capacity of eDNA metabarcoding to monitor HAB dynamics globally, contributing to the GOOS BioEco “Phytoplankton Biomass and Diversity” EOV sub-variable “number of HAB events”, and to the GEO BON EBV class “Ecosystem Function” (generic name “Ecosystem Disturbance”).

BioMonWeek 2026 The European Conference for Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Freshwater Monitoring — Spotlight on rivers, lakes and wetlands

FR04a Advances in freshwater biodiversity monitoring

Tuesday 5 May 11h30–12h30, Room Sully 1
Chair: Daniela Cortes Guzman

Broad-scale evaluations of biodiversity change need reference comparisons

Daniela CORTES, James S. Sinclair, Jukka Aroviita, Nathan J. Baker, Libuše Barešová, Catherine Bradley, Miguel Cañedo-Argüelles, David Cunillera-Montcusí, Hugh B. Feeley, Martial Ferréol, Mathieu Floury, Marie Anne Eurie Forio, Peter Goethals, Kaisa-Leena Huttunen, Ioannis Karaouzas, Aitor Larrañaga, S. Jannicke Moe, Ariane Moulinec, Diana Osadčaja, Petr Pařil, Andrés Peredo Arce, Marek Polášek, Michal Straka, Rudy Vannevel, Martin Wilkes, and Peter Haase

Abstract: Anthropogenic impacts threaten global biodiversity. However, our broad-scale and long-term understanding of these impacts commonly lacks important local context that may be essential to identify consistent biodiversity responses, specifically comparisons to an unimpacted, reference state. To evaluate the importance of references, we used 4,062 European river invertebrate time series from 23 countries to determine whether biodiversity trends depended on: (i) the initial impacts in each community (based on similarity to least-impacted reference communities, termed ‘ecological quality’); and (ii) the total degree of temporal degradation or recovery. Biodiversity and compositional changes were generally stronger and more consistent in initially poorer-quality communities that exhibited more extreme degradation or recovery, whereas they were weaker in initially better-quality communities, and highly inconsistent with lesser total change. Our findings highlight the key role of reference comparisons for ensuring comparable biodiversity trends, and for setting expectations of community responses to anthropogenic impacts and conservation actions.

Monitoring biodiversity and carbon responses to restoration in Paul da Goucha, a southern European peatland reserve

Ana TRINDADE

Abstract: Peatland restoration in Europe increasingly relies on rewetting to recover ecosystem functions and reduce greenhouse-gas (GHG) emissions, yet evidence from southern European lowland peatlands remains limited. Here we present an integrated monitoring approach from Paul da Goucha Local Nature Reserve, Portugal, where biodiversity and carbon fluxes were assessed across wetland, restored, non-restored and adjacent pasture habitats. We combined biodiversity surveys of mammals, birds, beetles, butterflies and bees with ground-level measurements of CO_2, CH_4 and N_2O using closed chambers, complemented by ecosystem-scale fluxes from eddy covariance. This design allowed comparison of biodiversity patterns and carbon dynamics across habitats and seasons. GHG fluxes differed significantly among peatland, restored and non-restored habitats for CO_2 ($H=32.36$, $p=9.42\times10^{-8}$), CH_4 ($H=35.32$, $p=2.14\times10^{-8}$) and N_2O ($H=10.01$, $p=0.00672$). CO_2 was higher in restored and non-restored areas than in the peatland, whereas CH_4 was higher in the peatland; N_2O showed a weaker gradient, with highest values in restored sites. Ecosystem-scale monitoring further showed marked seasonal dynamics, peaking in spring and autumn. Biodiversity responses were strongly taxon-specific. Bee abundance differed significantly among habitats ($\chi^2=34.79$, $p=2.789\times10^{-8}$), peaking in restored areas and lowest in wetland sites. Butterflies showed a similar trend, with higher abundance and diversity in restored areas. Medium- and large-mammal records revealed significant seasonal differences, with more winter observations in restored and wetland sectors. Overall, no single habitat state maximised all biodiversity components. These results show that restoration outcomes are taxon- and process-dependent, and that rewetting in southern peatlands cannot be guided by carbon metrics alone. Integrated biodiversity and carbon monitoring is therefore essential to support adaptive, site-specific restoration in southern Europe.

Assessing river quality using diatom metabarcoding: harmonizing methods with microscopy to improve stakeholders' acceptance

Laurine VIOLLAZ, Benjamin Alric, Frédéric Rimet

Abstract: Benthic diatoms are the most abundant photosynthetic organisms within microbial communities with excellent bioindicator properties due to their high sensitivity to natural and human-induced environmental changes. They are traditionally used to assess the ecological status of rivers and lakes using microscopic methods based on morphological identification. For over a decade, high-throughput sequencing techniques, including metabarcoding based on the identification of diatom species DNA, have been developed. The data produced by this type of method is of particular interest in the context of monitoring for the Water Framework Directive (WFD), as it can be used to calculate the environmental quality indices required by this directive, in particular the diatom biological index (DBI). Usually, the index is obtained using the national standardized calculation system (SEEE https://seee.eaufrance.fr/) based on morphological datasets. We used this calculation system with molecular data and compared with microscopy-based indices. We identified several sources of differences between both methods, including the over or under-estimation of abundant species, leading to a gap between indices. To address these issues, a gateway has been developed between the two approaches. This method corrects molecular abundances using a correction factor based on cell biovolume combined with a linear model. This strategy increased the similarity between DNA and microscopy quality assessments with the BDI. In addition to the recent advances in ISO standardization of the different stages of the workflow, diatom metabarcoding is now ready to be implemented in WFD monitoring networks, alongside classical diatom microscopy.

New ways to evaluate freshwater biodiversity using periphyton genomics

Hetty KLEINJAN, Lena Brouwir

Abstract: The objective of the present study (AquaBioSens, Wallonia ERDF/JTF 2021–2027) is the creation of a novel biological indice, derived from the genomic composition of periphyton. The development of this indice is driven by the underlying need for new methods that facilitate rapid, sensitive and field-based monitoring of freshwater biodiversity The project incorporates a case study of one year, conducted along two main rivers in the Walloon (Belgium) region, the Vesdre and the Ourthe. The rivers differ in terms of water characteristics and the types of pollution they are exposed to. In particular, the water quality of the Vesdre is severely affected due to the 2021 floods, which led to the destruction of key wastewater infrastructure situated along the river. During the case study, periphyton was collected monthly from standardized passive samplers that were installed on different locations in the rivers. The periphyton community composition was analyzed through the sequencing (nanopore, long-reads) of marker genes from bacteria (16S rRNA), eukaryotes (18S rRNA) and macroinvertebrates (CO1). The resulting dataset was subsequently used to identify bioindicator species suitable for the calculation of the biological indice. The presentation will cover the initial evaluation of the field data obtained from this case study, as well as the present methodology for converting this data into the new biological indice. An illustration will be given on how to use the indice as a diagnostic instrument for rapid in-field evaluation of freshwater biodiversity, and as a metric for biological water quality monitoring.

Comparing molecular and image-based approaches for standardized diatom biodiversity monitoring under the Water Framework Directive (WFD)

Maxime BEAUVAIS, Abdelmguid D., Beszteri B. and Rimet F

Abstract: Diatoms are well-established indicators of freshwater quality and play a central role in WFD biomonitoring. While light microscopy remains the reference method, advances in high-throughput molecular (eDNA metabarcoding) and image-based approaches (deep-learning models) offer new opportunities for fast and standardized biodiversity assessment. However, comparisons between these approaches and traditional microscopy remain limited, notably regarding their implications for ecological status evaluation. In this study, we compared three approaches for assessing diatom biodiversity at the genus level in 58 river stone biofilm samples from six European countries: expert microscopy, deep-learning model trained on microscope slides, and eDNA metabarcoding targeting rbcL marker. The results were compared in terms of alpha and beta diversity and based on the Generic Diatom Index (GDI) value. Metabarcoding showed the strongest correlation with microscopy, whereas model predictions were less consistent with the other methods. Shared genera represented over 90% of total abundance, while method-specific taxa accounted for only ~3%, indicating that discrepancies mainly involve rare taxa and are unlikely to affect GDI values. Metabarcoding detected more genera than microscopy due to its ability to capture rare, cryptic or fragmented organisms, whereas the deep-learning model predicted richer and more even communities, suggesting a theoretical community structure where observational and ecological constraints are reduced. Despite being trained on few samples from scattered European regions, the deep-learning model showed good diversity coverage highlighting its promising potential for biomonitoring, although requiring further calibration. Overall, comparable ecological signals were obtained for dominant taxa, suggesting that operational criteria (i.e., expertise, cost, reproducibility transferability, carbon footprint) should finally guide method implementation in WFD biomonitoring.

FR06a Freshwater habitats

Wednesday 6 May, 9h00-10h00, Room Joffre F

Groundwater Biodiversity Monitoring in Switzerland: from Case Study to Upscaling

Mara KNÜSEL, Roman Alther, Florian Altermatt

Abstract: Groundwater is globally one of the largest bodies of freshwater, and an essential provider of drinking water and other ecosystem services. It is generally well-monitored from a chemical and physical perspective, yet its biodiversity is largely unknown. Also compared to other freshwater ecosystems, groundwater remains understudied from a biological perspective and groundwater biodiversity is largely not integrated into regional or national monitoring programs in most countries. In Switzerland, we developed a novel citizen science approach to assess baseline groundwater biodiversity data and possible change with support from drinking water providers. Covering >900 sampling sites across the country we demonstrated a scalable and systematic sampling design suitable for groundwater biodiversity monitoring. Based on thousands of samples we demonstrated a high yet hitherto largely overlooked diversity and distribution of groundwater amphipods across Switzerland, identifying biodiversity hotspots and endemism. In parallel, we developed and tested eDNA methods for systematic groundwater biodiversity assessments. Combining eDNA and citizen science approaches, we are currently upscaling to future-proof these sampling methodologies and their integration into national monitoring programs in Switzerland. Eventually, through combined efforts in international programs such

as the Biodiversa+ DarCo project, we aim to advance knowledge, management and conservation of European subterranean biodiversity in general.

Unraveling metacommunity dynamics in European drying river networks through bulk DNA metabarcoding

Nieves LÓPEZ-RODRÍGUEZ, Csabai Z., Bonada, N, Leese, F, Buchner, D., & Datry, T.

Abstract: Drying river networks are the dominant type of water bodies on Earth and are expanding worldwide. Drying acts both locally as a master environmental variable and regionally as fragmenting river networks temporarily, influencing metacommunity dynamics. Fragmentation shapes intraspecific genetic diversity through dispersal limitation and recolonization dynamics. Bulk DNA metabarcoding allows us to capture these patterns with unprecedented resolution, detecting both taxonomic and molecular diversity that traditional methods may miss. We evaluated whether biodiversity patterns derived from molecular data matched those commonly described in drying river networks, where drying generally decreases local diversity (α-diversity) and increases differences among communities (β-diversity). Here, we analyzed aquatic macroinvertebrate metacommunities across six European drying river networks in countries (Croatia, Czechia, Finland, France, Hungary, and Spain) using repeated sampling conducted between 2021 and 2022 and modelled hydrological patterns. We calculated local taxonomic and molecular richness (number of exact sequence variants [ESVs] per site) and quantified community differentiation using mixed-effects models. We also assessed spatial structure using the Mantel test, relating community dissimilarity to flow patterns and network structure. We expected that drying would reduce local taxonomic richness and associated molecular diversity, while differentiation among sites was expected to increase due to limited dispersal and site-specific retention of ESVs, resulting in even stronger environmental filtering and isolation differentiation among sites than observed at the taxonomic level. By integrating taxonomic and molecular perspectives, our study illustrates how flow intermittence reorganizes biodiversity across scales in drying river network metacommunities, providing novel insights into how drying influences community assembly rules.

The TRANSPONDER project: towards a standardized protocol for monitoring biodiversity in freshwater ponds across Europe

Anna BADOSA SALVADOR, Brucet, S., Benejam, L., Cuenca-Cambronero, M., López-de Sancha, A., Sgarzi, S., Boix, D., Beklioğlu, M., Boissezon, A., De Meester, L., Horváth, Z., Mehner, T., Davidson, T.A.

Abstract: Ponds are small ecosystems but ecologically significant freshwater habitats, supporting high biodiversity relative to their size and often harbouring rare or singular species while providing multiple ecosystem services. Despite this, ponds remain largely overlooked in biodiversity monitoring programmes and in national and EU policy frameworks, highlighting the need for standardized approaches to assess their biodiversity status and dynamics. The EU Biodiversa+ project TRANSPONDER (2024-2027) aims to develop a standardized yet widely applicable monitoring protocol for ponds and pondscapes across different pond types, climatic zones, and land-use contexts, including Mediterranean temporary ponds, a priority habitat under the EU Habitats Directive. The protocol will integrate abiotic variables with biodiversity data across key taxonomic groups and multiple dimensions of diversity (taxonomic, functional and genetic), and will provide a much-needed tool to support implementation of the EU Nature Restoration Law. A key question is how many ponds must be sampled within a pondscape to obtain a reliable estimate of biodiversity. Initial work towards such a protocol was initiated within the H2020 project PONDERFUL (2021–2024), providing an important methodological foundation for sampling pond biodiversity and ecological status. PONDERFUL compiled a large freshwater biodiversity database, including eDNA data for amphibians and fish, spanning broad gradients of latitude, land use and eutrophication. Analysis revealed links between biodiversity and ecosystem functioning, and between zooplankton functional diversity (measured as body size) and trophic status, and positive associations between amphibian richness and pond conservation status. Monitoring protocols adopting this integrated approach are essential for the long-term maintenance of pond biodiversity and ecosystem resilience.

Airborne Infrared Thermography (TIR) and in-situ loggers for mapping thermal suitability: A study of brown trout (Salmo trutta) habitats in pre-alpine rivers

Emmanuelle CHEVALLIER, Baptiste Marteau, Stephen Dugdale, Arnaud Caudron

Abstract: Context: Increasing thermal stress in rivers resulting from climate change poses a critical threat to cold-water species like brown trout (Salmo trutta). In French pre-alpine rivers, understanding the availability and distribution of thermal refuges is thus crucial for species conservation and effective fisheries management. Material & Methods: We implemented a multi-methods approach on three distinct rivers to quantify the spatio-temporal variations of suitable and unsuitable thermal habitats for S. trutta. This approach integrated: - High-resolution airborne thermal infrared (TIR) mapping: To characterise surface water temperature patterns and identify groundwater upwellings and thermal anomalies. - In-situ temperature loggers: To calibrate the spatial snapshots captured by aerial surveys and to extend the analysis by providing continuous data throughout the summer. Key Findings & Applications: The combination of these technologies provides a spatial framework for managers to: - Identify and protect critical thermal refuges during heatwaves; - Prioritise river reaches for potential rehabilitation; - Quantify functional habitat suitability based on biological temperature thresholds, moving beyond simple physical habitat

metrics. This approach offers a perspective for amending current management methodologies, providing a framework to refine existing tools such as the definition of minimum ecological flows (eFlows). Conclusion: This technical contribution highlights how the synergy between remote sensing and in-situ sensors provides a powerful diagnostic tool for climate-resilient freshwater environment management.

FR06b Freshwater habitats

Wednesday 6 May, 10h00-11h00, Room Joffre F
Chair: Tiina Laamanen

Bioindication as a Tool for Evaluating the Environmental Health of Zhinvali Reservoir, Georgia

Bella JAPOSHVILI, MURVANIDZE Lali, EPITASHVILI Giorgi, ARABULI Lela, ASATIANI Ketevan, KOTOLASHVILI Tamta

Abstract: The Zhinvali Reservoir serves as a critical strategic water resource for Georgia, providing drinking water and hydroelectric power. Monitoring its ecological integrity is essential for sustainable management. This study, initiated in 2025, employs a multi-proxy bioindication approach to evaluate the environmental health of the reservoir, focusing on three distinct biological components: fish communities, benthic macroinvertebrates, and parasite assemblages. The research utilizes fish as long-term indicators of ecosystem stability, analyzing population structure and reproductive status through gonad examination to detect chronic environmental stressors. Complementing this, macroinvertebrate sampling provides high-resolution data on localized water quality and sediment health, as these organisms are highly sensitive to organic pollution and oxygen fluctuations. A novel aspect of this study is the integration of parasitological indicators; the diversity and prevalence of fish parasites are used as sensitive biomarkers to reflect both host health and broader environmental perturbations. Preliminary findings from the ongoing monitoring suggest that the synergy between these three taxonomic groups offers a more comprehensive "health report" than traditional chemical analysis alone. By correlating biological data with physico-chemical parameters, the study aims to establish a baseline for the reservoir’s current ecological status. This holistic bioindication framework provides a robust diagnostic tool for detecting early signs of environmental degradation. Ultimately, the results of this research will inform conservation strategies and policy decisions to ensure the long-term preservation of the Zhinvali Reservoir's vital ecosystem services.

Automatic identification and dry mass estimation of arthropods

Mikko IMPIÖ, Philipp M. Rehsen, Jarrett Blair, Cecilie Mielec, Tiina Laamanen, Arne J. Beermann, Florian Leese, Toke T. Høye, Jenni Raitoharju

Abstract: Arthropods are widely used as condition indicators for both freshwater and terrestrial ecosystems. However, routine monitoring remains labor-intensive, requires taxonomic expertise, and is difficult to scale globally. Advances in computer vision and deep learning have made it possible to streamline key components of monitoring. We present recent work demonstrating how computer vision supports biodiversity monitoring, with examples in species identification and biomass estimation. AquaMonitor [1] is a recent multimodal, multi-view dataset of benthic macroinvertebrates. It was collected using an unbiased setup by imaging all specimens sampled during two years of routine freshwater monitoring. The dataset was collected with the dual-image BIODISCOVER device that captures image sequences of specimens from two perpendicular angles. The dataset contains 2.7M images from 43,189 specimens, with smaller subsets of specimens DNA-barcoded and dry-weighed. This dataset has been used to train large foundational models for benthic invertebrate identification and can be used to benchmark new methods in a realistically challenging, real-world setup. We also present results from a recent study considering non-destructive dry mass estimation for arthropods [2]. We demonstrate that the BIODISCOVER device can be used to obtain predictors such as specimen area and sinking speed, which can be used together with images to fit both statistical and deep learning models. Results indicate that dry mass can be estimated with useful accuracy across diverse morphologies, enabling scalable biomass assessment. [1]: AquaMonitor: A multimodal multi-view image sequence dataset for real-life aquatic invertebrate biodiversity monitoring. ArXiv preprint: https://arxiv.org/pdf/2505.22065 [2]: Computer vision-based estimation of invertebrate biomass. ArXiv preprint: https://arxiv.org/pdf/2603.06362

Identifying high priority obstacles for longitudinal connectivity restoration in mainland Spain considering freshwater fish species

Lide DE IZETA ZALDUENDO

Abstract: Hydrological connectivity plays an important role in ensuring the functional integrity of river ecosystems. However, free-flowing rivers are increasingly rare due to the proliferation of artificial barriers that interrupt river connectivity. Artificial barriers alter the natural dynamics of fluvial ecosystems, modifying and fragmenting the habitat, and have an impact on freshwater biodiversity. With freshwater ecosystems at risk and one quarter of the world's freshwater fauna threatened with extinction, the restoration of river ecosystems, including the recovery of hydrological connectivity, is receiving increasing attention from administrations. In Europe, the aim is to reconnect 25,000 river

kilometres by 2030 through the removal or permeabilization of obsolete obstacles. The prioritization of restoration actions is essential to achieve this objective while maximizing ecological benefits. This study assessed longitudinal connectivity across eleven catchments in mainland Spain considering the distribution of freshwater fish species, with the aim of identifying particularly impactful artificial obstacles to fish fauna, confined to the river network and especially vulnerable to river fragmentation. Fish populations were estimated for 47 freshwater species, using presence data and binary predictions from species distribution models. Artificial obstacles were obtained from a database containing 9065 records for those catchments. Population estimates were used to calculate connectivity indices both under the current scenario and after simulating the removal of each of the barriers present in the catchment. The resulting rankings highlight the obstacles whose removal would yield the greatest improvements in connectivity, providing a valuable tool for effective river restoration and management.

Context-dependent benchmarks for the biological validation of freshwater typology systems

Jonathan JUPKE, Jürg Spaak, Kaisa-Leena Huttunen, Timo Muotka, Riku Paavola, Petr Pařil, Theresa Piana, Marek Polášek, Ralf Schäfer, Michal Straka, Janne Soininen

Abstract: Freshwater typology systems underpin biodiversity monitoring across Europe. They stratify sampling designs, calibrate ecological indicators, and define reference conditions. All these applications rest on a single assumption: that ecological communities within a type are more similar than communities from different types. Yet, despite decades of use, we lack agreed-upon standards for "how much more" similar they need to be. Current validation practices rely on statistical significance tests—which often conflate sample size with effect size—or visual inspection of ordination plots. Both leave the question of practical relevance unanswered: When is a PERMANOVA R^2 of 0.05 acceptable? We address this gap by deriving context-dependent benchmarks for twelve biovalidity metrics across four taxonomic groups (diatoms, macroinvertebrates, fish, macrophytes). We compiled over 470,000 field samples from across Europe, evaluating empirical datasets against seven established typology systems. To explore the design space beyond existing systems, we fitted Hierarchical Models of Species Communities to simulate over 700,000 additional community datasets. These simulations systematically varied typology scenarios—manipulating type separation, within-type compactness, and variable definitions—while constraining environments to remain ecologically realistic. Using Quantile Random Forests, we predicted expected metric values as a function of typology design, ecological context, spatial scale, and sample size. The resulting benchmarks are not universal thresholds but conditional predictions: for a given combination of system

properties, they indicate whether observed biovalidity is poor, mediocre, or good relative to comparable potential systems. We deliver these benchmarks through an interactive application, allowing users to input their 'system characteristics and obtain tailored ranges, making rigorous typology evaluation accessible to any monitoring programme.

FR04b Advances in freshwater biodiversity monitoring

Wednesday 6 May 11h30–12h30, Room Joffre F
Chair: Daniela Cortes Guzman

Monitoring of invasive macrophytes (Eichhornia crassipes and Hydrilla verticillata) in Coastal Wetlands using Sentinel-2 imagery improved by Artificial Intelligence algorithms

Alejandro CORRALES BARRERA

Abstract: Coastal wetlands are sensitive ecosystems, serving as vital buffers for populations and habitats in these specialized regions. Their position at the interface between coastal and terrestrial environments mitigates the effects of flooding and other adverse phenomena exacerbated by climate change. Within the Ciénaga Grande de Santa Marta (CGSM) Ramsar site, the interconnected lagoons of Pajaral, El Tigre, Pijiño, Cherle, and Majagualito act as immediate receptors of the Magdalena River's discharge into the protected area of the CGSM Flora and Fauna Sanctuary. By utilizing multispectral optical imagery from the Sentinel-2 constellation, enhanced through Artificial Intelligence (via the S2DR4 algorithm), it was possible to monitor the invasive growth of two macrophyte species: the surface-dwelling Eichhornia crassipes (locally known as 'tarulla') and the submerged Hydrilla verticillata (colloquially termed 'cola de caballo'). The expansion and growth of both species were analyzed using the Floating Algae Index (FAI). Furthermore, the invaded surface area was quantified by applying the Normalized Difference Water Index (NDWI), which enables the discrimination between open water surfaces and those effectively invaded. To validate the S2DR4 algorithm, the extent of the invasion was surveyed with UAV Multispectral imagery in order to assess signal answer from Sentinel-2 Super Resolution Algorithm around the stilt-house villages (pueblos palafíticos) of Nueva Venecia and Buena Vista, comparing the standard MSI (MultiSpectral Instrument) data from Sentinel-2 with the high-resolution outputs generated by the S2DR4 algorithm

BIMS - Biodiversity Information Management System

Timothy SUTTON

Abstract: BIMS is an open-access platform for serving, hosting, analysing, visualising, and sharing biodiversity data. It is designed to support data-driven ecosystem management and conservation. Who is it for? BIMS is shaped by the needs of water resource managers, biodiversity planners, conservation agencies, researchers, and environmental consultants. The goal is simple: get high quality biodiversity evidence into real decision-making pipelines. What kind of data? Species occurrence and abundance, habitat and abiotic parameters, freshwater taxa (fish, invertebrates, algae, anurans, wetland plants), SASS biomonitoring, physico-chemical parameters, water temperature time series, and more. Why was it built? To make biodiversity data usable — not just stored. To improve long-term conservation outcomes and guide real-world freshwater management.Origins and collaboration The platform began life as the Freshwater Biodiversity Information System (FBIS) in South Africa. It was developed by the Freshwater Research Centre in partnership with Kartoza and the South African National Biodiversity Institute, with support from the JRS Biodiversity Foundation (2017–2024).

Application of Unmanned Aerial Vehicles (UAVs-drones) for habitat and bird monitoring

Peter GOETHALS, Miel Bogaert, Andrée De Cock, Xingzhen Liu, Long Ho, Wouter Maes

Abstract: During 2024-2025 a set of flights with UAV's was executed to determine the potential for automated waterbird detection and counting. The automated bird detection was compared with manual counting on generated pictures from the drone flights, as well as with direct field observations. The results of this research indicated that this automated system based on UAV's and AI can be a valuable approach to identify and count waterbirds, and also make an association with the preferred habitat conditions.

NewtCAM - Underwater camera trap for freshwater wildlife monitoring

Xavier MESTDAGH, L'Hoste Lionel, Charles Cyrille, Didry Yoanne, Foucteau Mathilde, Gama Adriano, Michel Kélian, Minette Franck, Titeux Nicolas

Abstract: The emergence of camera trapping over recent decades greatly increased the availability of terrestrial field observations. However, comparable image-based approaches remain largely underdeveloped to underwater ecosystems, especially freshwater. We present NewtCAM, an underwater camera system composed of 4 funnel-shaped entrances connected to a single tunnel where specimen trigger image recording. Specimens remain free to exit at any time, while being positioned at a defined distance from the camera, with standardised background and lighting system (visible and/or near-infrared), thereby reducing sources of variance in image composition. NewtCAM can be set in the field to capture different specimen body sides. Since 2024, NewtCAMs have

been deployed worldwide in 36 sites, collecting observations of 12 amphibian species, grass snakes, 6 fish species, 6 insect orders, and 8 additional invertebrate orders. All adult vertebrates are identified at species level, whereas only part of the invertebrate observations reach this taxonomic resolution. Smallest recorded organisms include copepods. For many taxa, images clearly reveal life stage, sex, and natural body markings for individuation. The video mode enables the recording of intra- and interspecific interactions such as courtship, mating, fighting, and predation. NewtCAM also allows imaging of live specimens too small for safe handling, such as newt larvae displaying individual belly patterns. Like terrestrial camera trapping, AI-assisted data processing is essential to effectively handle and exploit abundant observations. Our RCNN sex classifier applied to adult Triturus cristatus reaches 99% accuracy on the training dataset (only 3,690 images) and 92% on the validation dataset. These advances open new opportunities for automated, in situ and in vivo ecological monitoring with high spatiotemporal resolution in freshwater organisms, delivering novel biological insights beyond the reach of traditional field approaches.

Freshwater DNA Monitoring in Slovakia: From Reference Library Research to Applied Biomonitoring of Aquatic Ecosystems

Fedor ČIAMPOR, Michaela Šamulková, Kornélia Tuhrinová, Olena Bielikova, Patrik Macko, Zuzana Čiamporová-Zaťovičová

Abstract: Freshwater DNA monitoring in Slovakia has recently developed along two closely linked lines: research and applied practice. The first includes building of reference DNA libraries, testing of different sample types, and evaluation of DNA metabarcoding for the biomonitoring. Slovak studies show that DNA barcoding significantly expands reference databases and reveals cryptic diversity, while metabarcoding provides a more detailed view of benthic invertebrate communities and environmental gradients in Carpathian streams and Tatra lakes. Sample-type comparisons are also important: bulk macrozoobenthos provides the broadest taxonomic coverage, water is suitable for practical eDNA monitoring, and sediment complements the picture by detecting biodiversity components missed by other sample types. The scond line is represented by environmental reports from rivers, tributaries, gravel pits, and other FW habitats across Slovakia, where DNA metabarcoding is used to assess biodiversity in areas with different levels of human impact. In practice, eDNA from water and sediment is analysed most often, and results repeatedly demonstrate the high sensitivity of the method for detecting aquatic invertebrates, fish, and selected species of conservation concern or non-native origin. Monitoring of the Váh and Revúca rivers confirmed the potential of eDNA to describe biodiversity patterns in detail, while also showing that DNA provides a richer picture of species composition than older conventional data. A key link between these two lines is their applicability to biomonitoring under the WFD. At 17 Slovak sites, DNA metabarcoding detected

30% more species than conventional monitoring, while differences in ecological metrics were generally small and often remained within a single ecological quality class. Freshwater DNA monitoring in Slovakia therefore represents a promising tool connecting basic research with practical conservation and aquatic ecological assessment.

FR08 PANEL Needs and future perspectives for the Water Framework Directive

Thursday 7 May, 9h00-10h30, Room Sully 3
Chair: Kristian Meissner
Description: As Europe advances into its 4th implementation cycle of the EU Water Framework Directive (WFD), this panel will examine the need to adopt molecular monitoring, with a focus on eDNA, to enhance water body status assessment, comparability of results, and integrative use of this monitoring approach across different environmental policies (MSFD, NRL, biodiversity strategy) in the EU and beyond. The discussion will explore whether standardized molecular tools can help transform biomonitoring—from local to regional scales. Can they really deliver the much needed rapid, scalable, and cost-effective detection of biodiversity and ecosystem status in aquatic and other ecosystems?

FR01 WORKSHOP From Freshwater Biodiversity Monitoring to Conservation Actions and Policy

Thursday 7 May, 10h30-12h30, Room Sully 3
Chair: Daniela Cortés-Guzmán
Description: This workshop aims to foster discussion on how freshwater biodiversity is monitored and how these assessments can inform conservation and policy decisions. Topics include key challenges and recent advances in using community-based monitoring for biodiversity assessment, identifying the causes and drivers of biodiversity change, detecting spatial patterns and temporal trends, and integrating data into decision-making. By linking assessments with policy, the workshop will explore how research and practice can guide effective conservation actions and contribute to bending the freshwater biodiversity loss curve.

PS01 Posters

Biological eDNA monitoring in watercourses with alternating lake and river reaches: effect of lake residence time and comparison with traditional methods

Henna SNÅRE, Kimmo Tolonen

Abstract: Environmental DNA (eDNA) methods are relatively novel monitoring tools that offer multiple advances in biodiversity assessment. Compared to traditional survey methods, eDNA sampling often provides broader spatial coverage. However, this spatial coverage may also be less precise, especially in riverine environments. In large river systems, eDNA can be transported over distances up to 100 km, whereas in smaller streams and rivers transport distances are typically shorter, ranging from a few hundred meters to several kilometers. Some modeling approaches have been developed to estimate eDNA transport distances (Altermatt et al., 2023; Pont, 2024). However, these models generally do not account for the presence of lakes and the potential sedimentation of eDNA in them. Consequently, the influence of lakes on eDNA transport distances remains poorly understood. In lakes with sufficiently long water residence times, eDNA can be expected to degrade or settle out of the water column. As a result, the upstream eDNA signal, such as the species composition originating from rapidly flowing stream sections, may not be detectable at the lake outlet. Therefore, an eDNA sample collected from a stream section located downstream of a lake is likely to reflect predominantly local biological communities rather than taxa transported from upstream reaches. In this study, we investigate how water residence time in lakes affects biological communities detected in eDNA samples in two watercourses in Finland. We hypothesize that beyond a critical residence time threshold, the upstream eDNA signal is effectively lost within the lake. In addition, we compare eDNA-based species detections with existing traditional monitoring data to evaluate the efficiency and suitability of eDNA methods for river system monitoring.

From eDNA to population genetics: resolving fine-scale structure in the Garonne minnow

Tom JAMONNEAU, Jérôme G. Prunier, Alizée Ossedat, Simon Blanchet

Abstract: Environmental DNA (eDNA) is increasingly used for biodiversity assessments, yet its potential for population-genetic applications remains underexplored. Here, we present ongoing work demonstrating the feasibility of retrieving fine-scale population genetic structure from freshwater eDNA, using nuclear microsatellite markers to characterize diversity patterns of the Garonne minnow (Phoxinus dragarum) in southeastern France. We collected eDNA using multiple sampling strategies (in-stream filtration and container-based filtrations with fish / enclosed filtration capsules and circular filters) to evaluate how protocols influence the recovery of fine-scale population-genetic information. Species-specific microsatellites were successfully amplified from eDNA extracts, yielding multilocus allele-frequency profiles for each site. These profiles discriminated populations separated by only a few kilometres, highlighting the strong potential of eDNA-based genotyping —well beyond simple species detection. Reliability was assessed through contamination controls (negative / cross-amplification), and eDNA-derived allele frequencies were compared against SNP-based genotypes obtained from tissue samples. Preliminary analyses (allele-frequency distances, PCoA) revealed strong concordance between eDNA-based and tissue-based population relationships, supporting the validity of eDNA as a tool for fine-scale population-genetic inference. This study provides one of the first empirical demonstrations that freshwater eDNA can capture intraspecific genetic diversity at a resolution relevant for population monitoring. Sampling methods were compared, contamination risks evaluated and eDNA-derived results benchmarked against tissue-based datasets, offering practical insights toward operationalising population-genetic monitoring from eDNA. Ultimately, we believe such approach holds strong promise for informing river-connectivity restoration plans and assessing their effectiveness.

PS02 Posters

EpiDNA: Unlocking Fish Age Structure through Environmental DNA Methylation

Nina MARSCHEL, Henrik Krehenwinkel & Till-Hendrik Macher

Abstract: Freshwater ecosystems are among the most threatened ecosystems worldwide, making their effective monitoring essential for assessing ecological status. In addition to species composition and abundance, population age structure represents a critical parameter in environmental monitoring, particularly under the EU Water Framework Directive (WFD). In recent years, environmental DNA (eDNA) metabarcoding has emerged as a powerful, non-invasive monitoring tool. However, it is currently limited to compositional biodiversity data and does not provide age-related information. Yet the age of an organism is also molecularly encoded, specifically in DNA methylation patterns at CpG sites (cytosine-guanine dinucleotides) in vertebrate genomes. These age-associated methylation patterns form so-called “epigenetic clocks,” which have been successfully established for various taxa. To date, however, such approaches rely on invasive tissue sampling. Recent studies indicate that methylation patterns remain stable in eDNA, highlighting their potential for non-invasive age-structure assessments of fish from water samples. The EpiDNA project aims to develop the first protocols for eDNA-based methylation analyses, using brown trout as a model species. To establish an epigenetic clock for the brown trout, we conducted whole-genome bisulfite sequencing (WGBS) on tissue samples from each two specimen across three distinct age groups. Our analyses identified thousands of significantly age-associated CpG sites, revealing increasing methylation levels with advancing age. Based on this epigenetic clock, targeted eDNA primers can be designed using the currently developed EpiPrimerMiner pipeline to assess population age structure based on non-invasive sampling. Environmental DNA methylation analyses thus offer a novel, non-invasive approach to meet the monitoring requirements of WFD fish monitoring, reducing the need for invasive and potentially harmful conventional methods such as electrofishing.

Developing monitoring strategies for aquatic fungal biodiversity

Andreas BRUDER

Abstract: The biodiversity of aquatic fungi is still largely unknown, including their taxonomy, biogeography and sensitivity to environmental changes. Aquatic fungi contribute substantially to ecosystem processes and services, and interact with other organisms in multiple ways, e.g. as decomposers, symbionts, pathogens, and parasites. Despite increasing recognition of their importance for ecosystems and societies, aquatic fungi remain excluded from most biodiversity monitoring programs, unlike other aquatic organism groups. The Biodiversa+ project MoSTFun aims 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 and samples, both from publicly available archives and previous sampling efforts. Additionally, we evaluate the procedures and experiences of existing biodiversity monitoring programs and concepts such as Essential Biodiversity Variables to add aquatic fungal biodiversity to them. MoSTFun also fills knowledge gaps in understudied ecosystems such as glaciers and estuaries and emerging issues, e.g., the spread of anti-fungal resistance. For this, we develop and test novel methods from -omics, earth observation approaches, and citizen science. While the project focuses on examples in Europe, we will generate scalable knowledge and recommendations, transferable to other regions. This knowledge transfer is ensured through collaboration with relevant stakeholder groups and will culminate in a Knowledge-to-Action Hub for aquatic fungi. This will also support collaborations with other ongoing initiatives on the conservation of aquatic fungi and ensure the continuation of our efforts after the project's lifetime.

Comparing different Species Distribution Models approaches for Iberian aquatic insects

Carlota SÁNCHEZ-CAMPAÑA, Núria Bonada, David Sánchez-Feránandez, Emilio García-Roselló, Raúl Acosta, Martiño Cabana, Tommaso Cancellario, Adolfo Cordero-Rivera, Jesús M. Evangelio Pinach, Antonio José García-Meseguer, Marcos

González, Manuel Jesús López-Rodríguez, Cecilia Díaz-Martínez, Jesús Martínez, Saray Mañas-Jordá, Xavier Maynou, Andrés Millán, Florent Prunier, José Manuel Tierno de Figueroa, Jorge M. Lobo

Abstract: Having reliable knowledge of species distributions is crucial for their conservation, especially in regions with high diversity and significant anthropogenic impacts. The Mediterranean Basin is one of the world's biodiversity hotspots, also for aquatic insects, which are key to the functioning of freshwater ecosystems. Distribution data for aquatic insects are sometimes insufficient and inaccurate, which challenges the implementation of effective conservation and management strategies. Species Distribution Models (SDMs) are a powerful tool to infer distribution patterns from incomplete occurrence datasets. Here, we evaluated which SDMs best fit aquatic insect species distributions, using a database with occurrences of Coleoptera (64.400), Odonata (631.848), Plecoptera (13.393), and Trichoptera (20.513) from the Iberian Peninsula. We used the ModestR software to model and compare two approaches (MaxEnt and Niche of Occurrence) across two spatial extents (the entire Iberian Peninsula, and river basins adjacent to each occurrence record). To improve model validation, we used inventory completeness. Species with 10 or fewer records were not considered, and models were calculated at a resolution of 5 minutes. SDMs that maximised specificity and sensitivity were considered optimal. Our results show that model performance varied even among congeneric species, and some species showed equal preference for two or more models. These findings emphasise that, to achieve conservation targets, it is necessary to have complete and accurate information on species' distributions. They also show that, under certain conditions, relatively simple modelling approaches can yield reliable predictive results. Future monitoring in poorly surveyed areas may also provide independent empirical data for model validation.

Integrated analysis of microbial diversity dynamics and environmental drivers in Lake Razim, Romania

Denisa IGESCU, Elena-Alina Olaru, Adrian Burada, Cristian Mihai Adamescu, Marian Radu, Ionela Avram

Abstract: Aquatic microbial communities play a central role in nutrient cycling and ecosystem functioning, yet the environmental factors structuring their spatial distribution remain incompletely studied, especially in freshwater ecosystems. Lakes connected to major river-sea continuum, such as Lake Razim (Danube Delta Biosphere Reserve, Romania), represent dynamic environments where physico-chemical gradients may differentially shape water column and sediment microbiomes. In this study, we examined microbial community composition in water and sediments across five representative sites using 16S Metabarcoding analysis in relation to key environmental variables. Sediment communities exhibited higher diversity and structural stability compared to the water column, according to Shannon and Simpson indices results. Some phylum groups, such as Proteobacteria and Ignavibacteriae appear to dominate in the sediments, while Bacteroidetes, Plactomycetes and Verrucomicrobia were more prevalent in the water column. Elevated Bacteroidetes abundance was associated with increased in total and water-soluble organic carbon, suggesting links between carbon availability and heterotrophic taxa distribution. Overall, environmental gradients were associated with distinct compartment-specific microbial assemblages across the lake. This study provides an integrated view of microbial distribution within a freshwater ecosystem and highlight the role of environmental gradients in structuring aquatic microbiomes, while also underscoring the persistent limitation in knowledge regarding the functional roles of specific microorganisms in aquatic ecosystems.

Applied eDNA for Cross-Taxa Biodiversity Monitoring: A Case Study from Megadiverse Ecosystems

Vincent PRIÉ

Abstract: Biological surveys in megadiverse tropical environments are notoriously difficult, particularly for invertebrates, which represent the bulk of biodiversity. Yet given the unprecedented pace of biodiversity loss worldwide, we urgently need tools that are efficient, cost-effective, rapid, standardisable, and capable of detecting virtually any taxon across the tree of life. Environmental DNA (eDNA) metabarcoding bears such a promise. By capturing genetic material shed by organisms directly from environmental samples, it bypasses the need for direct observation or collection, making large-scale biodiversity monitoring feasible even in remote or logistically challenging settings. Here we present methods and results from a large-scale eDNA biodiversity monitoring programme conducted along the Maroni River (Suriname and French Guiana) since 2017, combining broad-spectrum primer sets designed to cover the whole tree of life with more targeted primers for specific taxonomic groups. Results reveal a global decline in biodiversity even in the most pristine parts of the river, with contrasting responses to human activities across biological realms.

BioMonWeek 2026
The European Conference for Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Data Management for Monitoring — Frameworks, data standards and infrastructures

DT08 Data infrastructures, coordination and interoperability

Tuesday 5 May, 11h30-12h30, Room Joffre G

Chairs: Maxime Coupremanne and Wouter Addink

Description: This session showcases how national monitoring systems and major data infrastructures, including GBIF, OBIS, LifeWatch, and DiSSCo, are working to integrate new and diverse types of monitoring data. Through concrete examples, speakers will illustrate interoperability challenges and needs arising when connecting datasets for integrative uses. The session highlights practical approaches, standards, and workflows that help reduce fragmentation and support a more connected, FAIR biodiversity data landscape.

From Physical Specimens to Digital Intelligence: Navigating the Interoperability Landscape with DiSSCo

Wouter ADDINK

Abstract: How can 1.5 billion physical specimens across hundreds of institutions become a single, machine-actionable dataset for European biodiversity monitoring? Can we bridge the gap between a museum drawer and a genomic sequence? In this presentation, you will hear about the practical journey of the Distributed System of Scientific Collections (DiSSCo) as it transitions from a visionary project to a functional European Research Infrastructure (ERIC). You will discover how we build a unified data fabric that connects specimens, sequences and observations into a seamless ecosystem. You will hear about our cross-infrastructure integration efforts and how we move beyond "linking by name" to "linking by identifier," ensuring that a researcher investigating a decline in pollinator populations can trace every data point back to a verifiable physical voucher. We will dive into the technical core of our interoperability strategy. You will gain insights into: openDS Implementation: The successes and growing pains of deploying the open Digital Specimen (openDS) specification as a common language for diverse biological and geological collections. The Shift to Darwin Core Data Packages (DwC-DP): Moving to structured data packages to handle complex relational data without losing information in translation. You will hear about significant challenges we encounter regarding license fragmentation, technical debt of legacy Collection Management Systems and maintaining provenance and attribution. Finally, we will present how DiSSCo allows integration of historical baseline data from collections with real-time monitoring streams, enabling AI-driven models to predict ecosystem shifts with increased accuracy. By the end of this session, you will understand how DiSSCo is not just digitizing the past, but building a digital foundation that supports the future of European biodiversity research.

Insights from the UK offshore wind environmental data architecture to support strategic monitoring

Ellen JONES, Chloe Figueroa Ashforth, Emma Seal, Dan Lear

Abstract: The Marine Biological Association (MBA) Data Team has undertaken an analysis of the UK's offshore wind environmental data architecture, as part of a Defra-funded project to support the development of a strategic monitoring framework for offshore wind farms aiming to deliver a coordinated, ecosystem-based approach to environmental monitoring. The project collated information from existing literature and from interviews with key stakeholders in the offshore wind industry to build a picture of the current data flows, challenges and opportunities seen across the sector. The MBA engaged with 19 stakeholders including developers, environmental consultants, academic institutions, regulators and statutory bodies through an online questionnaire and an online interview to find out about the current journey of their data, their perspective and experiences. The questionnaire and interviewed covered their data collection, quality assurance, sharing, storage and reporting processes, any feedback loops currently being used to feed data back into regulatory processes and project design, key data sharing platforms, the main barriers across the data lifecycle, and leverage points that could be addressed to improve data governance, interoperability and future strategic monitoring. This talk will cover the methodology, and key findings uncovered during the project, highlighting the future opportunities for enabling better data flows and fostering collaboration and supporting innovation to help deliver projects more efficiently while meeting environmental regulations.

Biodiversity Knowledge Hub Bridging RIs, Aggregators & Communities: Past, Present & Future

Christos ARVANITIDIS, Joaquin Lopez Lerida, Cristina Huertas Olivares, Alberto Basset, Sara Montinaro, Lucia Vaira, Nikos Minadakis, Michalis Griniezakis, Julio Lopez Paneque, Niels Raes, Lyubomir Penev

Abstract: Between 2021 and 2024, the Horizon-funded project Biodiversity Community Integrated Knowledge Library (BiCIKL) demonstrated how interdisciplinary collaboration and FAIR data integration can transform biodiversity research. By connecting research infrastructures, scientific repositories and expert communities, BiCIKL reduced fragmentation and enabled centralized access to interoperable biodiversity knowledge. A major outcome was the Biodiversity Knowledge Hub (BKH), a platform providing seamless access to data, tools and workflows to support research and evidence-based conservation. Building on this foundation, the newly launched Biodiversity Meets Data (BMD) project significantly advances the BKH ecosystem. BMD focuses on integrating high-throughput biodiversity tools, AI-powered species identification services, and strengthened connections to global infrastructures such as GBIF. At its core, BMD prioritizes the standardization and harmonization of biodiversity data across spatial, temporal and taxonomic dimensions, ensuring interoperable and policy-ready outputs. BMD also mobilizes historical baseline data from literature and legacy reports, unlocking underused biodiversity knowledge for long-term trend analyses and restoration target setting. By combining contemporary monitoring data with historical evidence, BMD enhances the capacity to assess biodiversity change across terrestrial, freshwater and marine ecosystems, from local to national scales. All these functionalities converge in the BMD Single Access Point, designed as an integrated and scalable service within the BKH framework. Through this evolution, BMD moves from knowledge integration to biodiversity intelligence, strengthening Europe's capacity to deliver harmonized, data-driven solutions for conservation, restoration and environmental governance.

A flexible pipeline for using open biological data to create regional biodiversity maps

Sam Wenaas PERRIN

Abstract: Making effective use of the cornucopia of occurrence data that has been made available by the information age is vital in our efforts to reliably map biodiversity and prioritise areas for conservation and further study. The Global Biodiversity Information Facility (GBIF) contains over 3.5 billion occurrences, but the diversity of the datasets that make up such an infrastructure means that using this data in species distribution models can be difficult. Being able to leverage this diversity represents a huge step forward in biodiversity monitoring. GBIF is replete with spatially and temporally extensive occurrence data collected by citizen scientists, but this data lacks standardised sampling protocols and is often heavily biased towards more populated or accessible areas. On the other hand, structured datasets which include sampling protocols and species checklists are more informative, but are usually limited in taxonomic and spatial scope. Here, we present the Hotspots project, the centrepiece of which is a flexible pipeline for using open data to create biodiversity maps, using terrestrial Norway as a case study. The pipeline uses integrated Species Distribution Models (iSDMs) to incorporate both occurrence-only data and more systematically sampled data, employing the strengths of both in one modelling framework. The resulting models produce taxa-level species richness estimates, giving a broad view of biodiversity at the national scale. They can also produce estimates at more management-specific levels, such as threatened species, functional groups or species of cultural significance. In addition, our pipeline can output maps of both sampling intensity and estimate uncertainty. These give informed indicators of where a lack of data is most limiting our understanding of terrestrial biodiversity, and where increased biological monitoring can increase our understanding of the spatial distribution of biodiversity.

Parallel Publishing to GBIF & OBIS: Streamlining Marine Biodiversity Data Sharing

Stephen FORMEL

Abstract: Publishing marine to OBIS and GBIF simultaneously can save time and ensure your data reaches wider audiences, leveraging the distinct yet overlapping communities of each network. This presentation, part of the GBIF North America 2026 Nodes Meeting and Training, explores best practices for publishing marine-focused datasets simultaneously to the Global Biodiversity Information Facility (GBIF) and the Ocean Biodiversity Information System (OBIS). We highlight the benefits of parallel publishing, including broader visibility and improved data interoperability, and discuss key differences in data requirements between the two networks. Practical guidance is provided for using tools such as the Integrated Publishing Toolkit (IPT), aligning taxa with WoRMS, and managing flagged or dropped records. We discuss how OBIS and GBIF workflows can be harmonized, while maintaining data quality across platforms. This presentation offers actionable insights for researchers and data managers aiming to streamline marine data publication to global biodiversity repositories, while ensuring compliance with community standards.

DT07 Standardising and sharing survey and monitoring data through GBIF and OBIS

Tuesday 5 May, 16h30-17h30, Room Joffre G

Chairs: Kate Ingenloff and Dan Lear

Description: The Darwin Core Archives (DwC-A) and the emerging Darwin Core Data Packages (DwC-DP) provide practical solutions for making biological survey and monitoring data discoverable, interoperable, and reusable across platforms, institutions, and research programs such as the Global Biodiversity Information Facility (GBIF) and the Ocean Biodiversity Information System (OBIS). Join us to learn more about these data models from researchers, data managers, and/or practitioners who are applying the Darwin Core standard in real-world contexts. The session will conclude with an open Q&A and group discussion, allowing participants to share experiences and discuss opportunities and challenges in implementing these standards.

How a camera trap data standard enabled an ecosystem of interoperable tools

Peter DESMET

Abstract: Camera Trap Data Package (Camtrap DP, https://camtrap-dp.tdwg.org) is an open community-developed standard for the FAIR exchange and archival of camera trap data. Since its release in November 2023, the standard has been widely adopted by the camera trap community and is now the cornerstone of an ecosystem of interoperable tools. These include data management platforms (Agouti, Trapper, Wildlife Insights), R packages (camtrapdp, camtraptor, camtrapReport), publication tools (GBIF IPT) and visualization software (BioWatch, Wild Album). Together, they aid users in all aspects of the data life cycle and have become instrumental for meta-analysis in projects such as BIG_PICTURE. Camtrap DP has also gained the interest of the bioacoustics and image-based insect monitoring community. Through the Safe & Sound project and Insect AI COST action, we investigated how to extend Camtrap DP to facilitate their needs. We now plan to release a new version of the standard, while maintaining the existing software ecosystem.

Mobilising monitoring data to GBIF

Eva CORSSMIT, Jeroen Creuwels

Abstract: Effective biodiversity monitoring depends not only on robust field methodologies, but increasingly on how data are structured, standardised, and shared for reuse across scales and domains. Global infrastructures such as the Global Biodiversity Information Facility (GBIF) and the Ocean Biodiversity Information System (OBIS) provide essential platforms for integrating monitoring data, yet mobilising complex survey and monitoring datasets into these platforms remains a challenge for many data providers. In this talk, we present practical approaches and lessons learned from mobilising monitoring data to GBIF. We discuss the use of the DarwinCore to publish different types of monitoring data, including checklist data, occurrence data, and sample event data. Furthermore we discuss how to select appropriate extensions to the DarwinCore for datasets differing in monitoring objectives and study design. This includes differences in sampling effort, methodology, and temporal replication. We further address the specific challenges of structuring marine monitoring data for integration with OBIS, including the representation of sampling events, environmental context, and taxonomic resolution. By illustrating how marine datasets can be harmonised to meet both GBIF and OBIS requirements, we highlight opportunities to increase interoperability between terrestrial and marine biodiversity data infrastructures. The talk combines conceptual guidance with concrete examples, all aimed to support monitoring programmes, data managers, and researchers in making their data more FAIR (Findable, Accessible, Interoperable, and Reusable) and to increase the data quality in general. By improving data standardisation and sharing practices, biodiversity monitoring data can more effectively contribute to large-scale assessments, long-term trend analyses, and evidence-based conservation and policy decisions.

Standardising and sharing survey and monitoring data using DwC-A Event core with Humboldt extension

Salza PALPURINA, Kate Ingenloff

Abstract: Standardising the way we structure and share biodiversity monitoring data is essential for enabling large-scale synthesis, long-term trend analysis, and effective reuse across platforms such as GBIF and OBIS. The Darwin Core Archive (DwC-A) Event Core format has emerged as a powerful framework for representing multi-scale survey, sampling, and monitoring activities, yet many projects face challenges when attempting to capture environmental context, sampling design, and nested survey structure in a consistent way. The Humboldt Extension—developed through the Humboldt Core framework—offers an important enhancement, enabling richer, more explicit descriptions of sampling events, effort, and protocols. This presentation introduces the structure and logic of the DwC-A Event Core combined with the Humboldt Extension, demonstrating how this pairing supports complex monitoring datasets, including hierarchical events, standardised effort reporting, and comprehensive metadata about sampling methodologies. Through concrete examples, we will outline how this structure improves transparency, reproducibility, and interoperability across biodiversity monitoring programmes. Benefits such as enhanced comparability across surveys, improved suitability for modelling and trend analyses, and greater data discoverability will be highlighted, alongside potential drawbacks such as increased metadata requirements, steeper learning curves for data providers, and challenges when converting legacy datasets into the Event–Humboldt framework. By the end of the talk, participants will understand how the DwC-A Event Core with Humboldt extension supports robust, standardised sharing of biodiversity monitoring data, and how its adoption can strengthen the integration of survey and monitoring outputs across GBIF, OBIS, and broader research networks.

AURORA - A Shiny app designed to create Darwin Core Archives from messy biodiversity datasets

Álvaro Somensi, Sara M. Araújo, Heliana TEIXEIRA, Ana Hilário, Sofia Ramalho, Eva Ramirez-Llodra, Fábio L. Matos

Abstract: Biodiversity monitoring data are commonly stored in heterogeneous tabular formats, hindering standardisation, validation, and publication through public repositories. Researchers frequently encounter technical bottlenecks, including complex event hierarchies, taxonomic inconsistencies, and geospatial errors, that must be resolved before datasets can be submitted to global repositories such as GBIF and OBIS. To address these challenges, we developed an R Shiny application that provides an intuitive, end-to-end workflow for transforming raw datasets into publication-ready Darwin Core Archives (DwC-A). The application supports data ingestion from diverse tabular formats, enabling users to convert raw and tidy structures. An interactive mapping interface allows users to align user-specific fields with Darwin Core terms by combining manual

selection with automated suggestions and mandatory-field validation. The tool automates critical data cleaning tasks, including date standardization (ISO 8601), duplicate detection, and the validation and transformation of coordinates to the WGS84. Taxonomic integrity is ensured through integrated API calls to the WoRMS and GBIF Backbone Taxonomies, allowing users to select the most appropriate reference systems for marine or terrestrial datasets. The workflow generates core Darwin Core tables, including Event, Occurrence, and Extended Measurement or Fact (eMoF). Finally, a quality-control module provides diagnostics on data completeness and flags missing key fields. The resulting output is a standards-compliant Darwin Core Archive accompanied by structured metadata aligned with FAIR principles. By streamlining these time-consuming processes into a user-friendly interface, this application significantly reduces the technical barriers to biodiversity data mobilization and global sharing. The application is accessible to the public via a web browser and requires only an internet connection.

DT05a Tools for data use, curation, and management

Wednesday 6 May, 9h00-10h00, Room Sully 2
Chairs: Andrew Rodrigues, Dan Lear, Wouter Addink
Description: This session will showcase tools and approaches that support effective use, curation, and publication across the biodiversity data lifecycle, with a strong focus on the application of the FAIR data principles. Presentations will highlight tools and methodologies for data quality control, standardisation, documentation, and publication, as well as solutions that enable interoperability and reuse.

PlutoF platform enables FAIR management of ecological and eDNA data

Kristjan ADOJAAN

Abstract: PlutoF (https://plutof.ut.ee) platform is a web-based research data management solution designed to support a wide range of biodiversity data types and projects across multiple fields, including ecology, taxonomy, environmental monitoring, nature conservation, agriculture, and genetics. PlutoF provides modules for managing taxon occurrences (e.g., specimens in scientific collections, observations by citizen scientists, material samples, and DNA sequences from barcoding and metabarcoding studies), taxonomic classifications, measurements and traits, molecular experiments, and more. It allows users to manage datasets throughout the entire data lifecycle — from project design and data collection to publishing and archiving — in compliance with FAIR principles. PlutoF provides users with an easy-to-adopt and user-friendly interface for preparing their data for collaborative management and seamless publication.

Biodiversity repository

Reza ZAHIRI

Abstract: A biorepository is not merely a storage facility but an integrated research infrastructure that preserves voucher specimens, environmental samples, and associated metadata for long-term scientific use. By providing verifiable physical evidence, biorepositories underpin biodiversity assessments, enable taxonomic validation, and allow re-analysis with emerging methods. In this way, they transform short-term monitoring efforts into a lasting ecological record. Centralized repositories serve multiple functions: they safeguard reference material for taxonomic training, support the development of molecular and imaging technologies, and facilitate retrospective analyses and future projections under climate and land-use change. Through standardized sampling, documentation, and the integration of high-quality metadata—such as locality, habitat, and environmental parameters—biorepositories convert individual specimens into a coherent, accessible information system that strengthens biodiversity research and monitoring.

Adaptable Standardized Methods Reporting (ASMR) for fieldwork studies: lesson from a systematic review on visual-based investigation of mesophotic ecosystems

Claudia CAMPANINI, Martina Coppari, Cristina Gioia Di Camillo, Torcuato Pulido Mantas, Camilla Roveta, Daniel Gómez-Gras, Carlo Cerrano

Abstract: Research in many areas, such as biology, ecology, and conservation, often depends heavily on fieldwork. However, while rigorous and standardized method reporting has become increasingly applied for laboratory procedures and data analysis, fieldwork method reporting remains comparatively vague and heterogeneous, particularly in some systems such as the marine realm. For instance, a recent global systematic literature review analyzing 994 publications on mesophotic research found that the majority of studies either did not employ standardized protocols and/or provided insufficient details in their methodological descriptions. To contribute to filling this gap, we propose the Adaptable Standardized Methods Reporting (ASMR), a reporting guidance framework for fieldwork studies that consists of a reporting checklist, a flow-chart showing ASMR integration with other established standards, and a metadata term list. The latter encompasses terms related to 1) sampling design, methods, and equipment; and 2) ecological context, e.g. habitat, substrate, geomorphology. ASMR terms can extend the Darwin Core Standard by providing more detailed information on fieldwork methods. ASMR and its compilation guidelines will also favor machine readability, and data homogenization by referring to established classification schemes. While the checklist applies to all environments, the current version of the metadata list was designed to cover only marine fieldwork activities;

nevertheless, it can be refined through users feedback and adapted to better include other environments and methodologies. Moreover, it is expected that the research community will benefit from ASMR tools at different stages: documentation, revision, publishing, and data collation for synthesis research. Most importantly, ASMR will enhance methodological transparency, reproducibility, and comparability across marine studies, finally contributing to the adoption of standardized fieldwork protocols.

Tools and resources for the marine biodiversity community- Powered by EMODnet Biology

Joana Beja, Leen Vandepitte, Tobias Büring, Benjamin Weigel, Marina Lipizer, Bart Vanhoorne, Dan LEAR, EMODnet Biology consortium

Abstract: EMODnet Biology, the EU service for marine in situ biodiversity data and data products, was established in 2009 and currently comprises a consortium of 30 organisations spread across Europe and includes research, government and private organisations. The management of marine biodiversity data presents significant challenges due to the complexity of required metadata, the necessity of rigorous quality control procedures, and the adoption of standardized vocabularies. In parallel, data discovery remains difficult because of the heterogeneity and structural complexity of existing data infrastructures. To address these issues, the consortium has developed several key tools and resources, over the last 15 years, designed to support both data providers and end users. The continued development and refinement of these services will remain a strategic priority in the years ahead. In this work we will showcase the EMODnet BioCheck tool, which supports data providers in performing data quality control , present the changes currently being implemented and highlight additional resources including two R Packages (emodnet.wcs and emodnet.wfs) that allow data users to query and download data from not only EMODnet Biology but also other EMODnet thematics. Alongside these tools, there are a number of resources, training materials and informational content freely and openly available to all providers and users. To promote awareness of the developments achieved to date, the consortium's tools and online resources have been presented at numerous workshops targeting diverse stakeholder groups, ranging from Regional Sea Conventions to EU-funded projects, with the objective of fostering data sharing and facilitating data use.

TreMs Collect and IBP Collect: two new apps designed for collecting data on tree related microhabitats and the Index of Biodiversity Potential

Nicolas GOUIX, Bossaert M, Bütler R., Courbeau B., Emberger C., Marty P., Norel H., Larrieu L.

Abstract: The recording of tree-related microhabitats (TreMs) and the assessment of the Index of Biodiversity Potential (IBP) are increasingly being implemented by

foresters and protected area managers. Re-commendations aimed at maintaining a minimum density of habitat-trees are now integrated into most forest policies and certification schemes in Europe. An international database of TreMS mana-ged by French researchers currently contains data on around 260,000 trees recorded in many coun-tries. Similarly, the IBP has spread to 18 countries in Europe and beyond, under the guidance of an international expert committee. Given the wide diversity of users, data centralisation has become a key issue in supporting research aimed at better understanding the relationships between biodiversity and forest ecosystem characte-ristics. Nevertheless, consolidating data at an international scale remains challenging due to a lack of dedicated tools. Moreover, to ensure wider adoption, it is crucial to provide user-friendly data entry interfaces linked to databases that enable automatic analysis and graphical outputs. For this purpose, we have developed two forms based on the Android application ODK Collect to promote and facili-tate the field records of TreMs and the IBP data within a stable framework. TreMs Collect and IBP Collect have been already used in several research programs as well as by forest and natural area managers in Europe and North America in their routine diagnostics. Avai-lable in several languages, these tools simplify the flow fromof field data collect to databases and open up new possibilities for using these data in biodiversity monitoring and management planning.

DT05b Tools for data use, curation, and management

Wednesday 6 May, 10h00-11h00, Room Sully 2
Chairs: Andrew Rodrigues, Dan Lear, Wouter Addink

Description: This session will showcase tools and approaches that support effective use, curation, and publication across the biodiversity data lifecycle, with a strong focus on the application of the FAIR data principles. Presentations will highlight tools and methodologies for data quality control, standardisation, documentation, and publication, as well as solutions that enable interoperability and reuse.

Harmonising policy relevant species data with Catalogue of Life

Olaf BÁNKI, Camila Plata, Mette Palitzsch Lund

Abstract: Policy-relevant species checklists, established by national and regional governmental bodies, are essential inputs for biodiversity policy and decision-making. Built on scientific evidence, they also incorporate economic, regulatory, and societal considerations. Given their legally binding nature, these lists can define entire frameworks for biodiversity management and conservation, making them critical references for monitoring and planning. Despite significant progress by global non-profit initiatives in making species information

interoperable and openly accessible, national and regional governmental institutions have largely lagged behind in adopting similar strategies. Here we present the collaborative work, executed through the Horizon Europe project Biodiversity Meets Data (ID No 101181294), between the European Environment Agency (EEA) and the Catalogue of Life (COL) to pilot a strategy for mobilizing EU policy-relevant species data into ChecklistBank, COL's open data infrastructure. ChecklistBank already hosts over 400 policy-relevant checklists, establishing it as a key platform for improving the access, visibility, and reuse of biodiversity data globally. This pilot operated on two fronts: first, digitizing and structuring the taxonomic information embedded in European Commission legal documents, beginning with the Habitats and Birds Directives and the Invasive Alien Species Regulation; and second, exploring harmonization processes between these instruments and the Catalogue of Life, with the aim of facilitating data use by users like scientists, natura 2000 site managers, and EU member states responsible for biodiversity management. We present the results of this pilot and reflect on its broader implications for future work.

Breaking Biodiversity Data Silos: LUCA’s Unified Ingestion Pipeline and Taxon Richness API

Kristy DEINER

Abstract: Biodiversity data is currently trapped in "methodological silos." Acoustic recordings, camera trap footage, and eDNA samples provide different lenses on ecosystem health, but they rarely speak the same language. This fragmentation prevents a holistic view of species richness and slows down the adoption of nature-positive metrics. The challenge isn't just technical; it’s economic. Data providers lack sustainable incentives to share high-resolution datasets. LUCA addresses this by creating a unified ingestion pipeline that standardizes multi-modal data into a 1km-resolution species richness API. By introducing a revenue-sharing model where subscribers fund data providers, we can turn "isolated data points" into a "global nervous system" for the planet. In this talk we will show how we bridge the gap between fragmented raw data and the actionable, high-fidelity insights required for the next generation of MRV.

Flipping the Databerg: Surfacing Biodiversity Data Sunk in Environmental Assessment Reports

Maite TELLETXEA, Rafael MIRANDA, David GALICIA, Arturo H. ARIÑO

Abstract: The global biodiversity crisis, driven by human development factors such as habitat loss, climate change, and overexploitation, requires efficient data management and accessibility to monitor biodiversity and guide conservation efforts. Environmental assessment (EA) is an essential tool for minimizing the environmental impact of human development, generating vast amounts of biodiversity data during field surveys. However, much of this information, also in

Spain, remains imprisoned in technical reports and is often inaccessible after being partly included in Records of Decision (RODs). As a result, these dark data remain underused, limiting their potential to inform monitoring and decision-making processes. We mobilized—through GBIF—1,263 previously dark primary biodiversity records (PBR), from RODs published in the Spanish Official State Gazette between 2013 and 2023, related to species listed in the Spanish Catalogue of Threatened Species and the List of Wild Species under Special Protection Regime. Data were collected using automated text-mining techniques and manually curated to correct errors and to identify and georeference actual PBR. We examined the mobilization of EA-related dark data for 43 species listed in the Spanish Catalogue of Threatened Species to improve their digital accessible knowledge. Based on IUCN Red List criteria, we evaluated the impact of EA-related dark data on two required metrics: extent of occurrence (EOO) and area of occupancy (AOO). Our results show that incorporating dark data increased EOO and AOO for 23% and 93% of threatened species, respectively, including endangered species like Aquila adalberti. We highlight the importance of bringing to light data collected during EA processes and ensuring that data are findable, accessible, interoperable, and reusable (FAIR). Mobilizing EA-related dark data is a cost-effective way to strengthen biodiversity monitoring, support better decision-making, and justify biodiversity conservation.

Connecting the dots: the essential role of taxonomic names to enable connecting monitoring data over time, space and existing knowledge.

Donat AGOSTI, Ruch, Patrick; Sautter, Guido

Abstract: Robust biodiversity monitoring depends on the ability to compare data across space, time, and programs—yet this comparability is fundamentally constrained by inconsistent taxonomic practices. Despite advances in data collection and analysis, taxonomic identification often remains weakly standardized, poorly documented, and difficult to trace, limiting the reliability, interoperability, and long-term value of biodiversity data. We argue that taxonomic identification must be treated as a first-class, citable data object within biodiversity monitoring workflows. Each identification should explicitly link specimens or sequences to taxonomic names, their underlying taxonomic concepts, and the scientific evidence supporting them, such as traits and others listed in the taxonomic treatments. This is particularly urgent given the dynamic nature of taxonomy, where names and their interpretations evolve over time. Without such traceability, biodiversity indicators risk becoming irreproducible and incomparable. Using Metaplantcode as an exemplar Biodiversa+-project, we demonstrate practical solutions to this challenge. We show how to systematically cite taxonomic names, use TreatmentBank or the Catalogue of Life to link them to authoritative resources such as Catalogue of Life, and generate structured, machine-readable data in cases where digital copies of the respective taxonomic

works or treatments are lacking. By integrating these FAIR and AI-ready taxonomic data into infrastructures such as Biodiversity PMC, we enable scalable, transparent, and reproducible biodiversity monitoring. It enables furthermore to explore the published data known in publications. This approach directly supports Biodiversa+ priorities by strengthening the scientific foundation of biodiversity assessments and enhancing the policy relevance of monitoring data.

Literature triage to support Island Biodiversity Monitoring

Patrick RUCH

Abstract: Biodiversity research increasingly relies on vast quantities of scientific literature, therefore developing screening tools to better scan the literature is essential. We developed an automatic triage system that we apply to Biodiversity Island monitoring. Islands host 20% of the world biodiversity yet this is increasingly at risk from global change which makes island epicenters of species extinctions. Islands are by definition isolated and their essential biodiversity knowledge is stored in scattered publications. This knowledge needs to be liberated and synthesized to make informed decisions for monitoring and conservation. We started by querying OpenAlex with broad coverage Boolean equations. Further, a binary classifier for island ecosystem publications (BioMoQA project) was developed using pre-trained bidirectional language models. After manual selection, the articles are then indexed into SIBiLS/BiodiversityPMC (https://biodiversitypmc.sibils.org/). Using 5-fold cross-validation on 1,434 Abstracts, we compared domain-specific biomedical transformers (e.g., BioBERT, BiomedBERT) for life sciences against general-purpose models (e.g., BERT, RoBERTa), which are combined with ensemble learning. Binary cross-entropy ensembles achieved best performance with ROC-AUC of 0.926. The reported model performance is competitive with curator inter-rater agreement (expert kappa ~0.78). The classifier is now integrated in the SIBiLS\BiodiversityPMC platform, and through weekly screening ensures consistent up to date coverage of island biodiversity literature, thus supporting the harmonization of global island biodiversity monitoring efforts. The service platform is currently being applied to other biodiversity assessment projects and could likely serve a large set of biodiversity communities.

DT02 Data Workflows and Pipelines for WorkFlowHub

Wednesday 6 May, 11h30-12h30, Room Sully 2
Chairs: Sandra MacFadyen and Stephen Formel

Description: This session focuses on designing, documenting, and sharing reusable data workflows and pipelines through WorkFlowHub. It highlights practical approaches for structuring workflows that span data ingestion, management, integration, analysis, and dissemination, with reproducibility and transparency embedded throughout. Contributions will showcase exemplar workflows, reference architectures, and workflow patterns that support interoperability, standardisation, and reuse across domains. Emphasis is placed on making workflows findable, citable, and adaptable, enabling communities to reduce duplication of effort, strengthen data stewardship, and translate complex data streams into robust, decision-ready information products.

From Observation to Decision: A Reproducible Workflow Architecture for Biodiversity Monitoring

Sandra MACFADYEN

Abstract: Biodiversity monitoring operates in a notitian age (data-rich era), yet the evidentiary chain from observation to decision remains fragile. Rapidly expanding environmental data streams are dispersed across portals, delivered in heterogeneous formats, and accompanied by inconsistent metadata, limiting the translation of raw observations into decision-ready indicators. In protected areas, these challenges are compounded by uneven resourcing, fragmented data practices, and limited capacity for sustained data stewardship and reproducible analysis. Here, we present an exemplar workflow for transparent and reproducible environmental research that functions as a structured reference architecture for protected-area monitoring programmes. Our six-stage monitoring architecture maps onto recognised biodiversity informatics pipelines: field data collection (B) corresponds to data inflow (1), while research planning and design (A) operationalises the data management plan (2) by specifying standards, formats, conditions of use, roles, and resourcing. Data cleaning and quality control (C) supports data centralisation (3) through standardisation and validation of inputs. Data integration and analysis (D) aligns with information processed (4), transforming integrated datasets into decision-linked indicators and information products. Data sharing and dissemination (E) corresponds to data services (5) that enable discovery, querying, analysis, and export. These products then feed into research and development (6), knowledge synthesis (7), and implementation (8), providing feedbacks that refine monitoring objectives, standards, and outputs over time. WorkFlowHub provides a practical venue to curate the workflow as a findable, citable pattern. This supports consistency across landscapes, reduces duplication of effort, and provides reusable templates that strengthen protected-area monitoring capacity.

A Dream of a Lean Marine Metadata Machine

Stephen FORMEL

Abstract: Marine biodiversity researchers invest enormous care in experimental design, sampling protocols, and statistical analysis. But the metadata that would make their observations discoverable and reusable by other scientists and computational systems receives less attention. This is not always negligence; structured metadata modeling often falls outside the training and tooling available to most researchers. As a result, valuable scientific results and context remain invisible to the global data systems that depend on open web standards to function. Closing this gap requires not just better infrastructure, but workflows and tools that make rigorous metadata practice tractable for the scientists who need to use them. MARCO-BOLO's Work Package 1 is tackling this gap and pushing further. Rather than targeting a baseline of compliance with FAIR principles, WP1 is actively exploring how expressive and semantically rich biodiversity metadata can become when open standards, purpose-built tooling, and domain scientists are brought together, and pushed, deliberately. The result is an experimental metadata catalog that treats description not as an administrative burden but as a scientific output in its own right. The catalog is intentionally lean: built on LinkML, an open modeling language, and running entirely on free infrastructure: GitHub for version control and automated pipelines, Google Sheets for collaborative data entry. The model aims to capture the full complex actions and outputs of a large marine science project: datasets, documents, personnel, organisations, instruments, platforms, sampling locations, taxa, protocols, and the Essential Ocean Variables and Essential Biodiversity Variables they produce. The captured metadata is transformed through an automated pipeline into schema.org-aligned JSON-LD making MARCO-BOLO's scientific outputs legible to the crawlers and aggregators that index the internet's knowledge graph, including ODIS and search engines like Google. The approach and its components are openly available and designed for reuse by other biodiversity observation projects facing the same challenges. This presentation describes the catalog's architecture, the workflows developed to make metadata modeling accessible to domain scientists, and the lessons learned at the frontier of what structured biodiversity metadata can express.

Gbifgaps – An open-source R pipeline for identifying biodiversity data gaps

Lena THÖLE, Kevin Holston, Veronika Johansson

Abstract: GBIF provides unprecedented access to biodiversity occurrence data, yet spatial, temporal, and taxonomic biases are rarely assessed systematically at a national level. Without such assessments, monitoring efforts risk duplicating well-sampled areas and taxa while neglecting critical gaps, particularly for threatened species and under-surveyed regions. We present gbifgaps, an open-source R pipeline that provides a reproducible framework for identifying data gaps using GBIF occurrence cubes and national taxonomic backbones. The pipeline analyses three dimensions: spatial gaps (under-sampled grid cells using EEA reference grids), temporal gaps (seasonal biases, declining collection effort, and data staleness patterns), and taxonomic gaps (coverage of the national

species checklist in GBIF, with particular attention to threatened species on national red lists). All configuration is externalized to a single YAML file, making the pipeline adaptable to any European GBIF participant country. Results are delivered through reports as well as two interactive Shiny dashboards. A Gap Analysis Dashboard supports node managers in prioritizing targeted data mobilization by visualizing spatial coverage, temporal trends, taxonomic completeness, and ranked priority lists. A Biodiversity Explorer enables researchers and the public to search species, view distribution maps, and browse threatened species. We demonstrate the pipeline using Sweden as a case study, where analysis of the Dyntaxa taxonomic backbone against GBIF occurrence data reveals spatial biases toward population centers, temporal peaks driven by citizen science, and taxonomic gaps concentrated in under-recorded groups such as fungi and invertebrates. Template configurations for Norway and a roadmap for non-European grid systems are included. This work provides GBIF nodes with a practical tool to evaluate data fitness for use and communicate monitoring priorities through interactive visualizations.

Scaling biodiversity monitoring using GBIF species occurrence cubes

Andrew RODRIGUES

Abstract: Global biodiversity monitoring increasingly relies on large volumes of occurrence records aggregated from heterogeneous sources. The Global Biodiversity Information Facility (GBIF) provides access to billions of biodiversity observations, but transforming these raw records into analysis-ready datasets suitable for monitoring and reporting remains a major challenge. Species occurrence cubes provide a scalable approach to organize biodiversity data across space, time, and taxonomy, enabling efficient generation of datasets for biodiversity assessments. Occurrence cubes aggregate filtered GBIF records into multidimensional summaries of occurrence counts for combinations of user-defined taxa, spatial grids, and temporal intervals. This structure reduces data complexity while preserving key dimensions required for biodiversity indicators, trend analyses, and modelling workflows. We present the implementation of species occurrence cubes in GBIF and demonstrate how they support reproducible biodiversity monitoring workflows. By combining standardized aggregation rules with persistent query definitions, cubes enable analysis-ready biodiversity summaries to be regenerated and reused across monitoring pipelines. Occurrence cubes therefore help bridge the gap between large-scale biodiversity data infrastructures and operational biodiversity monitoring and reporting.

Supporting the biodiversity data lifecycle with the LifeWatch Italy digital infrastructure

Ilaria ROSATI, Martina Pulieri, Cristina Di Muri, Andrea Tarallo, Davide Raho, Francesco De Leo, Mariantonietta La Marra, Lucia Vaira, Alberto Basset

Abstract: Biodiversity and ecosystems services are declining at an alarming rate, a trend expected to intensify due to human-induced climate change. Addressing this crisis requires intensive data collection or mobilisation initiatives coupled with efficient methods for biodiversity data integration to support complex analyses and evidence-based decision-making. Ensuring that research data are FAIR (Findable, Accessible, Interoperable, and Reusable) is essential to enable their effective reuse. In this context, national research infrastructures play a key role in supporting the generation, management and publication of FAIR research data. This contribution presents the LifeWatch Italy digital infrastructure as a comprehensive solution for biodiversity and monitoring data management, by providing platforms and services sustaining the core stages of the research lifecycle, including data collection, curation, publication, analysis and reuse. At the core of the infrastructure lies the Data Portal, used to share and manage data and associated metadata through a curation workflow. The workflow includes comprehensive (meta)data validation, covering structural and syntactic checks, taxonomic match against national and international taxonomic backbones (Italian taxonomic backbone, CoL, WoRMs and WFO) and the use of controlled vocabularies for metadata annotation. Interoperability is ensured through the adoption of international standards (EML 2.2.0 and Darwin Core), persistent identifiers, and open formats (csv, txt, XML and JSON). Moreover, this contribution also presents new synergies and strategies that will be adopted, at national level, to boost the interoperability of cross-disciplinary research infrastructures and to reduce fragmentation of biodiversity data.

DT11 WORKSHOP How to handle derived data products and outputs for EBVs and EOVs

Wednesday 6 May, 16h30-17h30, Room Sully 2

Chairs: Wiebke Pressé, Dan Lear, Guillaume Body, Stephen Formel, Lisa Benedetti

Description: This interactive workshop will focus on practical approaches for handling derived data products and analytical outputs supporting Essential Biodiversity Variables (EBVs) and Essential Ocean Variables (EOVs), with a strong emphasis on making them FAIR (Findable, Accessible, Interoperable, and Reusable), a particular focus on temporal trends. Through guided discussion and examples, the participants will explore what should and could be standardized (linear, smooth trends, uncertainties, spatial éléments), data standard options, infrastructure options, and common challenges in publishing, displaying and reusing derived data at scale. Descriptions of metadata (provenance, workflows, versionning) could also be discussed.

DT01 Biodiversity Data Cubes

Thursday 7 May, 10h00-11h00, Room Joffre G
Chairs: Quentin Groom and Niels Raes

Description: Biodiversity Data Cubes offer a new way to transform diverse biodiversity data into analysis-ready products for monitoring and reporting. This session introduces the concept of Biodiversity Data Cubes, and explores how standardized, FAIR biodiversity data can be organized across space, time, and taxonomy. We aim to cover how data cubes support biodiversity monitoring, indicators, and policy-relevant assessments, and highlight practical use cases and current challenges in moving from raw data to operational monitoring workflows.

Operationalizing Biodiversity Data Cubes for Open Science and Informed Policy

Lina ESTUPINAN-SUARZ, H. M. Pereira, N. Fernandez, C. Langer, E. Oceguera-Conchas, Q. Groom.

Abstract: Rapid advances in data acquisition technologies, combined with expanding reporting obligations under European biodiversity legislation, require analytical infrastructures capable of efficiently handling complex, multi-dimensional datasets. Biodiversity data cubes represent a key data infrastructure component, enabling structured storage, scalable querying, as well as integrated analysis across spatial, temporal, and taxonomic dimensions. In this talk, I present how this approach has been operationalized through the implementation of species occurrence cubes deployed by GBIF within the Biodiversity Building Blocks for Policy (B-Cubed) project, alongside the EBVCube format developed by GEO BON. Based on open records shared through GBIF, species occurrence cubes are generated using SQL-based queries that efficiently aggregate and harmonize multiple data sources. This cube-based architecture enables rapid querying of species data across Member States, taxonomic groups, and temporal scales (from months to years), using standard computing resources. The resulting cubes contain data organized by 'yearmonth', 'eeacellcode', 'countrycode', 'specieskey', and other categories. Using this approach, we assessed data availability relevant to EU biodiversity legislation, identifying spatial and temporal gaps that can guide policy and monitoring prioritization. Results are interpreted within the European Essential Biodiversity Variables (EBV) framework, linking data availability to monitoring objectives and promoting standardized data sharing through enriched metadata and structured formats such as the EBVCube format. We demonstrate how biodiversity data cubes enhance analytical transparency, reproducibility, and interoperability while lowering technical barriers of big data analysis. By aligning biodiversity data infrastructures with policy needs, this approach advances open science practices and strengthens the evidence base for biodiversity governance in Europe.

The b3verse: Research Software as a Reproducible Engine for Transnational Biodiversity Indicators

Ward LANGERAERT, Damiano Oldoni, Hanno Seebens, Lissa Breugelmans, Maarten Trekels, Mukhtar Muhammed Yahaya, Peter Desmet, Sabrina Kumschick, Sandra MacFadyen, Shawn Dove, Toon Van Daele.

Abstract: The transition from raw monitoring data to actionable policy indicators must be transparent, reproducible, and scalable to effectively address the global biodiversity crisis. The B3 project (Biodiversity Building Blocks for Policy) demonstrates how research software can function as a first-class scientific output by developing the b3verse, a modular suite of twelve interconnected R packages that transform heterogeneous biodiversity data, such as GBIF occurrence records, into standardized occurrence cubes and policy-relevant indicators. Built around a shared occurrence cube structure, the b3verse enables interoperability across taxa, regions, and monitoring schemes while preserving methodological flexibility. Standardized interfaces allow specialized packages to implement diverse indicator approaches, including general biodiversity indicators (b3gbi), phylogenetic diversity (pdindicatoR), and alien species impact (impIndicator), while producing comparable and harmonized outputs. Integrated uncertainty estimation and validation procedures ensure statistically robust and reproducible results. Developed through collaboration across nine countries and twelve research institutes, the b3verse reflects interdisciplinary expertise spanning biodiversity science, ecological modelling, data engineering, and science-policy integration. A shared development guide defines standards for interfaces, testing, and documentation, ensuring consistent quality and long-term maintainability across packages. Distribution via R-Universe supports coordinated releases and straightforward adoption. All releases and associated data snapshots are archived on Zenodo to provide stable, citable references beyond the project lifespan. Framed as reusable research infrastructure rather than a single analytical workflow, the b3verse strengthens transnational biodiversity monitoring through open and reproducible software and supports coordinated, evidence-based policy action.

Biodiversity Meets Data: A data cubing engine for analysis- and modelling-ready data in biodiversity monitoring

Niels BILLIET, Mathias Dillen, Quentin Groom

Abstract: Biodiversity Meets Data (BMD) seeks to equip policymakers and natural resource managers with data-driven tools necessary to make evidence-based decisions regarding the environment and its inhabitants. These tools rely heavily on high-quality data that captures both the biotic and abiotic factors characterizing sites of interest. However, challenges arise when harmonizing data types from different sources: critical information is fragmented across multiple

providers and lacks interoperability due to differences in formatting and storage. To resolve this, the BMD data cubing engine implements robust pipelines designed to produce spatially and temporally harmonized datasets. By aligning biological records with Earth Observation (EO) data, the engine generates products that are immediately usable in downstream analysis workflows. Crucially, to handle datasets with asymmetrical temporal axes—such as discrete annual records versus multi-year ranges—we utilize a hierarchical data model (datatree). This approach successfully structures complex temporal granularity without relying on artificial interpolation, preserving the integrity of the original data. This presentation will explore the primary challenges encountered when integrating EO data with biodiversity records. Additionally, we will present our current data schema design, offering a practical architectural template for how multi-dimensional ecological data can be efficiently structured and stored.

Optimising the Habitats Directive top-down assessment and bottom-up reporting in Europe

Ana Luísa MACHADO, Heliana Teixeira

Abstract: Robust, comparable and timely assessments are essential to support implementation of the EU Habitats Directive and consistent Article 17 reporting across Member States and biogeographical regions. While national monitoring remains the cornerstone of assessments, persistent data gaps and uneven sampling effort affect many taxa. Meanwhile, citizen science and biodiversity infrastructures have rapidly increased open occurrence data availability, notably through GBIF—creating an opportunity to complement statutory evidence, provided fitness-for-purpose and bias are addressed. Within the B-CUBED project, we developed a reproducible workflow to integrate Article 17 reporting needs with GBIF data. The approach builds simple, standardised biodiversity "data cubes" from GBIF occurrences to structure records across space, time and taxa, enabling rapid visualisation of key occurrence and biodiversity parameters. Crucially, it also includes tools to evaluate robustness and diagnose spatial and temporal sampling biases, supporting informed interpretation by Member States and the European Environment Agency (EEA). In our case study, ~80% of species subject to obligatory reporting have GBIF-mediated distributional information, and coverage is increasing over time, largely driven by growing citizen science mobilisation. We illustrate how such cubes can help strengthen evidence for taxa with recognised monitoring challenges (e.g., marine mammals) and support the exploration of potential distribution shifts, including movement beyond traditionally reported biogeographical regions, potentially consistent with climate-driven change. Overall, cube-based, bias-aware integration of open occurrence data can improve consistency, transparency and scalability of both bottom-up reporting and top-down evaluation, while promoting FAIR data mobilisation.

DT03 Environmental DNA survey data publication, management and interoperability

Thursday 7 May, 11h30-12h30, Room Sully 1

Chairs: Birgit Gemeinholzer, Stephen Formel, Pieter Provoost, Rasa Bukontaite

Description: Biodiversity monitoring relies on data publication frameworks that can be automated and are aligned with established data standards to ensure compatibility and interoperability with existing data networks. Important are the establishment of routine data pipelines from sampling in the field to downstream analyses with corresponding metadata as well as the documentation of failures and data gaps. This session will explore the full spectrum of data availability in routine monitoring, from collection to integration, and highlight the critical role of standardised, automated workflows in advancing open and reusable biodiversity data.

Advancing eDNA Quality: Validation Frameworks and FAIR metadata

Katie CLARK, Lynsey Harper, Eulyn Pagaling, Anita Hashmi, Nick Dunn, Debbie Leatherland, Max John, Mike Prince

Abstract: Environmental DNA (eDNA) is transforming the way we monitor the environment. However, there is often variability within workflows generating DNA data, with sometimes limited understanding on how these changes may affect derived metrics. It is essential for national monitoring programmes that the data collected is robust and repeatable. DNA data generated by public bodies also needs to be open access where appropriate, with the species data mobilised to suitable repositories, such as the National Biodiversity (NBN) Atlas for UK terrestrial and freshwater species data. This presentation highlights two areas that Natural England (a UK Government Body) has been focussing on: 1) A metabarcoding validation framework developed with the James Hutton Institute and in consultation with the international eDNA community, which evaluates metabarcoding assays across diverse criteria, including climate-habitat, uses and limitations. We anticipate the framework will standardise the use of metabarcoding assays and widen the opportunity for the use of eDNA across ecological monitoring. 2) Our work to standardise DNA metadata and ensure data is Findable, Accessible, Interoperable and Reproducible (FAIR), including contributing to the FAIR eDNA working group led by Miwa Takahashi. Internally we also had a need to include fields that improved documentation of methods, particularly in the laboratory and bioinformatic stages. This led to working with the NBN Atlas to establish their provision for key DNA-related metadata with a focus on quality, improving the overall quality of DNA species records uploaded to the Atlas and developing processes to deal with sensitive records.

The digital ecosystem of eDNA data in Europe

Katrina EXTER, Emilie Boulanger, Antonio Camacho, Cedric Decruw, Pascal Hablützel, Tiina Laamanen, Arnaud Laroquette, Kristian Meissner, Veera Norros, Antonio Picazo-Mozo, Marc Portier, Laurian Van Maldeghem, Peter Woollard

Abstract: In the Europe Horizon project eDNAqua-Plan we have surveyed the ecosystem around eDNA data in Europe. We have mapped the connectivity, commonality, and differences for all the players in the game, including those who: sample, store samples and hold collections, process and create data, work on bioinformatics, build reference libraries, provide infrastructures for publishing data, provide and use (meta)data and taxonomic standards. A number of workshops have been held, soliciting feedback from various stakeholder groups on our landscaping and the gaps identified, and to incorporate their own ideas in our blueprint for an improved eDNA digital ecosystem. We will present this blueprint and our roadmap and sustainability plan, that together can help Europe achieve the goal of a smoother, less frustrating, more productive environment for those who want to publish their (meta)data, those who provide the publishing infrastructures, and those who want to find and use data.

dbDNA - An expert identifier and sequence distance-driven rating system for reliable taxonomic annotation of metabarcoding data

Arne BEERMANN

Abstract: Identifying specimens to species or higher taxonomic level is a key component of biological monitoring. In recent times, species identification has been facilitated through high-throughput genetic methods, in particular DNA metabarcoding. One key aspect, that limits direct comparability of data and in particular hampers the defensibility of the results as part of regulatory monitoring tasks are uncertain taxonomic assignments via reference sequence databases. While these should ideally be complete, open, well-maintained, curated and updated continuously, they often lack quality assurance of taxonomic annotations. Existing solutions to this problem are researchers, industry and agencies creating their own, often closed reference databases. This is highly problematic as in closed databases the direct comparability of data sets is limited, and by this the key advantage of (meta)barcoding as a simple comparable, open tool gets lost. In view of the problematic situation and the need to also formally implement metabarcoding into regulatory monitoring programs, authoritative reference databases that are compiled according to community standards, have a version number, quality control and are maintained over time are needed. The ultimate goal of the dbDNA project was developing a system that aids in achieving robust taxonomic annotations when using DNA (meta)barcoding. The strategy reaching that goal is twofold, creating a pipeline that allows for grading individual sequences deposited in reference libraries as well as using graded references sequences to generate curated lists of reference sequences. The backbone of the developed pipeline are criteria for robust taxonomic annotations worked out by experts in two workshops. We will introduce the developed pipeline and criteria in detail and demonstrate the effectiveness of the approach on an existing taxa list for monitoring freshwater invertebrates in Germany.

eDNA data structuration and good practices for public policies and biodiversity monitoring: the French use case

Sophie PAMERLON, Aurélie Lacoeuilhe, Louise d'Hollande, Noëlie Maurel, Chloé Vinet, Thomas Bouix, Yvan Le Bras, Olivier Norvez, Nicolas Buisine, Anne-Sophie Archambeau, Solène Robert

Abstract: In the French research and expert communities, data providers currently use diverse and often unstructured methods to collect eDNA data. Following 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 and reuse. A key part of this effort is a set of new tools (national data template, GBIF MDT), and updated data-sharing pipelines by adapting the mapping of the French national data standard and Darwin Core based on the GBIF/OBIS 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 data integration workflows. More broadly, this initiative is part of the "large scale inventory of French biodiversity using molecular techniques" objective of the National strategy for biodiversity, supporting the harmonization and structuring of biodiversity data, including those acquired through eDNA techniques. In addition to the national reference list of genetic sequences for French taxa, the French eDNA working group contributes to improving the overall quality, accessibility and interoperability of eDNA data, allowing for their better sharing, discovering, reuse and practical application in biodiversity monitoring contexts. In this session, we will present ongoing work and documentation available to eDNA data providers and users: data standards, data templates, workflows, and technical resources to support high quality data sharing and reuse.

How reliable are our reference databases? Gaining confidence in eDNA detections by filtering erroneous barcodes.

Gert-Jan Jeunen, Aurelia BENHAMADOUCHE, Thomas Hughes

Abstract: Environmental DNA metabarcoding has transformed the monitoring of biological communities worldwide. Because species are detected indirectly rather than through direct observations, accurate taxonomic assignments are essential for robust ecological inference. However, assignment accuracy is constrained by the quality of reference databases, which are known to contain errors, leading to false-positive detections, reduced confidence, and biased ecological interpretations. We present LIMPET (Label Inspection & Mislabelling Purification for Enhanced eDNA Taxonomies), a framework designed to quantify multiple independent signals of taxonomic inconsistency within curated local reference databases. LIMPET integrates sequence similarity profiling, barcode gap analyses, phylogenetic neighbourhood assessments, and metadata exploration to identify barcodes that deviate from expected taxonomic structure. We evaluated performance using simulation experiments with controlled labelling errors to quantify detection sensitivity and specificity. By filtering erroneous barcodes from reference databases, LIMPET aims to strengthen the reliability and interpretability of eDNA detections.

PS01 Posters

Ecotrends: an R package for monitoring biodiversity trends over time

Neftalí SILLERO

Abstract: The ecotrends R package implements a robust monitoring framework for assessing species vulnerability by analysing temporal trends in habitat suitability. The framework calculates ecological niche models successively on the same species occurrence data over time, using a time series of environmental variables, for any period and periodicity. Then, a habitat suitability trend analysis is performed with Sen's slope, based on non-parametric Kendall's rank correlation. ecotrends includes functions that automatically gather annual time series of environmental data from TerraClimate, calculate and assess Maxent models, evaluate habitat suitability trends over time, and estimate variable importance. While it features a specific environmental database and modelling methodology, the package is adaptable and can utilise any variables and algorithms provided by the user. This framework is versatile and applicable to any taxon or guild, study area, spatial scale, or temporal resolution, as long as the necessary data is available. ecotrends serves as a valuable resource for estimating species vulnerability over time and supports the evaluation of conservation strategies. It allows users to analyse habitat suitability trends effectively, requiring only species occurrence data and a corresponding time series of environmental data.

AI4WildLIVE: Integrating AI, Citizen Science, and Data Infrastructure for Global Biodiversity Monitoring

Celine JORDAN

Abstract: The accelerating biodiversity crisis calls for scalable, data-driven solutions to monitor and safeguard ecosystems. Biodiversity monitoring increasingly relies on audiovisual data, ranging from camera traps to acoustic sensors, which generate vast and heterogeneous datasets. Processing these data streams in real time requires robust, sustainable infrastructures coupled with adaptive AI solutions. The AI4WildLIVE project provides the first integration of a FAIR (Findable, Accessible, Interoperable, Reusable) repository, AI-based analysis pipelines, and citizen science engagement within a single open-access portal. Building on Senckenberg's long-term citizen science initiative and a DFG-funded camera trap data platform, AI4WildLIVE leverages human-in-the-loop learning to accelerate model retraining, improve species detection, and support large-scale biodiversity assessments. The platform incorporates web GIS tools for spatial visualisation, enabling rapid feedback loops from data collection to actionable insights. By combining data infrastructure, machine learning, and citizen participation, AI4WildLIVE creates a scalable, transparent, and sustainable framework for biodiversity monitoring. This holistic approach supports scientific discovery, informs conservation policy, and fosters public engagement, ultimately positioning AI not only as a tool for efficiency but as a driver of transformative action in biodiversity conservation.

TERRASTOCK : an open-source information system to centralize, enrich and valorize biodiversity monitoring datas.

Apolline CARTON, Arnaud ALBERT, Ophélie PETIT

Abstract: The growing proliferation of biodiversity monitoring protocols generates increasingly large and heterogeneous field datasets – including images, audio recording, videos, genetic data – whose management remains fragmented, time-consuming and underexploited. In the context of a global data volume surge (Badshah et al., 2024), organizations responsivle for biodiversity monitoring face a structural challenge : how to efficiently store, process and leverage dispersed data ? To address the tangible need, the French Biodiversity Agency (OFB) is developping TERRASTOCK, a centralize, scalable data warehouse specifically designed for biodiversity observations data. TERRASTOCK is build on a flexible microservices architecture capable of ingesting raw field datas in their native formats, without requiring prior harmonization. The platform natively integrates computational capabilities for AI-based processing – including automated species classification (DeepFaune, SpeciesNet, Pl@ntNet) and image interpretation – combined with human annotation, indexation and data dissmination features. Beyond storage TERRASTOCK aims to streamline and accelerate processing pipelines, facilitate data access for both OFB field agents and external partners, and lay the foundations for a modern, interoperable infrastructure compatible with existing professional tools. As a pionneering project within the OFB, TERRASTOCK is being developed following cloud native, open source and cloud agnostic principles, with a modular architecture based on container architecture. The platform aspires to become a shared infrastructure accessible to external partners, fostering a community around a tool dedicated to biodiversity monitoring. In a world where IA applied to biodiversity is rapidly expanding, TERRASTOCK represents a practical lever for modernizing information systems, reducing manual data processing workloads, and maximizing the value of field collected data. Apolline CARTON, Arnaud ALBERT & Ophélie PETIT

eDNAqua-Plan recommendations towards a future of federated, curated reference libraries and aligned eDNA (meta)data publishing infrastructure and practices

Emilie BOULANGER, Katrina Exter, Joana Pauperio, Saara Suominen, Pieter Provoost, Frédéric Rimet, Antonio Picazo, Antonio Camacho, Camila Babo, Joana Verissimo, Veera Norros, Pascal Hablützel, Christina Pavloudi, Kristian Meissner, Peter Woollard

Abstract: Harmonising monitoring practices and methodologies across Europe has become an increasingly pressing priority. Beyond standardising protocols, making monitoring data openly available and aligning the tools and pathways used to share it are essential steps toward ensuring that data generated through monitoring efforts is comparable across monitoring programs and countries, as well as reusable across the wider scientific community. In aquatic biomonitoring, environmental DNA (eDNA) methodologies, and metabarcoding in particular, have matured to the point where integration into routine monitoring programmes is now a realistic prospect. Realising this potential requires the availability of quality-controlled, curated reference systems for taxonomic assignment, and a digital infrastructure built on connected, interoperable data and metadata systems that allow eDNA data to be effectively reused in support of broader aquatic biodiversity monitoring goals. The eDNAqua-Plan project addresses these challenges systematically. The project evaluates the current landscape of aquatic eDNA data, develops recommendations to improve its accessibility, interoperability, and overall effectiveness, and will ultimately translate these findings into a concrete blueprint and roadmap for the infrastructure needed to bring the envisioned future landscape into being. This talk will cover the technical evaluations and recommendations made by the eDNAqua-Plan project towards a future of federated, curated reference libraries and aligned eDNA (meta)data publishing infrastructure and practices.

From Field Notebooks to Open Data: Digitizing and managing Six Decades of Common Gull Monitoring data

Kristjan ADOJAAN, Allan Zirk, Kessy Abarenkov, Urmas Kõljalg, Jeffrey Carbillet, Tuul Sepp, Lauri Laanisto, Hannah Métaireau, Richard Meitern, Lauri Saks, Jaanis Lodjak

Abstract: The continuous monitoring of the Common Gull (Larus canus) breeding colony on Kakrarahu islet in the Baltic Sea, Estonia, is one of the region's longest-running ecological research projects, dating back to 1962. With continuous breeding success data collected since 1968 and ringing and age data since 1971, this project holds a vast repository of longitudinal population dynamics. Historically, these data were recorded in field notebooks, systematized on catalogue cards, and later partially transferred to spreadsheets. Modern data collection has now transitioned to a specialized mobile application "Bird Colony" for real-time field use. This work-in-progress project outlines the ongoing effort to rescue and digitize this extensive legacy dataset using a hybrid approach of manual data entry and novel AI-based digitization techniques. Because the monitoring methodology has remained constant over the decades, the recovered data holds immense value for understanding long-term population dynamics. The primary goal of this initiative is to make these unique ecological data widely available. While multiple open-access publication approaches will ultimately be utilized - such as publishing structured spreadsheets to open repositories - we focus here on one highly robust pathway. By utilizing PlutoF, a comprehensive biodiversity data management platform developed by the University of Tartu, we establish a seamless pipeline to structure, store, and publish the historical dataset directly to the Global Biodiversity Information Facility (GBIF). This workflow demonstrates an effective framework for rescuing legacy mass-monitoring data and ensuring over six decades of ecological observations become globally accessible to study and reveal long-term ecological patterns.

PS02 Posters

Using Galaxy platform to operationalize EBV computational workflows

Coline Royaux, Pauline Seguineau, Arthur Barreau, Olivier Norvez, Nicolas Buisine, Jian-Sheng Sun, Marie Jossé, Claire Bissery, Romain Lorrilliere, Yves Bas, Alexis Martin, Laureen Eon, Marc Eléaume, Dominique, Björn Grüning, Jean-Baptiste Mihoub, Yvan LE BRAS

Abstract: Since 2018, French museum of natural history is leading the "Galaxy for Ecology" initiative, to coordinate contributions of source codes, computational workflows and related tutorials linked to Biodiversity data management and treatments. Using the Galaxy platform, we are focusing on one of the biggest open source ecosystem for science worldwide. We also take advantage of a particularly high level of FAIRness regarding Galaxy services with high transparency, traceability and reproducibility of processes. We propose here to

showcase the use of Galaxy and related platforms already deployed at national, regional and international levels to build, test and ameliorate computational workflows dedicated to Biodiversity metrics and indicators production and then facilitate workflow publication notably in WorkflowHub.

A data-driven framework for biodiversity prioritization: the Biodiversity Value Mapping (BVM) in Catalonia

Arnau TOLRÀ MONTERO, Helena Tauler, Gemma Gual, Martí Franch, Gemma Gual

Abstract: Effective biodiversity conservation requires spatial tools that consistently integrate the best available ecological information into decision-making processes. The Biodiversity Value Mapping (Cartografia de Valor de Biodiversitat, CVB) is a spatially explicit framework developed in Catalonia to identify priority areas for conservation and ecological restoration. The approach is based on a 1 × 1 km grid and combines standardized biodiversity data, including habitat cartography, species distribution models, and long-term monitoring datasets. A key strength of CVB lies in its capacity to systematically incorporate heterogeneous but complementary sources of information, ensuring that outputs are grounded in the most robust and up-to-date knowledge available. Biodiversity elements are weighted according to their ecological relevance and conservation status, generating synthetic indices of spatial value that allow consistent comparisons across territories. The resulting maps reveal strong spatial heterogeneity in biodiversity value and provide an operational basis for identifying conservation priorities, restoration opportunities, and potential mismatches with current land-use planning. By bridging biodiversity data and spatial planning, CVB supports transparent, evidence-based decision-making and facilitates the integration of ecological criteria into sectoral policies in Mediterranean landscapes.

Evaluating the potential of Large Language Models for biodiversity data integration in transitional water ecosystems under climate change

Martina PULIERI, Ilaria Rosati, Gianluca Sarà, Alberto Basset

Abstract: Transitional water ecosystems (e.g., lagoons, estuaries, and coastal wetlands) are biodiversity hotspots that provide essential ecosystem services, yet they are highly vulnerable to climate change. Rising temperatures, salinisation, extreme events, and hydrological alterations interact in complex ways, producing nonlinear biological responses. Understanding how biodiversity and ecosystem services respond requires integrating diverse ecological data, including environmental variables, species occurrences, functional traits, and long-term monitoring records. Despite increasing data availability, integration is hampered by fragmentation, heterogeneity, and limited interoperability. Relevant datasets are scattered across international repositories (e.g., GBIF, OBIS, PANGAEA), national platforms (e.g., LifeWatch Italy, NFDI4Biodiversity), and general-purpose

archives (e.g., Zenodo, Figshare). Differences in format, structure, terminology, and standards make traditional ETL-based integration time-consuming, hard to scale, and error-prone. Recent advances in Large Language Models (LLMs) offer promising tools for harvesting heterogeneous data, detecting structural inconsistencies, harmonising terminology and taxonomy, and matching schemas across datasets. However, their reliability and methodological robustness in ecological data integration are largely unexplored. This project proposes to evaluate LLMs as facilitators of biodiversity monitoring data integration within the Italian PhD program in "Biodiversity", aiming to develop more efficient, scalable, and interoperable data systems for ecological research and conservation.

Challenges and prospects in the management of biodiversity monitoring data in Bulgaria

Radoslav STANCHEV

Abstract: Within the framework of the Bulgarian National System for Monitoring the State of Biodiversity (NSMSB), data has been collected on a total of 962 species belonging to eight different biological groups, as well as on 93 types of natural habitat. Field data collection methodologies have been developed for each of these groups and habitats. For each object, designated monitoring sites and a field form containing mandatory and optional parameters have been established. Specific methodologies have been developed for each biological group to statistically assess the status of the observed species at the level of the monitoring site, biogeographic region and national level. In 2010, an information system was developed to store all primary monitoring data collected at NSMSB sites. This system is centralized, with a copy of the database created for each user. In accordance with the monitoring methodologies, standardized methods are applied to record biological species either by direct counting or by noting traces of their presence or life activity. One of the system's key features is its ability to verify data. This involves checking geographic coordinates and ensuring that all the necessary information has been provided. One of the biggest challenges is increasing the number of visits and surveys in order to collect sufficient data to assess the status of species and short- and long-term trends at all levels in line with the monitoring periods. Over the past year, efforts have been made to implement modern genetic methods for evaluating the population of the brown bear, a flagship species for Bulgaria. The number of users has grown over the past 10 years, consequently increasing the volume of data entering the national database. This is partly due to an increase in state-funded projects and greater involvement from volunteers in non-governmental organizations. For instance, volunteers have provided data on wintering waterbirds and monitored common bird species. This data is used to prepare reports in accordance with the requirements of the EU Nature Directives. A taxonomic database containing detailed information on the current names of all taxonomic categories has been

developed. Also, ten web database applications were made for mapping ecosystems and ecosystem services in Bulgaria. These databases, together with Darwin core standards, will form the basis of the next update to the Central Biodiversity Database.

Biodiversity data to GBIF

Eva CORSSMIT

Abstract: Effective biodiversity monitoring depends not only on robust field methodologies, but increasingly on how data are structured, standardised, and shared for reuse across scales and domains. Global infrastructures such as the Global Biodiversity Information Facility (GBIF) and the Ocean Biodiversity Information System (OBIS) provide essential platforms for integrating monitoring data, yet mobilising complex survey and monitoring datasets into these platforms remains a challenge for many data providers. In this talk, we present practical approaches and lessons learned from mobilising monitoring data to GBIF. We discuss the use of the DarwinCore to publish different types of monitoring data, including checklist data, occurrence data, and sample event data. Furthermore we discuss how to select appropriate extensions to the DarwinCore for datasets differing in monitoring objectives and study design. This includes differences in sampling effort, methodology, and temporal replication. We further address the specific challenges of structuring marine monitoring data for integration with OBIS, including the representation of sampling events, environmental context, and taxonomic resolution. By illustrating how marine datasets can be harmonised to meet both GBIF and OBIS requirements, we highlight opportunities to increase interoperability between terrestrial and marine biodiversity data infrastructures. The talk combines conceptual guidance with concrete examples, all aimed to support monitoring programmes, data managers, and researchers in making their data more FAIR (Findable, Accessible, Interoperable, and Reusable) and to increase the data quality in general. By improving data standardisation and sharing practices, biodiversity monitoring data can more effectively contribute to large-scale assessments, long-term trend analyses, and evidence-based conservation and policy decisions.

BioMonWeek
2026
The European
Conference for
Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Mass Monitoring — Large-scale methods and technologies for monitoring

MM12 Lessons learnt from camera-based sensors and their data

Tuesday 5 May, 11h30-12h10, Auditorium
Chair: Toke T. Hoye

Description: The use of novel sensor technologies is transforming the way we monitor and conserve biodiversity, favouring informed and effective decisions making processes to protect nature. During this session, we explore how different types of image-based sensors are being implemented for biodiversity monitoring and conservation. Talks will highlight applications and advances in the deployment of image-based sensors across realms, how data is processed using advanced techniques, such as machine learning and artificial intelligence, efforts towards standardization of protocols and workflows, and examples of success deployment with policy relevance.

Automated insect monitoring with camera traps is transforming ecological understanding

Toke T. HØYE

Abstract: With computer vision and deep learning, insect camera traps have become important tools to improve our understanding of insect responses to environmental change. Through computer eyes, it is possible to effectively, continuously, and non-invasively observe insects throughout diurnal and seasonal cycles and deep learning models combined with statistics can provide estimates of their abundance, biomass, and diversity. We highlight four key areas of ecological understanding: phenology, abundance, richness, and community dynamics, and show how automated data can correct phenological estimates by weeks and improve biodiversity assessments. Data from insect camera traps offer unprecedented resolution and scalability, making them powerful tools for tracking insect communities and in forming conservation strategies. I will also highlight outstanding challenges and future research avenues to facilitate the broad scale implementation of insect camera traps for day active and nocturnal insects.

Monitoring Biodiversity in Hard-to-Reach Places: Automated Insect Monitoring in Remote Ecosystems

Alyssa DUFFY, Tom August, David Roy, Jenna Lawson, Jonas Beuchert

Abstract: Monitoring biodiversity in remote and hard-to-reach environments remains a major challenge for ecological research and conservation. Many locations of high ecological value, including islands and protected areas, lack consistent long-term monitoring due to logistical constraints, limited infrastructure, and the cost of repeated field visits. Recent advances in automated sensor technologies provide new opportunities to overcome many of these barriers. Within the AMBER project and related initiatives, we have developed and deployed automated insect monitoring systems designed to operate in remote environments with minimal maintenance. These systems combine light-based attraction, automated imaging, and machine-learning pipelines to detect and classify insects from large volumes of images. Early deployments used the Automated Moth Identification (AMI) system, which demonstrated the potential of camera-based monitoring but also revealed challenges related to power supply, data transfer, environmental conditions, and system robustness. Building on these lessons, we developed next-generation systems, including LepiSense, designed to improve reliability, scalability, and long-term autonomous operation. We present lessons learned from deploying these systems across multiple remote environments (e.g. Singapore, Thailand, Japan, Kenya, Nigeria, Costa Rica and Panama) and highlight recent deployments in Anguilla, where automated monitoring has generated the first large-scale baseline dataset for nocturnal insects across several island sites. We also outline plans to build on this work through the INSPIRE project, integrating citizen science with automated sensors for large-scale insect monitoring. Together, these initiatives illustrate how camera-based sensor systems can enable scalable, long-term monitoring of insect biodiversity in remote ecosystems and support global biodiversity observation.

Towards a continent-wide harmonised estimation of wildlife density: lessons learnt from a large-scale camera-trapping network

Stefania ZANET, Guerrasio T, Vicente J, Acevedo P, Blanco-Aguiar JA, Casaer J, Ferroglio E, Jansen P, Liefting Y, Palencia P, Rowcliffe M, Scandura M

Abstract: The European Observatory of Wildlife (EOW), developed within the ENETWILD project funded by the European Food Safety Authority, is a collaborative network aimed at generating harmonised data on wildlife populations across Europe using standardised camera-trapping (CT) protocols and the Random Encounter Model (REM). A key lesson from this initiative is the importance of strict protocol standardisation across all steps, from field deployment to data processing, to ensure comparability among sites and countries. The integration of photogrammetry into CT workflows has proven essential to reduce uncertainty in key REM parameters, improving the robustness of density estimates. Another major insight concerns data management. The use of platforms such as Agouti enables semi-automated workflows for image annotation, parameter estimation, and data standardisation (CamTrap DP), reducing processing time while ensuring data quality and reproducibility. This standardisation supports scalable and automated analyses. The EOW also highlights challenges typical of large collaborative networks, including variability in field conditions, operator expertise, and data quality. Addressing these required continuous training, clear guidelines, and iterative protocol refinement, leading to

increased consistency and precision over time. Finally, adherence to FAIR data principles has been fundamental to maximise data reuse and interoperability, supporting integration with wildlife monitoring and disease surveillance initiatives. Overall, the EOW demonstrates that standardisation, robust data workflows, and coordinated collaboration are key to effectively scaling camera-based wildlife monitoring.

MM12 SPECIAL FEATURE New monitoring technologies: turning optimism into enactment.

Tuesday 5 May, 12h10-12h30, Auditorium
Chair: Rebecca COURT

MM03a Novel remote-sensing approaches for biodiversity monitoring using multiple sensors - Part I. Foundations and frameworks

Tuesday 5 May, 16h30-17h30, Auditorium
Chairs: Petteri Vihervaara & Sandra Luque
Description: Possibilities to use various remote sensing technologies to monitor biodiversity have increased enormously during the last years. The aim of this session is to demonstrate novel approaches to integrate data from various sensors (i.e., multi- or hyperspectral, LiDAR, radar etc.), together with in-situ data to help monitoring biodiversity at large scale. Preferably the emphasis could be either on ecosystem structure and functioning, or community composition, but also novel approaches to detect changes in species populations are welcome.

Introduction to the session

Petteri VIHERVAARA, Sandra LUQUE

Abstract: Advances in satellite imagery, remote sensing, species distribution models, and artificial intelligence are transforming biodiversity monitoring. Open-access data and improved analytical methods now enable more detailed assessments across broad spatial and temporal scales. Upcoming Earth Observation missions will deliver higher spatial and spectral resolution data, improving measurements of key biodiversity variables such as ecosystem extent and condition. These advances strengthen our ability to monitor and manage resilient forest ecosystems. Supporting global goals—including the EU Biodiversity Strategy for 2030, the Sustainable Development Goals, and the Kunming-Montreal Global Biodiversity Framework—requires integrated approaches that combine multi-sensor Earth Observation data, in-situ measurements, and ecological models that account for uncertainty. Such methods can better predict forest biodiversity change and its drivers, enabling more effective, evidence-based conservation.

Standardized algorithm benchmarking framework to advance production of RS-based Essential Biodiversity Variables

Lori GIAGNACOVO

Abstract: The ongoing biodiversity crisis requires systematic monitoring of Essential Biodiversity Variables (EBVs) to assess the state and dynamics of Earth's biodiversity and halt worldwide decline. In recent decades, Remote Sensing (RS) technologies have advanced rapidly and are increasingly being applied in biodiversity research. Current literature suggests that RS-based biodiversity products (RS bd-products) are viable candidates for many EBVs. However, with the proliferation of both experimental and mature algorithms for generating these products, determining which algorithm is most suitable for a given product is often challenging. Within the OBSGESSION project, we established a standardized benchmarking framework for RS-bd products and their associated algorithms. Our step-wise approach is designed not only to identify the most suitable algorithm to produce a RS-bd product, but also to evaluate which RS bd-product informs best about a specific EBV. The benchmarking framework considers diverse criteria categorized in four themes: scientific validity, policy relevance, internal project goals, and technical advancement. By combining these diverse objectives and a tailored weighing scheme, the framework ensures a holistic evaluation rather than focusing on a single domain of progress. While the framework ensures much-sought consistency and transparency within a single application, it also allows for flexibility as (particularly project-related) criteria can be adjusted to meet different application targets. Our standardized approach for product and algorithm evaluation and selection can perfectly be combined with open data services such as openEO and Bon-in-a-Box, aiming at on-demand mapping of RS biodiversity products using the best-performing algorithms. Such integration is relevant for operation-oriented policy applications as well as more experimental research projects, which seek to unify data from multiple sensor sources for robust biodiversity assessments.

An EO-based framework for monitoring ecosystem extent and condition in tropical forests

Simon BONNEFOY, Jean-Baptiste Féret, Florian de Boissieu, Rémi Cresson, Mairi Souza Oliveira, Samuel Alleaume, Sandra Luque

Abstract: An EO-based framework for monitoring ecosystem extent and condition in tropical forests Simon Bonnefoy, Jean-Baptiste Féret, Florian de Boissieu, Rémi Cresson, Mairi Souza Oliveira, Samuel Alleaume, Sandra Luque

INRAE, UMR TETIS Land, environment, remote sensing and spatial information Montpellier, France Next-generation biodiversity observing systems and science-based solutions aim to address the main drivers of biodiversity loss while supporting the conservation and restoration of vulnerable ecosystems. However, the rapidly growing volume of Earth Observation (EO) data presents significant challenges for both scientific research and operational biodiversity monitoring. To address this, the Committee on Earth Observation Satellites (CEOS) established the Ecosystem Extent Task Team (EETT) in 2023 to explore the use of EO data for monitoring the Essential Biodiversity Variable (EBV) of Ecosystem Extent. A key objective of this initiative is the development of data-cube-based demonstrators to support future biodiversity monitoring systems. Here we present results from forest ecosystems in Costa Rica, using data from Sentinel-1 and Sentinel-2 to build advanced data cubes integrating spectral indices and spectral diversity metrics. The influence of cloud cover on spectral index composites is assessed to improve the temporal and spatial consistency of derived products. Resulting spectral diversity maps are compared with ground-based observations of forest types and species composition, as well as species distribution models, to evaluate their potential for biodiversity monitoring and ecosystem characterization.

Boosting biodiversity monitoring using novel approaches

Stelios KATSANEVAKIS

Abstract: Effective marine biodiversity monitoring is constrained by high costs, limited spatial coverage, taxonomic bias, and logistical limits of traditional sampling. Emerging technologies enable a step change in ocean observation by integrating AI, robotics, eDNA, remote sensing, acoustics, and citizen science within coordinated frameworks. This talk synthesizes advances developed and implemented in the research projects GuardIAS, BioBoost+, CAMBioMed, and NEMO-Tools. Autonomous and remotely operated platforms equipped with high-resolution imaging systems enable non-intrusive seabed mapping and rapid surveys across large areas and depths, producing orthomosaics and continuous visual archives suitable for AI-assisted species detection. Computer vision and deep learning support automated identification of taxa and habitats, transforming large image streams into biodiversity indicators and Essential Biodiversity Variables. Networks of fixed cameras and cost-effective observatories further enable continuous ecosystem observation at unprecedented temporal resolution. Molecular approaches, particularly eDNA metabarcoding and targeted assays, enhance detection of rare, cryptic, and nocturnal species while enabling quantitative inference through digital PCR. Satellite and UAV remote sensing enable multi-scale mapping of habitat extent, fragmentation, and seasonal dynamics, while passive acoustics provides a complementary non-invasive dimension for detecting vocal species and assessing ecosystem pressures. Affordable sensors and structured citizen science initiatives further expand observational capacity and democratize data collection. Collectively, these innovations support scalable, cost-effective, and adaptive marine observation systems capable of detecting biodiversity change, informing conservation action, and improving ecosystem status assessments under accelerating environmental change.

The Radar Network for Aerial Biodiversity Monitoring

Dominik KLEGER, Johannes Nüesch, Felix Liechti, Silke Bauer

Abstract: Monitoring the movement of birds, bats and insects at meaningful spatial and temporal scales remains a major bottleneck for biodiversity assessment. Many policy frameworks rely on sparse counts, opportunistic observations, or lack the in-depth information or resolution of aerial biomass composition. We present an approach that uses a network of specialized vertical-looking radar systems specifically developed for aerial biodiversity monitoring. These sensors are based on latest radar technology and can automatically determine species-groups based on signatures captured from individual birds, bats and insects while calculating accurate quantification of bird and bat activity in real-time. Preliminary studies show that even a modest number of radar stations can resolve large-scale spatiotemporal patterns. By combining radar-derived movement traits with environmental and landscape data, we can quantify migration fronts, seasonal traffic rates, diel movement strategies, and longer-term behavioural shifts. Preliminary analyses show strong correlations in movement intensity between radar sites separated by tens to hundreds of kilometres, indicating that the system captures coherent regional-scale dynamics rather than isolated local signals. The potential applications are broad. Radar-based movement metrics support early warning systems for agricultural pests or declining pollinators, inform bat and bird collision risk assessments at wind energy facilities, contribute data about bird strike risks for aviation, provide near real-time indicators relevant to zoonotic disease surveillance, and enable long-term tracking of phenological and distributional change under climate pressure. Because the data stream is continuous and harmonised across sites, it can complement existing biodiversity reporting frameworks by supplying movement traits that are consistent, comparable, and policy relevant.

MM01 WORKSHOP Getting kick started with (e)DNA based methods

Tuesday 5 May, 16h30-17h30, Room Rondelet
Chairs: Florian Leese, Pedro Junger, Tiina Laamanen and Joanna Warwick-Dugdale

Description: This session explores how DNA-based approaches are transforming biodiversity monitoring across terrestrial, marine and freshwater ecosystems. We will showcase advances in DNA barcoding, metabarcoding, and emerging genomic tools that enable rapid, scalable and taxonomically broad species detection. Talks will highlight applications ranging from community-level assessments to detection of rare, invasive or cryptic species, alongside discussions of reference databases, bioinformatics, standardisation and policy relevance. The session aims to connect methodological innovation with real-world monitoring needs and conservation decision-making.

Upscaling of DNA-based methods for aquatic biodiversity monitoring

Florian LEESE, Arne J. Beermann, Dominik Buchner, Jan Koschorreck, Till-Hendrik Macher, Robin Schütz, Marie-Thérése Werner

Abstract: Environmental DNA (eDNA) analyses are rapidly transforming biodiversity assessment, unlocking the potential for exponentially growing datasets from ecosystems around the globe. Particularly in aquatic environments, eDNA has established itself as a novel and powerful tool to assess ecosystem state and functioning. However, despite its promise, the full potential of eDNA remains underutilized. A major barrier is the lack of comparability across laboratories and between eDNA-based and traditional assessment methods. Moreover, the proliferation of diverse analysis approaches - the current "wild west" of eDNA workflows - poses a significant challenge in particular for end users seeking reliable and standardized services. To ensure eDNA's effective integration into formal biodiversity monitoring frameworks, critical next steps include the development of formal minimum methodological standards and robust quality assurance and quality control (QA/QC) schemes. In this talk, I will draw on insights from international method comparisons to highlight key challenges that currently limit eDNA data quality and reliability to then present the work of the international eDNA Standardization Task Force (iESTF), which is driving the inclusive development of formal standards aimed at the International Organization for Standardization (ISO), with the goal of establishing internationally accepted minimum requirements for eDNA applications. I will use the Horizon Europe project eDNAqua-Plan and the Biodiversa+ project DNAquaIMG as an examples, how solutions for FAIR data are being developed within an open, digital ecosystem for eDNA-based biodiversity assessments. Finally, I will argue that embracing international collaboration, open science, and FAIR data principles is essential to fully unlock the transformative potential of eDNA methods for global biodiversity monitoring and conservation.

The Finnish national eDNA initiative and roadmap: Where are we on the road to routine implementation?

Tiina LAAMANEN, Kristian Meissner, Veera Norros, Petteri Vihervaara

Abstract: In 2022, we published the Finnish roadmap for implementing environmental DNA (eDNA) and other molecular monitoring methods in Finland. In this roadmap, commissioned by the Finnish Ministry of the Environment, we assessed the state of the art in molecular monitoring methods in Finland within an international context, identified remaining challenges and areas for development, and proposed an action plan to promote the coordinated implementation of molecular methods in national monitoring programs. In this presentation, I will describe the Finnish national eDNA initiative and roadmap, including its origins, purpose, impact, and lessons learned. I will also discuss recent national level developments, such as the Nature Information R&D project and the ongoing national ECOSTAT eDNA pilot, linking these results to recommendations developed through close international collaboration with colleagues, for example within the eDNAqua Plan project.

From Raw Data to Indicators: eDNA-based Essential Variables for Marine Biodiversity Monitoring

Pedro JUNGER, Gladys Ventre, Lucie Zinger, Daniel Kumazawa Morais, Mads Reinholdt Jensen, Joanna Warwick-Dugdale, Michael Cunliffe, Hanneloor Heynderickx, Jennifer Beatty, Fabrice Not, Luís Afonso, Isabel Sousa Pinto, Aubrie Onoufriou, Iveta Matejusová, Domenico D'Alelio, Daniele Iudicone, Saara Suominen, Emilie Boulanger, Kim Præbel, Chris Bowler

Abstract: Environmental DNA (eDNA) is increasingly recognized as a scalable, standardized tool for biodiversity monitoring, yet its integration into established observation and policy frameworks remains limited. Here, drawing on case studies from the EU-Horizon MARCO-BOLO project, we present how eDNA-derived data can be translated into Essential Ocean Variables (EOVs) and Essential Biodiversity Variables (EBVs), and evaluate their utility for European directives including the MSFD, WFD, and Habitats Directive. Using a global ocean survey (Tara Oceans), three coastal time-series, and a cetacean dataset from the Portuguese coast, we generated eDNA-based EOVs, spanning from phytoplankton to fish and marine mammals, formatted to Darwin Core standards for deposition in public repositories. These EOVs serve as standardized building blocks and EBV candidates, linking raw eDNA observations to policy-relevant biological indicators. Across case studies, eDNA metabarcoding successfully captured seasonal phytoplankton dynamics and harmful algal bloom events relevant to eutrophication assessments; revealed temporal variation in fish diversity and community composition; and detected cetaceans protected under the Habitats Directive, validated against visual surveys. Targeted ddPCR assays provided quantitative signals for sentinel fish species supporting regional indicator frameworks. eDNA also expanded known distributions of OSPAR-listed invasive species and detected multiple IUCN Red List fish species, demonstrating value in data-deficient areas. Comparisons with conventional monitoring data and global

biodiversity databases confirmed broad congruence between eDNA-derived patterns and established methods, while eDNA provided additional taxonomic resolution and temporal coverage. These results demonstrate that eDNA-based EOVs offer a practical, harmonized pathway toward more comprehensive and efficient biodiversity monitoring aligned with European and international frameworks.

MM20 WORKSHOP Successful Citizen Sciences approaches for long-term & cost-effective monitoring

Wednesday 6 May, 9h00-11h00, Room Sully 1
Chairs: Constantinos Phanis

Description: This interactive workshop explores how citizen science can deliver long-term, cost-effective biodiversity monitoring while maintaining strong volunteer engagement. Building on recent work within Biodiversa+, the session will move from evidence to practice by examining real monitoring schemes and identifying key cost drivers, efficiency bottlenecks, and retention challenges. Participants will collaboratively identify practical solutions, engagement levers, and core indicators to strengthen scheme sustainability. The workshop will also introduce the concept of a user-friendly cost-effectiveness toolkit designed to support project managers, funders, and policy actors in planning, assessing, and communicating the added value of citizen science. Through interactive exchanges, the session aims to foster harmonised approaches and enhance the strategic role of citizen science in European biodiversity monitoring frameworks.

MM11 Lessons learnt from passive acoustic recorders and their data

Wednesday 6 May, 11h30-12h30, Room Barthez
Chair: Gerard Bota

Description: We invite the monitoring community to submit abstracts for the session topic “Lessons learnt from passive acoustic recorders and their data”. This session aims to share experiences, best practices, and challenges related to the use of passive acoustic monitoring and the analysis and interpretation of the data they generate for biodiversity monitoring. Contributions are welcome on sampling design, data management and quality, automated analysis, ecological interpretation, applications across different taxonomic groups, and implications for conservation and management. We particularly encourage case studies, innovative methodologies applications, and critical reflections on the use of this novel technology.

A Transnational Sensor Network for Birds, Bats and Insects: The Automated Biodiversity Monitoring Stations (ABMS) Pilot

Jamie ALISON, Mark Gillespie, Jonáš Gaigr, Gerard Bota, Lluís Brotons, Luc De Bruyn, Stinna Danger, Domhnall Finch, Klara Grethen, Daniela Hamidovic, Guillaume Mougeot, Jarek Scanferla, Vladimír Nemček, Lars B. Pettersson, Jozef Šibík, Mária Šibíková, Mladen Zadravec, Rotem Zilber, Toke T. Høye

Abstract: To address biodiversity decline, we need to fill glaring data gaps. Automated methods promise to generate affordable, standardized data with extensive spatial, temporal and taxonomic coverage. However, the deployment of sensors and AI has rarely been coordinated at transnational scales. The Automated Biodiversity Monitoring Stations (ABMS) pilot implemented a transnational sensor network for bats, birds and night-flying insects, evaluating the potential of automation for scalable biodiversity monitoring across Europe and elsewhere. Deploying ~200 sensors at 70 sampling locations across 12 EU member states, it generated 5.43 recording-years of audible sounds, 1.58 recording-years of ultrasound, and millions of images of nocturnal insects. The pilot trialed a centralized data processing framework: Raw data were uploaded by partners and processed using open-source AI models including BirdNet, BatDetect2, and flatbug. AI generated over 1 million preliminary species records, but these were difficult to interpret without verification. To remedy this, we coordinated expert review of 8,690 bird and 3,048 bat detections, validating records of 127 bird and 24 bat species. Our data generated indicators to capture the annual rise and fall of bird, bat and insect activity across Europe, as well as dominant taxa and species richness at sampling locations. Crucially, the pilot built a community of practice around automated methods, and shed light on obstacles to automated monitoring related to technological readiness level, demand for expert verification, and data processing options. Still, the promise of transnational sensor networks is clear, as all partners agree that ABMS approaches can be integrated with national monitoring.

Upscaling Acoustic Monitoring through Citizen Science: 20 Years of Bat Monitoring in France

Yves BAS, Tiphaine Devaux, Ferdinand Petit, Christian Kerbiriou

Abstract: Vigie-Chiro is a citizen science programme based on recording bat echolocation calls across France. Established in 2006, it enables monitoring of bat populations at a national scale, and also non-target taxa such as nocturnal orthopterans, shrews and rodents. Over nearly two decades, the programme has demonstrated that deploying acoustic recorders through a network of more than 600 motivated participants can dramatically increase the volume of standardised data (exceeding 200 TB in recent years), achieve spatial replication at an unprecedented scale (over 30,000 sampled sites), and ensure long-term monitoring continuity through sustained volunteer engagement. Through continuous investment in participant training, the programme has produced more than 140,000 species-level annotations, supporting the development of machine learning algorithms that incorporate nightly contextual information. This has substantially improved classification performance and expanded monitoring to species that were initially poorly identified. All recordings were reanalysed in 2015 and 2019 using retrained algorithms (Tadarida software), generating more accurate datasets and enabling trend estimation across a broader range of species. The systematic storage of raw data has not only strengthened species identification but also enabled robust quality control, using proxies to assess protocol compliance and sensor performance, thereby ensuring data reliability despite large-scale deployment by non-scientists. Ongoing collaboration with other European teams points toward the emergence of a pan-European monitoring framework via batmonitoring.org. Building on this experience, new protocols targeting nocturnal bird migration and pollinators were also developped, with early results indicating strong potential for generating reliable long-term biodiversity trends across multiple taxa.

Contribution of large-scale acoustic monitoring to biodiversity monitoring and reporting needs

Luc BOHYN

Abstract: Initial involvement in the conservation of the great spotted kiwi (Apteryx haastii) in New Zealand highlighted the importance of robust, field-based monitoring to support species recovery. Motivated by these lessons, we next explored passive acoustic monitoring (PAM) combined with advanced machine learning as a scalable tool for biodiversity assessment. Building on research demonstrating strong individual distinctiveness in great spotted kiwi vocalisations, we developed AI-driven models capable of detecting species, managing environmental noise, and, where appropriate training data are available, identifying individuals. These models are designed to process very large acoustic datasets and convert raw recordings into structured, decision-relevant outputs. To illustrate this approach in action, this paper presents four operational case studies from New Zealand: (1) individual-level monitoring of the great spotted kiwi (Apteryx haastii); (2) multi-species biodiversity analysis at the landscape scale; (3) single-species monitoring of mohua (Mohoua ochrocephala) in alpine ecosystems; and (4) large-scale detection of kea (Nestor notabilis) across 609,541 15-minute recordings from 1,031 monitoring plots in the 'Department of Conservation Tier-1 acoustic dataset'. In the kea study, 129,528 call segments were detected across 544 plots, with resulting distribution patterns consistent with national survey maps derived from traditional field methods. Collectively, these examples show that AI-enabled acoustic monitoring can operate reliably at individual, species, and landscape scales. It transforms extensive audio archives into actionable biodiversity intelligence. Although the work was conducted in

New Zealand, the methodology is fully transferable. We now aim to expand it to European species and ecosystems. This will contribute to scalable, data-driven tools to support current biodiversity monitoring and reporting needs.

Vibrational Monitoring for Enhanced Arthropod and Pollinator Assessment

Rok ŠTURM, Ambrožič Žan, Bianco Lorenzzo, Gradišek Anton, Lopez Diez Juan Jose, Marolt Matija, Polajnar Jernej, Virant-Doberlet Meta

Abstract: Vibrational monitoring, as a very special version of acoustic monitoring, offers a highly effective and non-invasive approach to studying insect communities - especially those that rely on substrate borne vibrations as their primary mode of communication. More than 70% of all insect species use substrate-borne vibrations for communication, while less than 2 % use air-borne acoustic signals, which can be detected by existing PAM devices. We argue that vibroscape includes far more organisms than soundscape itself. We present two case studies: one addressing seasonal changes in arthropod community structure and other monitoring pollinators activity on flowering plants on a meadow. Both studies include deploying machine learning to automatically evaluate insect activity (signalling behaviour for arthropod communities and flower visit for pollinators). Recording of vibroscape would greatly benefit from the development of cheap, autonomous, and portable sensors, which already exist, but have not yet been adapted or optimised for monitoring purposes. We would like to emphasise how incorporating this non-invasive behaviour-based monitoring could accelerate the development of arthropod monitoring. It can be deployed on common species, which importantly contribute to ecosystem services, but also on rare, cryptic and/or protected species because of the non-invasiveness of the method.

MM03b Novel remote-sensing approaches for biodiversity monitoring using multiple sensors - Part II. Data integration and systems

Wednesday 6 May, 16h30-17h30, Room Joffre F

Chairs: Sandra Luque & Petteri Vihervaara

Description: Possibilities to use various remote sensing technologies to monitor biodiversity have increased enormously during the last years. The aim of this session is to demonstrate novel approaches to integrate data from various sensors (i.e., multi- or hyperspectral, LiDAR, radar etc.), together with in-situ data to help monitoring biodiversity at large scale. Preferably the emphasis could be either on ecosystem structure and functioning, or community composition, but also novel approaches to detect changes in species populations are welcome.

An Extended Biodiversity Data Cube: Integration of Multi-Spectral Imagary

Maarten TREKELS

Abstract: Climate change is rapidly reshaping ecosystems, shifting species distributions, community composition, and the environmental conditions that sustain biodiversity. Understanding and predicting the impacts of this change depends on our capacity to combine biodiversity observations with environmental drivers across space and time. However, biodiversity data are intrinsically sparse, unevenly distributed, and taxonomically biased: most records are opportunistic, clustered in accessible places and periods, and reflect strong taxonomic and geographic biases. Without careful aggregation, these observations remain difficult to interpret, compare, or use for robust modelling and indicators. By structuring occurrences into standardized, multidimensional, analysis-ready structures, data cubes transform fragmented observations into interoperable, policy-relevant evidence. This concept of biodiversity data cubes is developed in the Horizon Europe project B3 - Biodiversity Building Blocks for policy (ID No 101059592, b-cubed.eu). Built on GBIF's open infrastructure, cubes make data provenance and bias transparent, support reproducible workflows, and scale from local monitoring to continental assessments. Within the project, we extended the dimensions of the data cubes, by adding vegetation indices using multi-spectral imagery from Copernicus. They can be generated in cloud environments and produce digital, temporally explicit representations of ecosystems even when in-situ environmental histories are incomplete. A such they can form a solid and reproducible basis for species distribution analysis.

Behind the Scenes of GeoPl@ntNet: Generating High-Resolution, European scale Maps of habitats and plant species by combining satellite and in situ observation data

Christophe BOTELLA

Abstract: The lack of systematic, high-resolution monitoring of habitats and plant communities across Europe remains a major barrier to effective land-use planning and conservation strategies. Massive in situ species observation data are available but yet to scarce and heterogeneous across space, time, and taxa to be used directly. To address this, we have developed a cascading modeling pipeline that generates (i) species maps from remote sensing data, and then (ii) habitats maps from the predicted species assemblages. For the first step, we combined disparate in situ observations (presence-absence and presence only) with remote sensing data within integrated species distribution models powered by scalable deep learning. for species-to-habitat mapping, a Large Langage Model was built to learn the syntax of species assemblages determining habitats. This approach generates harmonized, robust, and repeatable predictions of plant species assemblages and habitats at a continental scale. This is the foundation of GeoPl@ntNet (https://geo.plantnet.org), a new web application from the

Pl@ntNet team. GeoPl@ntNet maps the potential presence of ~10,000 plant species, EUNIS habitats, and key biodiversity indicators at a spatial resolution of 50 meters across Europe for the period 2017-2021. This presentation will provide an overview of the data, modeling architecture and evaluation pipelines behind the platform. Current limitations include better leveraging presence-only data with dedicated bias correction to improve predictions in data-poor regions and produce interpretable uncertainty estimates. A crucial next step is extending the framework to model temporal trends, ultimately providing a dynamic tool to better support both biodiversity scientists and conservation stakeholders.

Empowering Biodiversity Monitoring: A Multiscale, Multisensor Approach for Germany's Natural Heritage supported by EO4Nature

Annett FRICK, Michael Foerster, Benjamin Stoeckigt, Sascha Gey, Gregor Weyer, Merlin Schäfer, Claudia Hildebrandt, Thorsten Laufhuette, Lena Schultz-Lieckfeld

Abstract: Monitoring the conservation status of German wilderness and natural heritage sites requires a comprehensive approach to capture the complex dynamics of these areas. We developed a multiscale, multisensor indicator framework for assessing habitat types and species habitats within and outside these protected sites. By combining high-resolution multispectral, LiDAR, and radar data, the methodology enables detailed monitoring across multiple spatial scales. The approach integrates remote sensing time series with field data and advanced analysis techniques to derive key indicators for habitat quality, e.g. vegetation dynamics, phytomass trends, soil moisture and habitat fragmentation. For example, the vegetation height indicator was derived using a UNet-based approach and very high-resolution LiDAR data and stereomatched orthophotos to gather large amounts of training data, which were then upscaled to the Sentinel-2 level. A transformer model with thermal encoding processed the full time series to produce robust, yearly vegetation height maps for Germany. This method ensures consistent monitoring of vegetation height dynamics across large, complex landscapes. These remote sensing-based indicators serve furthermore as a foundation for Species Distribution Models (SDMs) to assess habitat suitability for key species. The SDM results help to prioritize restoration efforts and monitor changes within and outside protected sites. The developed indicators and insights will be integrated into the EO4Nature platform, providing a stable, scalable foundation for continuous biodiversity monitoring at a national level. EO4Nature supports the long-term objectives of nature restoration and climate protection, ensuring data-driven decision-making for the protection of Germany's natural heritage.

Broadening the standardized retrieval of vegetation structure metrics from airborne laser scanning point clouds across Europe

W. Daniel KISSLING, Jinhu Wang, Yifang Shi

Abstract: The rapid expansion of national airborne laser scanning (ALS) programmes across Europe provides unprecedented opportunities for large-scale biodiversity monitoring. Yet transforming multi-terabyte point clouds into harmonised, analysis-ready habitat metrics remains computationally demanding and methodologically fragmented. We present a computational framework developed within the MAMBO project that enables standardized, scalable retrieval of vegetation structure metrics from ALS data across diverse European landscapes. Building on the open-source Laserfarm workflow, we implemented automated, parallel and distributed processing in cloud and cluster environments to derive 10 m resolution metrics describing vegetation height, cover, vertical complexity, and structural heterogeneity. The pipeline was deployed across demonstration sites in Denmark, France, the Netherlands, the United Kingdom, and Malta, ensuring consistent metric extraction despite differences in acquisition parameters, landscapes, and point clouds. Beyond workflow automation, we produced harmonised geospatial data products at site level and national-scale, multi-temporal wall-to-wall products for the Netherlands from repeated ALS surveys. These datasets are findable and accessible through established data portals, facilitating integration with in-situ biodiversity observations and complementary remote-sensing sources. The framework is being extended to scalable tree individualization from ALS point clouds, enabling broad-scale mapping of trees at individual level. Our results demonstrate how distributed cloud computing and reproducible workflows bridge the gap between raw ALS data and operational biodiversity indicators. By broadening standardized metric retrieval across Europe, this approach lays the foundation for future pan-European, wall-to-wall vegetation structure products derived from harmonised ALS archives.

MM07a Citizen Science for biodiversity monitoring

Thursday 7 May, 9h00-10h00, Room Auditorium
Chair: Gitte Kragh

Description: This session explores the potential of citizen science as a transformative approach contributing to biodiversity monitoring for policy, research and natural resource management. By involving the general public, communities, and organizations through citizen science and community-based approaches, there is the possibility of addressing biodiversity and environmental challenges at larger scales with an impact on more effective and inclusive conservation practices and strategies. Talks will highlight good practices, how citizen science helps strengthen capacity and foster synergies for biodiversity monitoring, current challenges for implementation across Europe, and how citizen science can enhance our scientific understanding as well as support natural resource management and policy promotion, monitoring and enforcement.

A feedback loop framework for flexible citizen science biodiversity monitoring

Caitlin MANDEVILLE

Abstract: Citizen science supports biodiversity monitoring through both data collection and positive outcomes for citizen science participants and stakeholders. It is also increasingly valued for its responsiveness to evolving data needs and emerging monitoring technologies. However, the integration of new data needs and technologies into citizen science affects not only data collection but also the experiences of participants and stakeholders. Therefore, an understanding of interactions between these two types of impact is needed to inform the design of citizen science programs that meet emerging needs while minimizing trade-offs and maximizing win-wins across impact pathways. We present a feedback loop framework for exploring this question and demonstrate the use of this framework in FOOTPRINTS-CITSCI, a cascade funding project associated with Horizon Europe project TETTRIs. In this project, we developed technological tools to address persistent challenges in citizen science biodiversity monitoring and applied them in a new citizen science program. An AI-driven species identification model and interactive identification key were designed to support participant training in surveying mammals from animal tracks, responding to the common challenge of taxonomic bias. These tools enabled the design of multiple structured monitoring schemes tailored to varied monitoring objectives, responding to the common challenge of limited knowledge of sampling structure. To complete the feedback loop, we assessed the impact of these approaches on participant and stakeholder impact pathways with the aim of identifying opportunities to reinforce positive outcomes. Finally we contextualized our results against ongoing research on flexibility in citizen science, drawing lessons on how to balance specific data needs with intended outcomes for participants and stakeholders.

Using environmental sensor networks and citizen science to monitor priority species in Flanders, Belgium

Stijn VAN ONSEM

Abstract: Systematic and standardized species monitoring in support of European and regional legislation represents a complex challenge, even at relatively small spatial scales. In Flanders, Belgium, we apply innovative sensor networks (including camera traps, biologgers and passive acoustic monitoring) and citizen science to monitor population trends, distribution and ecology of a significant part of protected or threatened species, and to survey the spread of invasive alien species. We present our overall experience with both sensor networks and citizen science to comply with monitoring obligations for the Birds, Habitats and Water Framework Directives and the Eel and Invasive Alien Species

Regulations, and consider their potential role in future monitoring programs under the Nature Restoration Regulation. In Flanders, monitoring through sensor networks includes the wide-scale use of camera traps, biologging of migratory fish species and sea birds (LifeWatch, Biodiversa+) and experimental pilot studies using passive acoustic monitoring for bats and birds or image recognition techniques for moths and plants (Biodiversa+). Citizen science projects like Vespa-Watch, Craywatch and several eDNA initiatives allow us to map the distribution of invasive alien species, while the citizen science projects 'Species Monitoring Schemes' and 'Monitoring Agricultural Species' provide long-term, standardized data for protected species. Innovative sensor networks and citizen science for mass surveillance and monitoring in support of nature policy have a large potential in the Flemish region, but often face challenges in terms of upscaling, data management, integration into derived indicators, durability of the volunteer network, and, most notably, sustainable funding.

FunDive: pan-European fungal monitoring enriched by structured citizen science engagement backed by molecular-based identification

Igor SIEDLECKI, Dima Bálint, de-Miguel Sergio, Dueñas Margarita, Dziurzyński Mikołaj, Furtado Ariadne N.M., Gonçalves Susana C., Kochanowski Michał, Martín María P., Quintanar Alejandro, Rinaldi Andrea C., Rivas-Ferreiro Mauro, Rusevska Katerina, Tischer Marta, Zervakis Georgios I., Pawłowska Julia, Heilmann-Clausen Jacob

Abstract: Despite their ecological importance, fungi remain severely understudied. This limits conservation efforts and leaves fungi vulnerable to environmental and anthropogenic pressures. Consequently, there is an urgent need for large-scale monitoring. However, monitoring based on ephemeral sporocarps requires repeated surveys and substantial human resources. While volunteer mycologists can generate data that would be difficult to achieve through professional monitoring alone, many citizen science initiatives are grassroots, locally coordinated, and rely solely on morphological identification. As morphological identification is often difficult, DNA barcoding has become an essential tool for identifying and validating fungal taxa. FunDive is a pan-European initiative that brings together 42 academic institutions and NGOs from 26 countries to improve fungal monitoring across Europe. The initiative relies heavily on methodologically coherent citizen science engagement supported by molecular identification. Activities are organized into 16 projects that require different levels of taxonomic expertise and target specific taxa or environments. These targets are defined with scientific and conservation goals in mind. Publicly available guidelines describe the procedures for collecting specimens and metadata. Project participants have access to 36 educational materials and identification keys. Since 2024, citizen scientists have collected approximately 5,000 specimens from 32 European countries. Each specimen has been photographed and deposited in recognized fungaria. Citizen scientists assist partially with DNA isolation, while scientific institutions perform Nanopore sequencing of the fungal ITS barcode using custom protocols. All data are openly shared through the FunDive portal and will be published in GBIF. FunDive develops and tests solutions for efficient DNA-assisted fungal monitoring, and engages citizen scientists to improve knowledge and conservation of fungi in Europe.

Data Integration for Species Distribution Models Under Spatial and Environmental Separation

Pablo UBILLA PAVEZ, Diegos Marcos, Christophe Botella

Abstract: An important part of ecology is understanding where species occur in relation to their environment, a question addressed through Species Distribution Modelling (SDM). These models provide spatially explicit estimates of species distributions, which are essential for understanding biodiversity at large scales. SDMs extend far beyond what direct observation can capture and help identify which sites should be prioritised for monitoring or conservation.SDMs are typically supported by two types of data: Presence–Absence (PA) and Presence-Only (PO). PA data, collected through structured surveys, provide high-quality information but are costly and therefore sparse. PO data, by contrast, come from opportunistic observations and contain only positive detections, making them abundant but biased. These datasets present a clear trade-off between quality and quantity, and data-integration approaches seek to combine PA and PO information so that models can exploit the complementary strengths of both.It is not yet clear how much integration can improve our models, particularly when the available PA training data are geographically or environmentally distant from the prediction region. This issue is especially relevant for under-sampled areas, where PO data may be more readily available. Previous studies have explored this problem using simulations, but these lack the complexity and noise of real ecosystems. Using real data is therefore essential for understanding how these methods behave in practice and for assessing their value in biodiversity modelling.Our work studies this question using real-world datasets. We propose a partitioning framework that creates controlled spatial separation between PA training and prediction regions while respecting the environmental constraints of each dataset. Using this framework, we evaluate several state-of-the-art SDM approaches, including deep neural network models adapted to support integrated PA–PO training through specialised loss function

Leveraging opportunistic data to monitor the status of dragonflies

Lisa NICVERT, Aletta Bonn, Diana Bowler, Jason Bried, Aurélie Coulon, Geert De Knijf, Thore Engel, Maxime Fajgenblat, Roy van Grunsven, Alienor Jeliazkov, Marie Lamouille-Hébert, Colin Fontaine, Martin Jeanmougin, Reto Schmucki

Abstract: Standardized monitoring programs are the gold-standard to monitor biodiversity status. However, they are heavy and costly to set up and maintain, and very few programs are deployed at the European scale. In the pressing context of the biodiversity crisis, evaluating biodiversity status often has to rely on imperfect data for rapid assessment. In this context, opportunistic data collected by volunteer naturalists are a very precious resource, especially to leverage large-scale monitoring for charismatic species popular among naturalists. In this talk, I present how we assessed dragonflies distribution trends at the European scale with the DRAGON project. We first gathered data from 27 organizations across Europe, totaling more than 15 million observations for 128 European dragonflies species. To correct biases inherent to opportunistic data, we used occupancy modelling: I briefly present this method and its strengths and weaknesses. I also discuss our first results and their relevance for conservation at the European scale. Finally, I reflect on the comparison between opportunistic and standardized monitoring.

MM07b Citizen Science for biodiversity monitoring

Thursday 7 May, 10h00-11h00, Room Auditorium
Chair: Gitte Kragh

Description: This session explores the potential of citizen science as a transformative approach contributing to biodiversity monitoring for policy, research and natural resource management. By involving the general public, communities, and organizations through citizen science and community-based approaches, there is the possibility of addressing biodiversity and environmental challenges at larger scales with an impact on more effective and inclusive conservation practices and strategies. Talks will highlight good practices, how citizen science helps strengthen capacity and foster synergies for biodiversity monitoring, current challenges for implementation across Europe, and how citizen science can enhance our scientific understanding as well as support natural resource management and policy promotion, monitoring and enforcement.

Scaling up marine biodiversity monitoring through large-scale participatory events, the BioMARathons

Berta COMPANYS, Xavier Salvador, Rocio Nieto Vilela, Rita da Silva, Sara Riera, Catia Monteiro, Jaume Piera

Abstract: Marine citizen science monitoring requires a well established Community of Practice (CoP) reporting observations throughout the year. Here we present the BioMARathons as a participation engagement tool which increases the participant's retention rate after each edition. As a result, sustained

observations' are registered all year around. BioMARathons are large-scale participatory monitoring events during the summer period, implemented in two sites at the Catalan coastline (ES) and at the continental Portuguese coast (PT). For the past 5 years, the consolidated Catalan CoP reached outstanding numbers including a cumulative of 1.300 participants who contributed with over 400.000 observations and registered more than 3.800 species. Last year, a complete coverage of the Catalan coastline on 10x10 km grid cells resolution was achieved. The participatory event model has been successfully replicated in the Portuguese coast. Starting with pilot activities in 2023, and then the implementation of the BioMARathon event for the past two years. Focused on the Portuguese intertidal rocky shores, the event gathered over 200 participants who reported more than 8.300 observations registering 760 species, cumulatively for the past three years. Marine biodiversity participatory monitoring is key to covering large extensions of coastline with high temporal frequency and obtaining a huge amount of biodiversity information. Among the BioMARathon results, species occurrences with special interest, including threatened, protected and non-indigenous species were reported. These data is valuable input in marine spatial planning for conservation and restoration.

Vigie-Nature: reflecting on 20 years of citizen science monitoring in France

Charles THÉVENIN

Abstract: Vigie-Nature (Nature's Lookout) is a citizen-science programme for monitoring biodiversity in France, managed by the French National Museum of Natural History. The programme relies on data collection schemes focusing mainly on common species and involving a variety of citizens (general public, naturalists, teachers, practitioners, farmers) in order to track changes in biodiversity at the national scale. With the help of over 40 000 volunteers over the years, the Vigie-Nature programme collected millions of observation data of flora and fauna. I will show how these structured or semi-structured schemes help us achieve 3 main objectives: promote citizen empowerment and public learning on biodiversity, provide indicators and tools for conservation policies, and enhance our scientific understanding of biodiversity patterns at large scale. First, I will present an overview of the 23 existing data collection schemes developed by Vigie-Nature, their similarities and differences, particularly in terms of sampling strategy, characteristics of participants, as well as trends and indicators they produce. I will also discuss the challenges in data synthesis and openness that arise thanks to the multitude of stakeholders involved (institutions, participants, NGOs and researchers). Finally, I will provide some examples of trade-offs that we face when trying to help strengthen capacity at the local scale while also contributing to national surveyance schemes, and managing derived data products to align with biodiversity monitoring standards at the European scale.

“DNA macht Schule” – a citizen science eDNA biodiversity monitoring project for schools

Marie-Thérése WERNER, Svea Isabel Kleinert, Nora Lösing, Justin Timm, Philipp Schmiemann, Dominik Buchner, Florian Leese

Abstract: Biodiversity monitoring is the foundation for ecological status class assessments of freshwaters. These bioassessments are essential for achieving the “good ecological status” target of surface and groundwater bodies as required by the EU Water Framework Directive (WFD). However, many freshwater ecosystems are not monitored at all. In North Rhine-Westphalia (NRW), Germany’s most densely populated state, only 27% of the total length of all running waters fall under the WFD and are monitored, neglecting the vast majority of small streams and rivers. To address this gap, the German Federal Environment Agency (Umweltbundesamt) funds the citizen science project “DNA macht Schule” (i.e. DNA makes it into school). The project aims to explore the potential of citizen science to enable long-term and cost-effective biodiversity monitoring and at the same time pupils to participate in research, apply innovative methods and become aware of the natural environment. In the project, environmental DNA (eDNA) samples are taken by pupils according to specific guidelines and analysed in the molecular laboratory of our university. The data are used to evaluate the ecological status of the small rivers and streams based on the resulting Biological Quality Element (BQE) data for fish and benthic macroinvertebrates. The processed molecular data are send back to the participating schools, completing a full circle of knowledge transfer and enabling pupils to understand how their sampling contributes to scientific analyses and environmental decision making. We present the first results of our project to gain attention for the biodiversity of neglected small water bodies, demonstrate the potential of citizen science combined with eDNA, and discuss both opportunities and challenges for large-scale implementation.

Citizen[OC1.1] Science butterfly monitoring along a sharp climate gradient reveals rapid declines, seasonal shifts and high percentage of species becoming threatened

Orr COMAY, Oz Ben Yehuda, Ofir Tomer, Dubi Benyamini, Israel Pe’er, Guy Pe’er, Ittai Renan, Tania Bird, Shira Grossbard, Victoria Yael Miara, Udi Segev, Gilad Ben Zvi, Dotan Rotem

Abstract: National Citizen Science Butterfly Monitoring Schemes (BMS) are expanding globally due to their public appeal, and their correlation with other insects contributes invaluable knowledge on trends and underlying causes of insect declines. The Israeli BMS (BMS-IL) was established in 2009, spanning from the Mediterranean Upper Galilee to the hyper-arid Arava valley[AP2.1]. National data from Pollard Transects indicated a decline of 34% (abundance) and 18% (species richness) with an annual mean 3.4% and 1.6% respectively from 2010 to

2022. Fifty-five of 138 native species are now defined as threatened. Over this period, seasonal abundance peak was delayed from April 13th to May 13th, and richness peak from April 21st to June 4th. Furthermore, the mean species-specific mid-season date (date by which half the annual individuals were expected) was delayed from June 16th to July 1st. To our knowledge, these declines are the second highest among all BMS, after Illinois. We attribute these losses mostly to high human demographic growth which has driven rapid anthropogenic land-use changes. The seasonal delays we found differ from those reported in temperate climates, (which occur mainly as activity extending into November-December), but align with those found in Iberia[3.1אק], with a similar climate. High elevation areas in Israel were most species rich and harbored the highest percentage of threatened species. [AP4.1]Most butterfly species here are Palearctic, with many reaching their southern global distribution edge in Israel. We therefore expect the above-average warming pace found in the Levant to place severe pressure on Israel's butterfly fauna, likely driving rapid alterations in species' community in the coming years for both butterflies as well as many other insect species already threatened by habitat loss and pesticide usage.

SoilRise: Citizen Science for Earthworms – A Case Study of Urban Parks

Agnieszka JÓZEFOWSKA, Pacanowski P., Potthoff M., Greifenstein N., Randecker, L., Euteneuer P., Sturm L., Stuhler, J.,Schmidt O., Clune S., Fertil A., Le Callonec L.

Abstract: SoilRise is an international research project dedicated to soil biodiversity, with earthworms as the central focus because they act as key "ecosystem engineers" and bioindicators of soil quality. The project develops a mentor-based citizen-science approach: students are trained as mentors and, together with farmers, gardeners, and green-space managers, they conduct standardised surveys in arable soils, on green-area lands, and in urban gardens across five European countries. By combining classic morphological identification with DNA barcoding of the COI gene, the programme harmonises taxonomy and detects cryptic, threatened and invasive species. SoilRise also has a strong educational dimension, building networks of citizen science and raising soil literacy. A concrete application of this methodology is the study of earthworms in urban parks. In parks in Poland, Austria, Germany, France, and Ireland, SoilRise mentors followed an identical protocol: at each site, five soil blocks (20 × 20 × 25 cm) were excavated; earthworms were hand-sorted, identified to species, and assigned to ecological groups (epigeic, endogeic, anecic). The same blocks were subsampled for analysis of pH, organic matter content, texture and other physicochemical properties. The data yielded earthworm density, biomass, species richness and diversity indices (e.g., Shannon, Simpson). Results revealed clear differences among parks linked to management regimes, soil characteristics, and climatic gradients. Despite intensive use, urban parks proved to be important habitats for functionally diverse earthworm communities that sustain essential ecosystem services such as soil structure formation, water retention and nutrient cycling. The study demonstrates that a well-designed citizen science framework can reliably monitor below-ground biodiversity across many cities and support evidence-based green space planning.

MM03c Novel remote-sensing approaches for biodiversity monitoring using multiple sensors - Part III. Applications and case studies

Thursday 7 May, 11h30-12h30, Room Auditorium
Chairs: Petteri Vihervaara & Sandra Luque

Description: Possibilities to use various remote sensing technologies to monitor biodiversity have increased enormously during the last years. The aim of this session is to demonstrate novel approaches to integrate data from various sensors (i.e., multi- or hyperspectral, LiDAR, radar etc.), together with in-situ data to help monitoring biodiversity at large scale. Preferably the emphasis could be either on ecosystem structure and functioning, or community composition, but also novel approaches to detect changes in species populations are welcome.

Mapping, monitoring and enhancing BCEs biodiversity at large scale through the ESA Coastal Blue Carbon project.

Benoit BEGUET, Elodie BLANCHARD, Ghali BEN-BOUZID, Rémi BUDIN, Olivier REGNIERS, Nicolas Debonnaire, Nicolas COELHO, Meghana Paranjape, Marlow PELLATT, Karen KOHFELD, Oscar SERRANO, Miguel A. MATEO, Marie-Aude SÉVIN, Christine DUPUY, Christophe PROISY, Thibault CATRY, Aurélie DEHOUCK, Virginie LAFON

Abstract: As part of the ESA Coastal Blue Carbon project, we present large-scale mapping of coastal blue carbon ecosystems and associated carbon stocks using a transferable Earth observation framework across multiple coastal regions. We developed an operational framework for multi-site habitat mapping and carbon assessment using Sentinel-2 time series and Pléiades very high-resolution imagery. The study targets three key ecosystems: (i) Posidonia oceanica meadows in the Mediterranean, (ii) intertidal seagrass meadows and salt marshes along the French Atlantic coast and Canada, and (iii) mangroves in French Guiana. The pipeline integrates bi-monthly compositing, feature engineering, supervised classification, and spatial structuring within a 20 m hexagonal grid to harmonize reference data from field surveys, photo-interpretation, and existing maps. Key methodological choices address optical noise, tidal variability, and temporal aggregation, while validation protocols assess spatial transferability using extensive in-situ datasets. Applied to 2015, 2020, and 2025, the framework enables

consistent multi-date mapping and medium-term ecosystem dynamics analysis. Tested across diverse ecological, geomorphological, and tidal contexts, it demonstrates strong scalability and generalization. Overall accuracies range from 0.84 to 0.91, with mean F1-scores between 0.75 and 0.93 depending on site, year, and habitat. By linking mapped habitats to carbon storage estimates, the project moves from cartography toward ecosystem service quantification, supporting climate mitigation, biodiversity monitoring, and coastal management at regional to continental scales.

Wall-to-wall and through time: towards dynamic habitat monitoring with Earth observation foundation models

Sara Si-Moussi, Wilfried THUILLER

Abstract: Habitats integrate the abiotic conditions, vegetation structure, and biological communities that underpin biodiversity and sustain ecosystem services. Tracking their extent and condition over time is central to European conservation policy — from the Habitats Directive to the Nature Restoration Law — yet available maps remain largely static and coarse, reflecting the difficulty of characterising hundreds of ecologically distinct types continuously across a continent. Earth observation foundation models, pre-trained on large satellite archives, offer a new capacity for automated, large-scale habitat characterisation that generalises across landscapes and seasons. We present a pan-European application producing wall-to-wall maps at 100-metre resolution for 260 EUNIS Level 3 types across the EEA39 territory, and discuss the potential of the growing satellite archive for reconstructing historical habitat trajectories and anticipating future dynamics. We reflect on the key barriers to operationalising this vision and on what the monitoring community can do to help overcome them.

Unsupervised handling of acquisition artefacts for large-scale forest mapping

Paul TRESSON

Abstract: Tropical forests play a key role in Earth biogeochemical cycles and host a large portion of terrestrial species. Due to the scale of forests such as the Congo Basin Forest and the difficulties to access these ecosystems, large scale monitoring requires the leverage of remote sensing acquisitions such as Unmanned Aerial Vehicles (UAVs) or satellites. However, the clouds, aerosols and intricate shadows of the canopy make the analysis of remote sensing products over tropical forests very susceptible to acquisition artifacts that hinder the large-scale mapping of the forest. Deep learning has shown great success in handling various acquisition conditions in a variety of image analysis tasks but this is always constrained to large scale annotated dataset that can be hard to obtain when working with expert labelled data and remote terrain. Here we propose a method to make a pre-trained model robust to acquisition artifacts with no labels using Joint-Embedding Predictive Architectures. We test this method on Sentinel

2 and UAV imagery to assess its versatility and show improvement of the model's feature space and robustness to acquisition artifacts. Along with robustness, this pre-training setup leads to the adaptation of the models to new domain and improved accuracy in low and imbalanced data regimes. This method provides robust spatial features which can then be merged with fine temporal data such as produced by geostationary remote sensing for a finer monitoring of species and Essential Biodiversity Variables in the Congo Basin Forest.

Vallu - Finnish monitoring system for habitat types

Topi TANHUANPÄÄ

Abstract: Nature Restoration Regulation builds on knowledge about the location and condition of Natura 2000 habitat types. At present, many European countries do not have this information ready and hence need efficient tools to fill this knowledge gap. Remote Sensing (RS) and Earth Observation (EO) methods have been widely acknowledged as the only viable option for developing wall-to-wall maps that can offer both the location and quality estimates for habitat types. Critically, these methods need reliable and unbiased data for training and validation that can only be measured in the field. However, most of the key habitat types and their essential quality characteristics are rare, scattered, and clustered in the landscape, which makes them hard to capture in field surveys with sampling designs used in, for example, traditional forest inventory. This talk demonstrates a system that is built specifically for collecting nation-wide data from habitat types for a) inventory and monitoring, but also to be used as b) training data for RS and EO methods. The system builds on locations of known habitat type occurrences and uses them to stratify the landscape into most favorable areas for collecting data from rare and scattered habitat types. The talk will give an outlook on combining drone technology with traditional field work, which can be used to support more efficient collection of EO training data.

PS01 Posters

Lessons for Europe from a feasibility case study of a national scale satellite survey for savanna elephants in Botswana

Rebecca WILKS, Ruth King, Stuart King, Michael Chase, Kelly Landen, Niall McCann, David Williams, Murray Collins

Abstract: The majority of Africa's savanna elephants are found in Botswana (Chase et al, 2016) where they roam freely across the whole northern extent (120,000km^2). Critical abundance estimates are currently obtained via stratified aerial survey once every 4 years, however this is a logistically challenging operation and leaves large temporal data gaps for the endangered species. Satellite's significant benefits include easy scalability and permit-free imaging, whilst elephants had previously being shown detectable by very high resolution (VHR - 30cm) satellite (Duporge et al, 2021). We therefore investigated the feasibility of directly replacement by AI-enabled satellite survey, and provided a generalised species-agnostic framework for applications in heterogeneous vegetated environments such as savannas. Lessons to discuss include (i) accounting for satellite image characteristics upon AI performance and abundance estimates, (ii) what counts as "obstructive" vegetation in VHR, (iii) making justifiable corrections for hidden individuals, (iv) trade-off between very high cost of imagery and conservation budgets, (v) analysis uncertainty and trust from conservation managers, and (vi) realistic fusion of survey modalities towards increased temporal monitoring. As satellite resolutions increase towards drone capabilities (<10cm), such lessons provide transferable benefit for future planning of biodiversity monitoring at-scale across the EU.

Implementation of standardized monitoring protocols at eLTER sites in Austria

Lisa REISS

Abstract: Addressing complex and interlinked environmental challenges such as climate change, biodiversity loss, and socio-ecological transformations requires collaborative, transdisciplinary, and data-driven approaches. The European Long-Term Ecosystem, Critical Zone and Socio-Ecological Research Infrastructure (eLTER RI) responds to this need through a continental-scale 'whole system' approach. A central component of this framework is the eLTER Standard Observations system, which standardises data collection across 65 variables covering six ecosystem spheres (geosphere, pedosphere, hydrosphere, biosphere, socio-econosphere, and lower atmosphere), as well as major abiotic, biotic, and socio-ecological characteristics and fluxes of matter, energy, and water. This standardisation ensures consistency and comparability across sites, facilitating large-scale data products and cross-site analyses. In eLTER, biodiversity will be surveyed using novel biodiversity monitoring protocols for understudied taxonomic groups by applying eDNA metabarcoding (e.g., insects and soil biota) and fully automated workflows focusing on passive acoustic monitoring for high-resolution bird and bat data. The Research Infrastructure will be launched in 2027 and will cover 250 sites across Europe when fully rolled out. In Austria, the protocols, logistics and organizational framework is currently implemented at ten eLTER sites. In this pilot project, we are gaining practical experience that will inform the Europe-wide eLTER community and support the optimization of monitoring approaches in related projects and research infrastructures through the creation of toolkits, scripts, and improved protocols.

Citizen Science–Driven Acoustic Monitoring of Mosquitoes Using AI-Assisted Species Identification

Dorottya Kovács, Julie Augustin, Sándor Zsebők, Zsóka Vásárhelyi, Zoltán Soltész, László GARAMSZEGI

Abstract: Effective surveillance of mosquito populations is critical for managing vector-borne diseases, yet traditional monitoring approaches are often resource-intensive and spatially limited. Here, we present a novel, citizen science–based framework that integrates mobile technology and artificial intelligence (AI) to enable large-scale acoustic monitoring of mosquitoes under real-world conditions. Building on prior experience with participatory surveillance programs, we develop a dedicated smartphone application that allows volunteers to record mosquito flight sounds, collect standardized metadata, and upload observations to a central database. These crowd-sourced recordings are combined with laboratory-generated, expert-validated datasets to construct a comprehensive acoustic library of mosquito wingbeat sounds. We then use these data to train and optimize next-generation AI models capable of robust species identification despite environmental noise, device heterogeneity, and biological variability. Special emphasis is placed on improving model generalizability through diverse training data, advanced signal processing, and adaptive learning techniques. Our approach addresses key limitations of existing acoustic identification systems, which are typically based on controlled laboratory recordings and fail to perform reliably in field conditions. By leveraging citizen science, we capture a wide range of ecological contexts, including variation in temperature, habitat, and species composition, thereby enhancing model performance and ecological relevance. Beyond methodological innovation, this framework fosters public engagement and awareness of vector ecology and emerging health risks. The resulting tools—including an open-access sound repository and a scalable AI-based classification system—have strong potential for integration into existing mosquito surveillance networks. Ultimately, this work contributes to more efficient, data-driven monitoring strategies.

Bio-dIv(A): Leveraging Environmental Noise Measurements for Biodiversity Assessment in Anthropized Environments

Abbes KACEM, Olivier Taugourdeau, Pierrick Devoucoux, Maxime Esnault, Guillaume Labeque

Abstract: Monitoring biodiversity at large scale requires opportunistic methods capable of capturing ecological dynamics continuously and non-invasively. Passive acoustic monitoring (PAM) offers a powerful approach to complement traditional field surveys, particularly in human dominated environments where observer presence and limited sampling windows restrict data collection. The Bio-dIv(A) project investigates how professional environmental noise sensors, originally deployed for regulatory acoustic assessments, can be repurposed as bioacoustic devices for biodiversity monitoring. A comprehensive benchmark compares bioacoustic recorders, class-1 sound level meters, databases, and AI

models for species identification. Results show that professional sound level meters record high fidelity audio across the full audible spectrum (20 Hz–20 kHz), enabling detection of birds, amphibians, mammals, and part of orthopteran activity. A two stage processing pipeline is developed: automatic discrimination of biological vs. anthropogenic sound events using generalist classifiers, followed by taxonomic identification through dedicated models such as BirdNET. Two 24 hour measurement campaigns were conducted along railway and road corridors, combined with expert ornithological validation. Results confirm the feasibility of extracting biodiversity indicators from environmental noise measurements and highlight both the robustness and limitations of current AI models under real world, noisy conditions. This work reveals the potential of leveraging existing environmental noise sensor networks for large-scale biodiversity monitoring. Integrating long term acoustic recordings with automated species identification enables continuous biodiversity assessment, detection of discreet or nocturnal species, and the development of new soundscape-based ecological indicators. This approach opens the path toward integrated acoustic observatories that connect noise monitoring and biodiversity conservation.

Cost effectiveness of citizen science in monitoring biodiversity

Constantinos PHANIS

Abstract: This report evaluates the importance and cost-effectiveness of citizen science in biodiversity monitoring schemes across Europe, within the framework of the Biodiversa+ partnership. By reviewing existing methodologies and analysing case studies, the report demonstrates how citizen science complements professional monitoring, enhances public engagement, and provides cost-efficient solutions for large-scale and long-term biodiversity data collection. Methods such as Cost-Effectiveness Analysis (CEA), Benefit-Cost Ratio (BCR), and Multi-Criteria Analysis (MCA) could be employed in the assessment of the scientific and economic contributions of volunteers, highlighting the value of integrating citizen science into mainstream monitoring strategies. The report underscores the dual benefits of citizen science: it produces robust environmental data and fosters environmental stewardship among participants. Best practices for ensuring data quality, sustaining volunteer engagement, and leveraging digital technologies (e.g., mobile apps, AI-assisted identification, and participatory platforms) are explored in depth. Moreover, the report identifies critical challenges - such as retention, logistics, and long-term sustainability - and provides actionable recommendations to address them. Overall, the deliverable strengthens the case for embedding citizen science in EU biodiversity policy, advocating for structured support, harmonisation of data standards, and greater visibility for volunteer-based contributions in pan-European monitoring frameworks.

Two approaches to long-term citizen science biodiversity monitoring: lessons learned from the RitmeNatura and FenoCat networks

Ester PRAT, Domingo-Marimon C, Formoso A, Gaya G, Busto M, De Yzaguirre X, Cunillera J

Abstract: Citizen science has emerged as a powerful approach for monitoring biodiversity, enabling large-scale data collection while fostering public engagement with environmental change. However, its effectiveness strongly depends on project design and implementation. This contribution presents a comparative analysis of two citizen science initiatives devoted to phenology monitoring in Catalonia: RitmeNatura, managed by CREAF, and the FenoCat Network, managed by the Catalan Meteorological Service (SMC), which represent contrasting yet complementary approaches. RitmeNatura follows an open, highly participatory model that prioritizes scalability and broad engagement, generating large volumes of observations across wide spatial and temporal scales. In contrast, the FenoCat network is based on a more structured framework, with defined protocols and systematic monitoring, resulting in more consistent and standardized datasets. Through this comparison, we identify shared challenges, including participant recruitment and retention, data validation, and the integration of citizen-generated data into scientific workflows. We also highlight how these challenges manifest differently depending on the approach. Our analysis emphasizes key lessons learned: while structured protocols enhance data quality, they may limit participation; conversely, open models increase engagement but require robust validation mechanisms. In both cases, sustained participation depends on effective feedback and participant recognition. We argue that the choice of citizen science approach should be guided by research objectives, as different questions require different types of data. Structured models support high data consistency, while open approaches better capture broad spatial and temporal patterns. Aligning the model with intended outcomes is therefore essential, providing practical guidance for designing and scaling citizen science initiatives in biodiversity monitoring.

PS02 Posters

pdindicatoR - calculate phylogenetic diversity indicators from GBIF species occurrence cubes

Lissa BREUGELMANS

Abstract: To achieve the Global Biodiversity Framework's (GBF) ambitious 2030 targets to halt biodiversity loss, 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 preserve the full range of 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 and Goal B. Within the B3 project, a workflow was developed which combines a user-provided phylogenetic tree and a GBIF species 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 used a comprehensive angiosperm phylogeny and GBIF occurrence data, generated spatial maps of phylogenetic diversity and overlaid them with current protected area boundaries. In addition, national red list status data were used 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.

Co-producing Marine Knowledge through Blue Citizen Science for Biodiversity Monitoring

Tereza FONSECA, Sedef Korkmaz, Ayçe İdil Ağca, Inês Cardoso.

Abstract: Marine ecosystems are increasingly exposed to cumulative pressures from human activities, climate change, and emerging pollutants. Addressing these challenges requires robust and spatially comprehensive biodiversity data; however, existing monitoring systems often remain limited in coverage, frequency, and accessibility—particularly in coastal and nearshore environments. Blue citizen science has emerged as a promising approach to complement conventional monitoring by expanding data collection and fostering inclusive participation. Yet, challenges remain regarding data quality, standardization, and integration into scientific and policy frameworks. DiverSea is a Horizon-funded initiative focused on European coasts (including Türkey Norway, & Portugal) with complementary activities in Africa. It co-produces marine biodiversity knowledge through participatory monitoring, engaging communities, divers, and other volunteers in structured biodiversity assessments and water quality monitoring, using digital tools. The approach integrates three key components: (1) community engagement and capacity building; (2) data collection; and (3) data validation and integration with scientific workflows. Particular attention is given to ensuring data reliability through training, protocol harmonization, and expert validation mechanisms. This model aims to improve spatial and temporal data coverage

while strengthening ocean literacy and stakeholder engagement. Integrating citizen-generated data into monitoring frameworks also supports more inclusive and adaptive marine governance, including contributions to Marine Protected Area management. By bridging scientific knowledge and local experience, DiverSea demonstrates how blue citizen science can move beyond data collection to support evidence-based, participatory conservation, while highlighting key opportunities and challenges for scaling across diverse ecological and institutional contexts.

Towards a continent-wide harmonised estimation of wildlife density: lessons learnt from a large-scale camera-trapping network

Stefania ZANET, Guerrasio T, Vicente J, Acevedo P, Blanco-Aguiar JA, Casaer J, Ferroglio E, Jansen P, Liefting Y, Palencia P, Rowcliffe M, Scandura M

Abstract: The European Observatory of Wildlife (EOW), developed within the ENETWILD project funded by the European Food Safety Authority, is a collaborative network aimed at generating harmonised data on wildlife populations across Europe using standardised camera-trapping (CT) protocols and the Random Encounter Model (REM). A key lesson from this initiative is the importance of strict protocol standardisation across all steps, from field deployment to data processing, to ensure comparability among sites and countries. The integration of photogrammetry into CT workflows has proven essential to reduce uncertainty in key REM parameters, improving the robustness of density estimates. Another major insight concerns data management. The use of platforms such as Agouti enables semi-automated workflows for image annotation, parameter estimation, and data standardisation (CamTrap DP), reducing processing time while ensuring data quality and reproducibility. This standardisation supports scalable and automated analyses. The EOW also highlights challenges typical of large collaborative networks, including variability in field conditions, operator expertise, and data quality. Addressing these required continuous training, clear guidelines, and iterative protocol refinement, leading to increased consistency and precision over time. Finally, adherence to FAIR data principles has been fundamental to maximise data reuse and interoperability, supporting integration with wildlife monitoring and disease surveillance initiatives. Overall, the EOW demonstrates that standardisation, robust data workflows, and coordinated collaboration are key to effectively scaling camera-based wildlife monitoring.

Engaging School Communities in Biodiversity Monitoring through Citizen Science: A Case Study from Cyprus

Constantinos PHANIS

Scaling biodiversity monitoring with audio-ML

Burooj GHANI

Abstract: The ecological crisis is reshaping biodiversity at a rate that outpaces our ability to measure it. Machine listening, the use of artificial intelligence (AI) to interpret sound, offers a powerful approach to expand the scale of monitoring efforts. From dawn chorus to bat calls, passive acoustic monitoring can capture the acoustic information of ecosystems across vast areas and long time spans. The sheer volume of audio data produced creates a bottleneck that AI shows immense promise in resolving. Machine listening inherits many general machine learning limitations: algorithms depend on large collections of annotated recordings from which they can learn to recognize species. Yet, real-world training data is limited by taxonomic imbalance, a lack of 'strong' labels, and domain shifts that prevent models from generalizing across habitats and recording devices. Current tools favor birds, leaving significant gaps for European bats, amphibians, and insects. This talk introduces our sound recognition models and publicly available datasets for four major European taxa: birds, bats, anurans, and orthopterans. We demonstrate how these tools close the existing monitoring gaps by strengthening both the models themselves and the data foundations upon which they are built. Our bird model AvesEcho is directly integrated within Xeno-Canto, one of the world's largest repositories of wildlife sound. Through this partnership with Xeno-Canto, we further address the transition from weak labels to the strong labels necessary for the next generation of multi-taxa AI. Our efforts aim to improve classification performance and reduce taxonomic and geographic blind spots. We will also discuss our experiments with AI-assisted audio transect walks as an efficient alternative to PAM for data collection. By uniting open data, collaborative infrastructure, and machine listening, we aim to transform how Europe listens to - and safeguards - its biodiversity across taxa, habitats, and borders.

BioMonWeek
2026
The European
Conference for
Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Public policy and funding for monitoring — Science-policy dialogues

PP01a Role of monitoring in the Nature Restoration Regulation

Tuesday 5 May, 11h30-12h30, Room Sully 3
Chair: Colombe Warin

Description: Nature restoration is vital for reversing ecosystem decline and ensuring both environmental and economic resilience across Europe. The Nature Restoration Regulation (NRR) entered into force on the 18 August 2024, setting a bold and necessary framework for restoring Europe's degraded ecosystems. Its goal is to reverse biodiversity loss, strengthen climate resilience, and ensure long-term environmental and economic sustainability. Key targets include restoring at least 20% of degraded ecosystems by 2030 and all degraded ecosystems by 2050. In this session, we welcome abstracts to show successful stories of nature restoration projects and initiatives, in all ecosystems (forest, aquatic, coastal, freshwater, etc). Considering the recently approved Nature Restoration Regulation, we will explore questions such as, how to get towards a successful implementation? What is needed? Which indicators can we use?

What are the key issues in biodiversity monitoring in light of the challenges posed by the EU Nature Restoration Regulation?

Catherine JULLIOT

Abstract: As part of the implementation of the EU Nature Restoration Regulation, the French government has identified significant needs in the area of biodiversity monitoring. Against a backdrop of budgetary constraints, monitoring systems must be prioritised and designed to directly address regulatory and operational objectives. This raises the issue of pooling monitoring systems, whether at land-sea or land-freshwater interfaces, but also within each type of ecosystem. Differences in historical regulatory frameworks or implementation constraints explain why the challenges may vary depending on the type of ecosystem. For marine environments, the organisation of monitoring for restoration purposes is a key issue at national level. For terrestrial and aquatic environments, the European regulation requires a massive consolidation of monitoring of natural habitats whose protection or restoration is deemed a priority (grasslands, peatlands, old-growth and riparian forests, lakes and rivers, habitats of species of Community interest such as amphihaline migratory species, etc.). For any ecosystem, this implies having the capacity to locate these natural habitats and assess their conservation status at a sufficient scale to plan their restoration. For the European regulation to be fully operational, it also raises issues relating to the coordination of different levels: i) harmonisation of monitoring at European level (to be taken into account in particular in the context of the forthcoming revision of the Marine Strategy Framework Directive), ii) monitoring mechanisms designed specifically to drive action: ensuring the involvement of local stakeholders, who are the main drivers of restoration, and extending monitoring to the pressures on biodiversity and to the practices in place, whether beneficial or not. Finally, to ensure the long-term effectiveness of restoration policies, public operators and decision-makers must take the effects of climate change into account.

Incorporating genetic monitoring into nature restoration can can meet practitioners' needs

Julia GEUE, Jill Sekely, Tsipe Aavik, Astrid Böhne,Jessica da Silva, Robert Ekblom, Jannis Feigs, Martin Fischer, Katrin Heer, ,Aveliina Helm, Christina Hvilsom, Aapo Kahilainen, Alexander Kopatz, Deborah Leigh, Joachim Mergeay, David O'Brien , Ivan Paz-Vinas, Ricardo Pereira, Gernot Segelbacher, Madlen Stange, Jasmine Tschan, Julia von Gönner

Abstract: Global commitments to halt biodiversity loss and restore degraded ecosystems, including the Kunming-Montreal Global Biodiversity Framework and the EU Nature Restoration Regulation, have driven recent momentum for large-scale ecological restoration. These initiatives emphasize not only habitat recovery but also ecological connectivity. Maintaining long-term resilience, adaptability, and persistence in populations and ecosystems requires standing genetic diversity. Yet, despite its importance, this key dimension of biodiversity is often overlooked in restoration planning and monitoring. Without incorporating genetic diversity into restoration programs, populations may remain vulnerable to inbreeding and reduced adaptive potential in the face of environmental change. Thus, maintaining genetic diversity is essential for ensuring nature's contributions to people in a rapidly changing world. Genetic monitoring, the systematic tracking of genetic diversity changes over time and space, provides a practical tool to improve restoration outcomes. By analyzing changes within and among populations, genetic monitoring can reveal threats not captured by traditional measures such as species presence or habitat extent. It can act as an early-warning system for genetic erosion and fragmentation, and help evaluate whether restored populations are demographically and evolutionarily viable and in need of genetic restoration. In this talk, we present how genetic monitoring can support nature restoration in Europe, drawing on practical examples and outlining pathways for its broader integration into restoration efforts. We also identify key barriers to its uptake, including limited awareness among stakeholders and a persistent disconnect between scientists and practitioners. By addressing these challenges, we demonstrate how genetic monitoring can directly inform conservation decisions and strengthen adaptive management, ultimately enhancing the long-term success of restoration efforts.

Targeting restoration needs through a national habitat map generated by modelling (CarHab) and pressure data

Idaline LAIGLE, Aurélien Carré

Abstract: The Restoration law requires a comprehensive assessment of the condition of all Annex I habitat areas by 2030. Currently, data is limited to biogeographical regions provided by the reporting under Article 17 of the Habitats Directive, or sparse information from local initiatives. To address this gap and establish a national overview of habitat conditions, we are developing strategies gathering local data to a national modeling program. Our approach is grounded in the CarHab program, a national initiative that models the distribution of Annex I habitats. While CarHab localizes habitats at a 1:25,000 scale, the underlying models require validation before they can support regulatory objectives. Consequently, we are launching an expertise project combining GIS analyses with fieldwork to verify CarHab predictions. To optimize this process, we are also developing a methodology using pressure data as a proxy for habitat condition. Our hypothesis posits that higher intensity and frequency of pressures correlate with deteriorating habitat conditions. At a critical threshold, habitats may be completely destroyed, yet the area might retain potential for habitat recreation. The expected outcome of this project is a national map of 5x5 km grids detailing the probability of occurrence of Annex I habitats, their potential minimum and maximum area, and their condition potential. This map will be calibrated against local data (e.g., Natura 2000 reporting) and compared with national surveys used in the reporting framework. Although the primary objective is to establish a national baseline of habitat area and condition, this methodology could also be applied longitudinally to monitor trends in habitat condition in relation to evolving pressure dynamics.

Use of reporting under the EU Nature Directives (and other EU directives) in the context of the EU Nature Restoration Regulation

Mikkel SCHWARTZ

Abstract: This talk reviews how reporting under the EU Nature Directives supports the implementation of the EU Nature Restoration Regulation and the potential for other directives to do so. It describes how the reporting under these directives is structured, what data it draws on, and what role the European Environment Agency plays in compiling and analysing the data reported under these EU directives. On that basis it scopes the potential for these data sets to be utilised to provide feedback on the national nature restoration plans that the EU Member States are expected to submit by September 2026. Monitoring and assessment under the EU Habitats and Birds Directives mobilise around 200 000 people across Member States and underpin one of the world's most extensive and coherent biodiversity assessments. This talk provides insights into the development of a harmonised EU-wide dataset from the 2019–2024 Nature reporting cycle, highlighting how national monitoring efforts are integrated to assess status and trends of birds, species, and habitat types at European scale. We demonstrate how monitoring data are translated into policy-relevant knowledge

products, including the State of Nature Report, and how they support implementation of both the Nature Directives and the Nature Restoration Regulation. Drawing on findings from the latest Nature reporting cycle and early experiences with implementation of the Nature Restoration Regulation, we discuss opportunities for integrating other EU reporting streams and biodiversity monitoring data sets into an overall EU picture.

PP06 National monitoring examples: from data to policy

Tuesday 5 May, 16h30-17h30, Room Sully 3
Chair: Julien Touroult

Monitoring terrestrial biodiversity in France: what can a national scheme achieve?

Julien TOUROULT, Antoine Lévêque, Erika Beaugeard, Olwen Falhun, Zelmira Gaudillat, Camille Gazay, Johan Gourvil, Manon Ghislain, Lise Maciejewski, Margaux Mistarz, Valentine Ouroux, Victor Robin-Havret, Stanislas Wroza

Abstract: Several public policies, resulting from European and national commitments (e.g. Nature Directives, French national biodiversity strategy), require accurate and regular information on the status and trends of different biodiversity components. In France, various monitoring protocols, sometimes for several decades, seek to meet these needs (e.g. temporal monitoring of common birds, of forest habitats, etc.). These programs often face the challenge of administrative and financial sustainability in order to ensure their long-term monitoring function. Furthermore, some compartments of biodiversity are still not covered by harmonised national monitoring protocols (e.g. open habitats) or their geographical coverage needs to be extended (e.g. amphibians and reptiles), despite the significant conservation challenges associated with them. In order to develop and sustain long-term terrestrial biodiversity monitoring systems, the French Ministry of the Environment has entrusted the French Biodiversity Agency with the task of implementing a national biodiversity monitoring scheme. In early 2024, France published its reference document, which outlines the issues and proposes principles of governance between stakeholders (including the key role of civil society in biodiversity monitoring, with associations and volunteering). It also looks to coordinate several monitoring scales, such as sub-national (administrative regions) and supra-national, in a dynamic European context (Biodiversa+). Faced with increasingly high monitoring challenges, such as required by the Nature restoration law (habitats, pollinators), this national framework must be regularly adapted and improved, while maintaining the stability of existing protocols. It must also ensure that the data are available and

useful (by sharing raw data, essential biodiversity variables and indicators) to fulfil its role of informing public debate and supporting public decision-making on biodiversity conservation.

Public Involvement in Monitoring the Kunming–Montreal Global Biodiversity Framework in Denmark

Gitte KRAGH, Finn Danielsen

Abstract: The Kunming–Montreal Global Biodiversity Framework (GBF), adopted under the Convention on Biological Diversity in December 2022 by 195 countries and the EU, mandates Parties to report progress on four goals and 23 targets aiming to halt and reverse biodiversity loss globally by 2030. Biodiversity observations are key to monitoring progress towards this ultimate goal, and the agreement explicitly promotes citizen science as a tool to enhance monitoring and decision-making. Of the 365 GBF indicators in the GBF monitoring framework, 185 (51%) could potentially be informed by citizen-generated data (Danielsen et al., 2024). This presentation draws on findings from the EU-funded more4nature project to assess the role of citizen science in supporting GBF monitoring, with a focus on Denmark. We investigate two key questions: (1) To what extent has the Government of Denmark integrated citizen science data into its official 7th National Report to the CBD, due 28 February 2026? and (2) How effectively can existing Danish biodiversity citizen science programmes contribute to populating GBF indicators in practice? Our analysis provides actionable insights for policymakers and practitioners seeking to leverage citizen science for robust biodiversity monitoring and reporting.

Introducing the Portuguese Pollinator Monitoring Scheme (PT-PoMS): A National Response to the EU Nature Restoration Law

Andreia MIRALDO, Eva Monteiro; Helena Ceia; Silvia Castro; João Loureiro

Abstract: Pollinators are in global decline, yet Portugal, a recognised Mediterranean biodiversity hotspot, has until now lacked a comprehensive national monitoring programme. Population trends for the vast majority of pollinators remain unknown, creating a critical evidence gap at a moment of urgent policy action. The EU Nature Restoration Law places legally binding obligations on Member States to reverse pollinator declines by 2030, underpinned by scientifically robust monitoring data. The Delegated Regulation (EU) 2025/2188, formalising the European Pollinator Monitoring Scheme (EU-PoMS) methodology, requires national programmes to be operational from January 2027, with the first national report due in 2030 covering at least four years of data. The Portuguese Pollinator Monitoring Scheme (PT-PoMS) was developed within the PolinizAÇÃO project, financed by the Ministry of Environment and Climate Action, to directly fulfil these obligations. Coordinated by the CFE at the University of Coimbra in partnership with ICNF, I.P., and built through a participatory process involving

over 130 experts, the PT-PoMS is fully harmonised with EU-PoMS requirements and validated through a national pilot study conducted in 2024. The scheme comprises two mandatory modules and four complementary modules, covering 80 monitoring sites across mainland Portugal, and the Azores and Madeira archipelagos. Core methods include standardised transects and light traps, complemented by Malaise traps and flight interception allied with DNA barcoding and metabarcoding for broader community-level detection and taxonomic resolution. It integrates professional monitoring with citizen science to maximise geographic reach and cost-efficiency. Full implementation is estimated to require between €1.2 and €1.85 M annually, depending on the staffing model adopted. This presentation will outline PT-PoMS's design, pilot findings, budget scenarios, and its role as a model for EU-compliant national pollinator monitoring.

From Science to Action: Lessons from Seven Years of Biodiversity Monitoring in South Tyrol

Andreas HILPOLD, Matteo Anderle, Elia Guariento, Chiara Paniccia, Julia Seeber, Magdalena Vanek, Ulrike Tappeiner

Abstract: Biodiversity monitoring programs are increasingly important for species and nature conservation in both lowland and mountain regions. They provide continuous, large-scale, standardized data to assess the impacts of land-use and climate change on biodiversity and to evaluate ecosystem status at local and regional scales. A key challenge, however, is translating these scientific findings into concrete conservation measures and policy decisions. In 2019, the Autonomous Province of South Tyrol (Italy), together with Eurac Research, established a permanent, standardized long-term biodiversity monitoring program. Interdisciplinary experts conduct systematic data collection and communicate results to scientific and institutional stakeholders. Monitoring sites are distributed using a stratified random design and cover a wide range of habitats, from near-natural systems such as alpine grasslands, running waters, and forests to human-influenced areas like meadows, apple orchards, and urban environments. The program surveys multiple taxa, including vascular plants, cryptogams, birds, bats, and invertebrates (e.g., grasshoppers, butterflies, soil and freshwater macroinvertebrates), alongside abiotic and landscape variables. After seven years, the dataset supports diverse ecological analyses and has led to numerous scientific publications that underpin evidence-based recommendations. Results show that agri-environmental schemes can sustain high biodiversity in meadows, while landscape heterogeneity enhances mobile taxa such as birds and bats. Conversely, intensive riparian management reduces aquatic macroinvertebrate diversity in lowland ditches. These findings have been translated into practical guidance for practitioners, policy makers, and conservation stakeholders. The presentation summarizes key results and

highlights policy-relevant recommendations from the first seven years of monitoring.

Long-term and large-scale diversity monitoring and policy evaluation in Switzerland

Noémie PICHON

Abstract: Biodiversity monitoring and policy evaluation is an important component of both international treaties signed by Switzerland and national legislation. Switzerland therefore set up three complementary biodiversity monitoring schemes to inform federal and cantonal authorities, policy makers and the general public on trends in biodiversity and to advance our general understanding of current biodiversity changes and impact of conservation policies in Switzerland. The three monitoring schemes are: (1) the 'Biodiversity Monitoring Switzerland' program, which started in 2001, studies mainly the common habitats; (2) the program 'Monitoring the effectiveness of species conservation' has its focus specifically on protected areas and started in 2011; (3) the program 'Agricultural Species and Habitats' has its focus on the agricultural landscape and started in 2015. Methods for biodiversity sampling have been standardized as far as possible across the three programs to allow comparisons of trends, for example between protected areas and the surrounding non-protected landscape. For example, in all three programs, circular plots of 10 m^2 are used to monitor changes in vascular plant diversity. Using these data, we recently showed that both protected dry grasslands and extensively manged grasslands, promoted through agricultural policies, exhibit common encouraging trends: the abundance of habitat specialists increased and mean nutrient indicator values decreased. In contrast, no positive developments were detected in grasslands without policies promotion or protection policies. In this talk, the three biodiversity and evaluation monitoring programs are introduced and selected results are presented.

PP05 WORKSHOP Cluster Event: The landscape of EU monitoring Project

Wednesday 6 May, 9h00-12h30, Room Rondelet

Chair: Gilles Doignon, Lucie Vidonne, Colombe Warin, Caroline Pottier, Emanuela de Menna, Bénédicte Blaudeau & Maria Blasi

Description: During a three-hour workshop, this event will focus on fostering collaboration among different monitoring disciplines, maximizing the impact of participating projects, and addressing key EU policy priorities, such as the European Biodiversity Strategy 2030 and the EU Nature Directives.

PP04 Combining needs of monitoring from different policies

Wednesday 6 May, 16h30-17h30, Room Rondelet

Description: The increasing need to monitor biodiversity across different scales and realms has reflected in increasing public European policies in recent decades. One of the most recent examples is the approval and implementation of the Nature Restoration Regulation across Member States. In this session, we will explore the potential links and connections shared among current established policies dealing with biodiversity monitoring, including the Birds and Habitats Directives, the Water Framework Directive, and the EU Marine Strategy Framework Directive. At the same time, global agreements, including the Global Biodiversity Framework, also require monitoring efforts that should be reported by the Member States. In order to avoid duplication of efforts and reach for effectiveness and resource efficiency, how can we better link ongoing initiatives for the harmonization of monitoring? What are the most common needs? How to obtain our targets in the most efficient way?

How to use the data from the French national forest inventory to meet both needs from DHFF and Nature Restoration law

Lise MACIEJEWSKI, Ingrid BONHÊME, Olivier Argagnon, Thomas Brusten, Eugénie Cateau, Fabrice Coq, Marion Gosselin, Benoit Renaux

Abstract: The French national forest inventory (NFI) carries out a permanent inventory of national forest resources, as long as gathering ecological information such as habitats identification and floristic composition. Those data enable a statistically robust assessment of the area occupied by half of the largest forest habitats of Community interest (HCI) in France. With the help of a group of experts and an in-depth analysis of NFI data, we have developed a method with 12 indicators to assess the conservation status (CS) of forest HCIs at the biogeographical scale, enabling the French government to meet the EU obligations of the DHFF (art.17) in 2024. Indeed, we have assessed the CS of 34 HICs within their biogeographical region, using 4 criteria: presence of habitat-structuring species, production and decay of structuring species, spatial and temporal continuity of the habitat, and soil functionality. However, for the Nature restoration law voted in 2024, each Members states need to produce figures for the surfaces of HCIs in “good” and “not good” conservation status. The indicators produced for the DHFF report do not directly allow us to estimate these areas, as NFI data are collected on statistical plots from a systematic sampling of French mainland forests. To do so, we had to calculate a CS assessment per plot, which required to modify the method. Most of the indicators had to be reshaped for local assessment, by adapting the calculation method and sometimes proposing new thresholds. For indicators that cannot be used at local level (such as very large trees, which cannot be expected in every plot), we decided to use the biogeographical mean in the local assessment. Finally, many special cases in the plots encountered by field agents required choices to be made on a case-by-case basis (e.g. plots temporarily deforested). Using this unique and innovative method, we were able to produce an estimation of the area of forest HCIs which required restoration measures.

Scoping the Future of Long-Term Ecological Data for Biodiversity Action into a Collaborative Research Action (CRA)

Laurent BERNADOU, Eric Pante

Abstract: Biodiversity loss continues to accelerate due to anthropogenic pressures such as land-use change, pollution and ocean acidification. Although Europe benefits from extensive long-term ecological monitoring infrastructures and datasets, efforts remain fragmented across disciplines, countries and sectors. This fragmentation limits the integration of ecological, social and economic knowledge and constrains the capacity of research to effectively inform biodiversity policy and action. This talk explores pathways to mobilise resources and strengthen coordination for a future international Collaborative Research Action (CRA) focused on long-term biodiversity monitoring and its contribution to biodiversity action. It will discuss how European research communities, infrastructures, funders and decision-making bodies could work together to develop a coordinated and transdisciplinary research framework. Particular attention will be given to how priorities emerging from the European research community can be translated into the multilateral landscape of international environmental research and funding. By framing long-term ecological data as a strategic resource for biodiversity governance, the talk aims to stimulate discussion on how coordinated investments and partnerships can enhance the impact of biodiversity monitoring on policy and societal decision-making.

The Carpathian Convention: translating GBF into regional context

Klaudia KURAS

Abstract: The Carpathian Mountains constitute one of Europe's most important biodiversity hotspots, spanning seven countries and providing essential ecosystem services to millions of people. This presentation highlights the role of the Carpathian Convention as a key regional governance framework for translating and implementing the Kunming–Montreal Global Biodiversity Framework (GBF) in a specific mountain context. It outlines how the Convention facilitates cross-border cooperation, aligns global biodiversity targets with regional priorities through the Carpathian Biodiversity Framework, and supports countries in integrating these objectives into national biodiversity strategies and reporting processes. The presentation further demonstrates how the Carpathian Convention bridges EU and non-EU countries, supports EU policy implementation, and advances coordinated action on biodiversity conservation, sustainable land use, climate resilience, and ecosystem restoration, positioning the Convention as a regional implementation arm of global and European biodiversity commitments.

Harnessing Monitoring Capabilities using the Digital Twins approach

Gabriela ZUQUIM

Abstract: While traditionally the processing of biodiversity data and modelling for monitoring has not required substantial computing resources, actions in the field are becoming increasingly data-intensive, requiring the use of supercomputers. This is connected to a need for improved modelling approaches that can handle data streams and produce reliable predictions of biodiversity shifts in response to anthropogenic pressures. A digital twin can be defined as a virtual, interactive replica of a real-world process, comprised of data, a model and ways to connect the data and model. Digital Twins allow automated data flows into modelling pipelines towards graphical user interfaces to support decision making and therefore represent a highly promising solution to address the needs of modern monitoring of biodiversity. In the biodiversity domain, prototypes of digital twins (pDTs) have already been developed for several purposes, from biodiversity monitoring to development of what-if and future scenarios under different climatic conditions in terrestrial and marine environments. Digital Twins in biodiversity can be designed to benefit from the developments from other DT initiatives, such as Destination Earth to build highly accurate digital twins of the Earth by integrating massive datasets to simulate future scenarios of climate, weather, and human impact. One clear example of the potential to leverage DestinE products for biodiversity monitoring and the DT concept is the use of ClimateDT data, one of DestinE's core components, focused specifically on simulating climate scenarios at very high resolution. In this talk, I will present a few examples of prototypes of DTs and the possible connections with broader EU initiatives and how it can help scientists and policymakers to explore how climate change will affect different biodiversity processes such as shifts in habitats and species distributions and ecosystem vulnerability.

PP02 Policy implementation to bridge the gap from data to action

Thursday 7 May, 9h00-10h00, Room Joffre G
Chair: Giovanni Strona

Description: In this session, we welcome abstracts to showcase examples of biodiversity indicators and EBVs used in policy and management. This session also welcomes innovative toolkits to support policies at national, European, and global levels, helping us to bridge the gap between data and biodiversity protection.

GINAMO: Operationalising Genetic Diversity Indicators for Biodiversity Reporting and Monitoring

Christina HVILSOM, Archambeau, A.-S., Battilani, D., Brown, I. Cai, X., Carlsson, I., Cousins, S., Ehrenmann, F., Galbusera, P., Garnier-Gere, P., Geue, J.C., Harribey, M.-G., Heuertz, M., Hoban, S., Kopatz, A., Laikre, L., Le Bras, Y., Leus, K., Lundmark, C., Martinez-Anton, L., Mergeay, J., Mouton, C., Noble, L. R., Raeymaekers, J., Raspail, F., Segelbacher, G., Theunissen, E., Vejlgaard, C. R., Vernesi, C., Westram, A. M.

Abstract: GINAMO is an international Biodiversa+ research project supporting countries in implementing indicators of genetic diversity, an essential but often overlooked component of biodiversity monitoring and policy reporting. The project strengthens the scientific and operational basis of genetic diversity indicators under the Convention on Biological Diversity (CBD), helping countries assess whether species and populations are sufficiently large and connected to maintain genetic variation, adaptive potential, and long-term ecosystem resilience. To improve the integration of biodiversity data into policy implementation, GINAMO engages stakeholders to map biodiversity reporting workflows and identify practical barriers to indicator use, highlighting challenges such as data accessibility, methodological consistency, and institutional coordination. Based on these findings, GINAMO is co-developing practical tools and guidance to support countries in operationalising genetic diversity indicators. This includes a method for selecting species for reporting and a workflow enabling the calculation of genetic diversity indicators using both DNA-based and non-DNA data sources. The project is also developing best practices for indicator calculations using genomic datasets combined with species life-history traits, as well as approaches using existing monitoring data (e.g. for bird species listed under EU legislation). In addition, we explore the potential of satellite Earth observation data to complement genetic datasets for large-scale assessments of genetic diversity. By combining scientific development, stakeholder co-creation, and practical guidance, GINAMO aims to provide policy-relevant methods and toolkits that enable countries to translate biodiversity data into actionable indicators for national and international biodiversity, reporting, monitoring and management.

How Essential Variables Can Inform MSFD Policy Criteria and Guide Marine Monitoring Priorities

Juan Camilo CUBILLOS M.

Abstract: Achieving Good Environmental Status (GES) under the Marine Strategy Framework Directive (MSFD) requires consistent assessments across criteria addressing ecosystem state, pressures, and impacts, yet current reporting

remains uneven across regions, with gaps in data and indicators limiting integration. This is particularly relevant given the MSFD requirement to assess predominant pressures, including their cumulative and synergistic effects, as part of an ecosystem-based approach to managing human activities within levels compatible with achieving GES. Essential Variables (EVs), including Essential Biodiversity Variables (EBVs) and Essential Ocean Variables (EOVs), are increasingly promoted as a framework to harmonise marine monitoring by standardising key measurements of ecosystem state and processes. Here, we evaluate how EVs can support MSFD assessments by developing expert-derived linkages between 55 EVs and MSFD criteria, identifying where these variables can contribute to reporting and where gaps remain. These results are implemented in an interactive web-based dashboard that allows scientists, stakeholders, and managers to explore how EVs can complement existing monitoring and help identify gaps in MSFD reporting. While based on an initial expert contribution, this work represents a growing effort to assess the potential of EVs to support policy-relevant frameworks. This approach helps connect monitoring frameworks with MSFD requirements, supporting more consistent and practical marine assessments.

Is One Health Plant-Blind? Bridging the Gap Between Biodiversity Monitoring and Health Policy

Louise HENDRICKX, Quentin Groom, Sofie Meeus

Abstract: The One Health framework recognises the interconnections between human, animal and environmental health. Yet in practice, implementation remains largely focused on humans, animals and pathogens, while plants are implicitly treated as a passive background component of “the environment.”. This plant-blindness represents a critical implementation gap: biodiversity data exist, but plant health and plant diversity are rarely translated into actionable health policy. Plants are foundational determinants of health. They underpin food security and nutrition, provide medicinal resources, regulate water and air quality, stabilise ecosystems and shape environmental microbiomes linked to immune function. Simplified plant systems—such as genetically uniform crops or low-diversity landscapes—reduce resilience to pests, climate extremes and disease outbreaks, with direct and indirect health consequences. Despite this, plant indicators (e.g. crop genetic diversity, vegetation diversity, ecosystem integrity) are largely absent from One Health monitoring frameworks. This talk argues that failing to integrate plant health into monitoring systems limits One Health to reactive crisis management rather than preventive action. Using examples from agroecosystems, nature-based solutions and biodiversity–microbiome research, it demonstrates how overlooking plant systems leads to misidentification of health drivers and missed opportunities for early intervention. To bridge the gap from data to action, plant diversity and plant

health must be explicitly embedded in One Health governance, indicator frameworks and funding priorities. Recognising plants as active health determinants is not an expansion of scope, but a necessary correction to strengthen prevention, resilience and policy coherence across biodiversity and health agendas.

Integrating biotic integrity, ecological processes and legal protection into a Universal Nature Indicator

Jesper BLADT, Andersen, C., Baaner, Bille, R.A., L., Brunbjerg, A.K., Bruun, H.H., Båstrup-Spohr, L., Chetcuti, J., Fløjgaard, C., Greve, MCS., Levin, G., Moeslund, J. E., Norrild, A.K., Oddershede A., Søndergaard, S.A., Ejrnæs, R.

Abstract: Reliable indicators are essential for translating biodiversity monitoring data into policy-relevant information. We present the Universal Nature Indicator, a recently developed framework that integrates multiple dimensions of biodiversity status into a single, transparent metric. The indicator evaluates three complementary components: biotic integrity (the status of species and habitats), ecological processes (the functioning of natural processes and ecosystem dynamics), and legal protection (the extent and strength of formal conservation measures). Each component is assessed through a dedicated sub-indicator based on multiple monitoring datasets, environmental information sources, and data on legal designations and regulatory frameworks. The three sub-indicators are reported individually in order to retain their ecological and policy relevance, but are also combined into a single aggregated indicator that provides an overall assessment of the state of nature while reflecting interactions and synergies among the three dimensions. This presentation introduces the conceptual framework behind the indicator, the integration of heterogeneous monitoring data across the three dimensions, and the methodological approach used to aggregate them into a unified metric. Although developed using Danish data, the framework is designed to be conceptually transferable and applicable to biodiversity monitoring and assessment in other countries.

Quantifying Complexity: Towards a Biodiversity Valuation Framework for Biogenic Reefs as Nature-based Solutions

Liselot BREYNE

Abstract: Marine biogenic reefs, built by habitat-forming species such as bivalves, worms, and corals, provide important ecological and socio-economic benefits as nature-based Solutions (NbS) for coastal resilience. They deliver key ecosystem services, including shoreline protection, water filtration, habitat provision, and carbon sequestration. Importantly, their complex structures support high levels of biodiversity, which in turn underpins essential ecosystem processes such as productivity, resilience, and stability. Valuing biogenic reefs is therefore closely linked to the wider challenge of valuing biodiversity. Despite their importance, the full value of biogenic reefs is rarely integrated in management or investment frameworks, resulting in limited funding for conservation and restoration. To attract investment, biodiversity benefits must become visible, measurable, and financially relevant. Yet methods to quantify and monetize biodiversity, especially in complex systems like biogenic reefs, remain underdeveloped. To address this gap, we conducted a systematic literature review on biodiversity valuation to support the creation of a robust framework for assessing the value of biogenic reefs as NbS. Our review synthesizes current approaches and identifies which benthic components, including microbial communities, benthos, and fish, are most suitable for monitoring, valuation and management. We also examine how these components shape structural and functional biodiversity, and how these relate to co-benefits such as habitat quality, ecosystem stability, resilience to environmental change, and productivity. By consolidating biodiversity valuation approaches and identifying key knowledge gaps in biogenic reefs, this work lays the foundation for integrating biodiversity into a valuation framework for biogenic reefs, supporting stronger financial and policy decision-making.

PP03 PANEL Links to funding, at national & EU levels for biodiversity monitoring

Thursday 7 May, 10h00-11h00, Room Sully 1
Chair: Michele Bresadola

Description: Biodiversity monitoring aims at ideally establishing long-term programmes to obtain trends over time and be able to continuously monitor the state of nature. However, this is a challenging task, since continuation of monitoring initiatives often depends on rapidly changing funding mecanisms and systems that often do not guarantee stable, long-term funding. During this session, we aim to explore funding mechanisms at regional, national and European levels to support biodiversity monitoring initiatives, especially those supporting in the long-term and public and private collaboration.

PP01b Role of monitoring in the Nature Restoration Regulation

Thursday 7 May, 11h30-12h30, Room Joffre G
Chair: Maria Blasi

European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL): a tested, in-situ methodology to deliver harmonized, EU-wide monitoring data

Laura SUTCLIFFE, Luca Kleinewillinghöfer, Lars Roggon, Carsten Haub, Rainer Oppermann

Abstract: The severe decline of biodiversity in European agricultural landscapes over the past century has led to the development of various policies and initiatives to restore the ecological integrity of farmland, such as the Common Agricultural Policy, as well as more recently the Nature Restoration Regulation. These policies and targets must be measured by monitoring systems tracking changes over time and space. While numerous biodiversity-relevant monitoring methods are used in the EU, these are either region-specific (e.g. the High Nature Value Farmland indicator in Germany) or target limited species groups (e.g. the Farmland Bird Index). To provide harmonized monitoring of broader agricultural biodiversity that is representative for the Member States, the European Commission launched the EMBAL survey (European Monitoring of Biodiversity in Agricultural Landscapes). EMBAL was first piloted in 2020, and rolled out to all EU27 countries in 2022 and 2023 with 3000 sampling locations based on the LUCAS grid. Surveyors collect data in a 25-ha sampling window relating to land cover, land use (intensity), pollinator forage (flower diversity and density), plant diversity (indicator species), landscape heterogeneity and density of landscape features. The data can, e.g., show changes in extent of landscape features over time, or differences in grassland plant diversity between Member States. As well as analysing parameters individually, we also developed a composite nature value indicator for agricultural landscapes (ANVI) that can be tracked over time or between regions. The EMBAL data also provides an essential basis for interpreting trends in other key biodiversity indicators such as farmland birds or grassland butterflies, or investigating the impact of Natura 2000 areas. This presentation outlines the EMBAL methodology, discusses the results and their relevance to track the success of different European policies, and makes recommendations for future enhancements to the survey.

Earth Observation for the EU Nature Restoration Regulation: building a stronger community of practice for monitoring

Michelle Hermes, Ruuta SKUJINA, Phillip Harwood,

Abstract: Earth Observation (EO)-based solutions, including those from the EU Copernicus programme, are explicitly referenced as tools to support the implementation, monitoring, and reporting under the EU Nature Restoration Regulation (NRR). As countries prepare draft National Restoration Plans, due by September 2026, the European Space Agency's Stakeholder Engagement Facility (ESA SEF project) has been connecting a wide range of actors affected by the regulation, facilitating exchanges on best practices and challenges encountered. Satellite-based remote sensing can provide free, standardised and transparent datasets that support reporting requirements and generate valuable insights for both planning and implementation. However, the uptake of EO-based solutions remains uneven, and their potential for monitoring is still underutilised. While many national authorities already use EO effectively, barriers remain, including the complexity of the EO ecosystem and challenges related to the full operational adoption of such solutions. To address these obstacles, the EO community has been increasing efforts to showcase capabilities and practical applications. A major initiative was the ESA BIOSPACE conference, the first international event dedicated to satellite remote sensing for biodiversity across ecosystems. Copernicus services (C3S, CAMS, CLMS) have also showcased practical applications supporting biodiversity monitoring and the NRR. In parallel, the European Association of Remote Sensing Companies (EARSC) has established a working group to define the EO industry's role and map relevant services for implementation. This talk aims to bridge the EO and biodiversity monitoring communities and gather perspectives on the current use of EO data as evidence in policy planning and reporting. It will explore barriers to uptake and discuss how a stronger community of practice could help unlock the potential of EO for monitoring and implementing the NRR.

From volunteer transects to EU policy: how the eBMS network delivers indicators for the Nature Restoration Regulation

Reto SCHMUCKI, Chris van Sway

Abstract: Translating biodiversity monitoring into harmonised data flows for policy-relevant indicators requires robust science and a framework that connects data providers, institutions, and policy users across scales. The European Butterfly Monitoring Scheme (eBMS) demonstrates how a distributed network of national and regional schemes, coordinated by Butterfly Conservation Europe, can deliver key policy outputs, most notably the Grassland Butterfly Indicator, now embedded in the EU Nature Restoration Regulation (NRR) to track progress in reversing biodiversity decline. eBMS was established as a collaborative effort in which local and regional schemes contribute data, knowledge, and expertise to a shared database while retaining ownership and agency. This distributed coordination model has been essential for building trust among stakeholders – from volunteer recorders and national agencies to EU institutions – and for addressing data-sharing challenges across the network. By providing shared infrastructure for data collection, validation, and management, eBMS accelerates new monitoring initiatives and enables local coordinators to redirect resources towards data mobilisation and volunteer networks. Accessible and transparent tools enable efficient calculation of rigorous and widely accepted indicators. Butterfly Conservation Europe, whose membership spans many European states, provides essential links between national conservation communities and EU-level coordination. Support from the European Commission has been instrumental in sustaining the network. As the NRR moves into implementation, the eBMS model shows that sustained investment in collaborative monitoring infrastructure –

combining community engagement, institutional partnerships, and federated governance based on shared data stewardship, rigorous standards, and equitable partnership – can maximise the value of collective efforts and deliver the evidence base required for biodiversity policy and nature recovery.

From existing biodiversity monitoring schemes to a pan-European biodiversity monitoBuilding a fit-for-purpose pan-European biodiversity monitoring network: gaps, inefficiencies and priorities

Martina Marei VITI, Jeremy Dierten, Jose Valdez, Piero Visconti, Henrique Miguel Pereira

Abstract: Pan-European biodiversity monitoring is increasingly needed to support conservation policy and, ultimately, to establish a Biodiversity Observation Network in Europe, yet it remains unclear how well existing monitoring schemes represent Europe's biodiversity. We assess the joint capacity of existing pan-European schemes to underpin an integrated terrestrial biodiversity monitoring network, and identify where complementarity is required to fill coverage gaps. We evaluated six schemes in representing 338 rare and 1,003 common species listed under the Nature Directives, and 79 rare and 169 common EUNIS habitat types. Using species occurrence data and habitat probability maps, performance was benchmarked against hypothetical, environmentally stratified monitoring networks. Existing schemes provide a useful starting point, but spatial coverage remains uneven, with notable gaps in Southern, Eastern and Northern Europe. Under realistic assumptions, the existing network represents approximately 80% of common habitats but only around 30% of rare habitats. Comparable habitat coverage could be achieved by stratified networks with far fewer sites (around 1,000 for common and just over 4,000 for rare habitats), despite the existing network comprising more than 82,000 sites. For species, coverage reaches approximately 65% for common taxa (comparable to a stratified network of roughly 4,000 sites) while rare species remain poorly represented at less than 10% coverage. Overall, the existing network lacks the spatial optimisation required to adequately represent rare species and habitats at the European level. Spatial prioritisation approaches can complement existing efforts by identifying sites that maximise representativeness gains while minimising expansion costs, supporting a more efficient and policy-relevant pan-European monitoring network.

PS01 Posters

Bright Spots and Bridge Building: Co-Designing Marine Biodiversity Knowledge to Inform Conservation, Stewardship, and Action

Eric PANTE, Laurent Bernadou

Abstract: Marine conservation increasingly depends on biodiversity monitoring systems capable of detecting ecological change across large spatial and temporal scales. Many monitoring initiatives remain fragmented, short-term, or limited to species inventories, constraining their capacity to reveal the mechanisms driving biodiversity responses to global change. Short-term studies often fail to capture ecological variability or detect reliable population trends, which may require monitoring over decades to emerge. Here we present a new call for collaborative research from the Belmont Forum, BIODIVERSITY III. The Belmont Forum, an international partnership of funding agencies, international scientific councils, and regional consortia dedicated to promoting transdisciplinary and transnational research to help understand, mitigate, and adapt to global environmental change. Belmont Forum funding opportunities —known as Collaborative Research Actions (CRAs)— are co-designed with the global research community and societal actors to identify research priorities addressing major sustainability challenges. The CRA BIODIVERSITY III aims at addressing a critical challenge in marine conservation: transforming biodiversity monitoring from isolated scientific observations into integrated socio-ecological knowledge systems that support decision-making. BIODIVERSITY III emphasises the need to combine natural sciences with social sciences and stakeholder / societal actor engagement in order to understand biodiversity dynamics within complex socio-ecosystems and to co-produce conservation solutions. Such approaches are essential for implementing global biodiversity commitments, including the Kunming–Montreal Global Biodiversity Framework and the UN's Sustainable Development Goals related to ocean conservation. Long-term monitoring also provides the empirical foundation for identifying ecosystem tipping points, assessing conservation effectiveness, and guiding adaptive management. By bringing tog

BioMonI - Biodiversity monitoring of island ecosystems: a spotlight on biodiversity hotspots

Nathaly R. GUERRERO RAMÍREZ

Abstract: Islands contribute disproportionately to global biodiversity, harbouring outstanding levels of endemism and evolutionary adaptations to island life. Yet, these ecosystems are epicenters of biodiversity change. Given their uniqueness and fragility, island-focused monitoring tools are urgently needed to inform conservation, restoration, and policy. In BioMonI, we build the foundation for a global long-term biodiversity monitoring network tailored to islands' specific needs. We combine diverse approaches, such as literature reviews, novel methodologies, and e-infrastructure. Based on the literature, we defined island-specific EBVs, laying the foundation for an Island Biodiversity Observation Network (IslandBON). Our evaluations of the Kunming-Montreal Global Biodiversity Framework (KM-GBF) reveal substantial gaps: over 70% of KM-GBF targets lack well-aligned indicators, and only 7 are tracked by headline indicators.

This highlights a need for improved metrics to monitor progress toward global biodiversity goals on islands. Using novel methodologies, including DNA-based monitoring, we establish reference genetic resources and analytical workflows to facilitate biodiversity assessments of understudied taxa (bryophytes, green microalgae, and flying arthropods). In parallel, terrestrial LiDAR extended our understanding of vegetation structural complexity beyond forests to other insular vegetation types. By integrating palaeoenvironmental indicators, we provide evidence that island ecosystems can shift rapidly under coupled human and environmental pressures, highlighting the importance of incorporating palaeoecological data into current biodiversity assessments. Finally, we are developing BioMonI-Plot, a community-driven network of plots across islands worldwide. This network, hosted in an interoperable e-infrastructure, aims to assess biodiversity and ecosystem change, inform evidence-based policy measures, and help close critical gaps in island biodiversity monitoring.

PS02 Posters

The Ecosystem Capability Unit (ECU) : an integrative metric that combines localised data on land use, water, bio-carbon and biodiversity in order to measure the potential of Ecosystem Natural Capital and its degradation at different scales : Application in Africa

Didier BABIN

Abstract: The Ecosystem Capability Unit (ECU) is an integrative metric that combines localized data to measure the potential of ecosystem natural capital and its degradation at different scales. It was developed to address a long-standing international demand, notably from the Convention on Biological Diversity (Aichi Biodiversity Target in 2010 and Kunming-Montreal Global Biodiversity Framework in 2022), to incorporate biodiversity into national accounts compatible with the United Nations System of Environmental Economic Accounting (SEEA). This metric does not describe the state of biodiversity sensu stricto, nor assign monetary values to Nature or Ecosystem Services, but rather evaluate and measure ecosystem degradation in terms of ecosystem capability of functional ecozones (socio-ecological landscape unit or SELU). It allows for the identification of observed and localized trends in potential biodiversity degradation (as ecological infrastructure) linked to other essential ecosystem elements (land use, water, biocarbon). This indicator offers a diagnosis approach to ecosystem health, based on qualitative aspects (pollution, degradation, fragmentation, etc.) and to sustainable use based on quantitative aspects (overexploitation, resource depletion, etc.) with core accounts in bio-physical terms. It allows for the integration of numerous parameters and data into a single indicator, depending on their availability, similar to other integrative metrics such

as Gross Domestic Product or the Human Development Index. It can be calculated using existing, available, and free data over time, but will improve with higher-quality or more specific data. The ECU is a useful indicator for decision-making processes at different scales. A decrease in the ECU value of an ecozone reflects a decline in its total ecostystel capability (TEC) and thus a decrease in its ability to provide its services sustainably. A first series of results for Africa and Madagascar are presented showing changes in different main regions between 2005 and 2019.

Monitoring gaps and schemes in long-term monitoring across taxa in the European Alps: preliminary results from the AlpsLife project

Michele BRESADOLA

Abstract: The European Alps host biodiversity of global importance, but climate change and land-use pressures, together with uneven biodiversity knowledge across the Alpine arc, challenge effective conservation and restoration in mountain environments. Current monitoring schemes vary by country, institution, taxon, method, and spatial scale, hindering Alpine-wide comparisons and the development of a coherent status-and-trends picture for decision-making. AlpsLife aims to strengthen science-based conservation and restoration by integrating existing monitoring schemes, downscaling and adapting relevant EU indicators to the Alpine context, and supporting comparable biodiversity assessment across borders. We developed three taxon-specific questionnaires to collect quantitative and qualitative information about long-term monitoring schemes currently in use for pollinators, mammals, and birds. Namely, we designed each questionnaire with feedback readily provided by three Working Groups formed by taxon-specific experts. Each questionnaire aimed at localizing where long-term monitoring of biodiversity occurs, and which monitoring methods and techniques are commonly used across the European Alps. Preliminary results reveal a paucity of long-term monitoring above the 2,500 m a.s.l. across all taxa, with taxon-specific target preferences and notable gaps. For example, hoverflies and moths among pollinators, and terrestrial and semi-aquatic insectivores among mammals. While certain mammal and bird indicators are already monitored, many small- and medium-sized mammals remain underrepresented, with a substantial methodological heterogeneity persisting across multiple scales. Our preliminary results highlight the need for strong harmonization of long-term monitoring protocols to enable coherent Alpine-level analyses and a shared evidence base for conservation and restoration planning.

BioMonWeek
2026
The European
Conference for
Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Monitoring and the private sector — Cooperation with and for non-state-owned enterprises

PV02 Tech or No Tech? How NatureTech can leverage traditional surveys - insights from the private sector experience

Tuesday 5 May, 11h30-12h30, Room Joffre F

Biodiversity monitoring on reforestation sites

Esther PEETERS

Abstract: Growing private sector interest and investment in nature restoration demands credible, decision-useful biodiversity monitoring. In practice, biodiversity monitoring remains methodologically fragmented, operationally challenging, and highly context-dependent. Land Life is a nature restoration company, focused on reforestation. We built experience in biodiversity measurement and analysis, across several regions. For the Conference, we can select from three private-sector case studies across Europe, Indonesia, and Australia. In Northern Spain we measured biodiversity on a post-wildfire restoration site. The project was implemented for carbon, but with strong biodiversity features (i.e. mixed native tree species). We established the biodiversity baseline with soil eDNA, field surveys, and remote sensing. Differences in soil fungi and moisture conditions against a healthy reference highlighted the required restoration trajectory and the opportunity to integrate biodiversity metrics alongside carbon outcomes. In Borneo, Indonesia, we piloted bioacoustics, and conducted vegetation surveys and remote sensing analysis on an orangutan habitat restoration site. It revealed that the planting site was significantly drier and structurally less developed than the reference forest, confirming both the need for intervention and the importance of ecosystem-specific indicators in tropical settings. On a site in South Australia, biodiversity monitoring supported registration and future certification under the Australian Accounting for Nature framework. We apply field-based assessment of native woodland birds and vegetation, complemented by remote sensing. The use case demonstrates how biodiversity evidence can underpin verified co-benefits and potential commercial value. We are happy to talk about what works, what does not, and what could be improved for biodiversity monitoring across landscapes and regions for the private sector.

BioDiMoBot: Autonomous Robotic Monitoring for Aquatic Biodiversity - A Science-Industry Partnership

Werner ROM

Abstract: Aquatic ecosystems are highly sensitive to the triple planetary crisis - biodiversity loss, climate change, and pollution - making them critical indicators of broader ecological change and priority targets under key EU policy frameworks. Systematic, long-term monitoring of aquatic biodiversity is therefore essential for

detecting early ecosystem degradation, assessing human impacts, and informing effective conservation and restoration strategies. Yet conventional approaches remain slow, costly, and spatially fragmented, leaving persistent data gaps that constrain both scientific understanding and timely policy responses. The EU Horizon-funded BioDiMoBot project addresses these challenges by developing an autonomous, modular robotic platform for continuous biodiversity and ecological assessment across freshwater and marine environments. The system integrates advanced sensing technologies - including novel biohybrid sensors, acoustic and optical systems, and physicochemical probes - to simultaneously capture biodiversity indicators, pollution signatures, and abiotic stressors in real time. AI-based onboard and server-side analysis converts raw observations into actionable ecosystem health insights, with data interlinked with e.g. GBIF and OBIS to ensure compatibility across European biodiversity monitoring infrastructures. Built on a transnational science-industry consortium and co-designed with stakeholders from research, policy, and the private sector, BioDiMoBot aims to shift aquatic monitoring from reactive, low-frequency snapshots to continuous, scalable, and autonomous surveillance. Deployments across contrasting freshwater and marine environments will rigorously validate the platform under real-world conditions. Underpinning the project's long-term vision, a comprehensive business plan will guide the path toward mass production of the BioDiMoBot robotic platform, ensuring wide accessibility and sustained environmental impact well beyond the project lifetime.

Assessing the role of eDNA in ecological monitoring : insights from France and Canada on best practices, barriers and long-term monitoring

Alix ALIAGA, Heather VEILLEUX

Abstract: eDNA is rapidly shifting from experimental applications to operational use in freshwater biodiversity monitoring. Yet questions remain regarding methodological reliability, regulatory acceptance, and integration with existing monitoring frameworks. Drawing on amphibian monitoring in France and fish biodiversity assessments in Canada, this presentation shows how eDNA can strengthen ecological monitoring when methods are rigorously validated and aligned with management objectives. In France, eDNA has complemented traditional amphibian surveys by detecting species frequently missed during visual or auditory fieldwork, particularly in ponds with high turbidity, dense vegetation, or limited accessibility. It is effective for identifying cryptic or hard-to-observe taxa but cannot assess reproductive success, so it must be paired with conventional methods. In Canada, an optimized extraction protocol was applied across targeted and metabarcoding approaches to evaluate its influence on eDNA performance. Sensitive assays improved detection across remote watersheds, increasing reliability relative to conventional methods and helping shift stakeholder perception toward adoption. Metabarcoding surveys showed

that extraction methods and sample volumes strongly influence detected community composition, with improved approaches enhancing detection and complementing traditional surveys. Together, these applications demonstrate how eDNA supports both large-scale baseline biodiversity assessments and targeted population monitoring. Despite these advances, barriers remain. Technical limitations include interpreting DNA transport and persistence and a lack of methodological standardization. Regulatory frameworks remain built around traditional surveys, and operational uncertainty persists. When validated and strategically applied, eDNA can significantly enhance freshwater monitoring, offering broad spatial coverage, long-term applicability, and low-impact biodiversity assessments.

PV01 PANEL Robust long-term monitoring for Nature credit viability

Wednesday 6 May, 11h30-12h30, Room Sully 1
Chair: Eric Rieux

Description: This panel session will cover what biodiversity credits are, how they mobilize private finance for conservation and restoration, and how rigorous long-term monitoring ensures real-world impact.

PV06 WORKSHOP THRIVE toolkit

Wednesday 6 May, 16h30-17h30, Room Sully 1
Chair: Niels Raes

Description: THRIVE—the Toolset for Hierarchical Reporting and Insightful Validation of Ecosystems—is a spatially explicit, modular tool that helps private sector companies and financial institutions assess their impacts and dependencies on biodiversity. Developed by Naturalis Biodiversity Center in collaboration with KPMG, THRIVE supports Environmental, Social and Governance (ESG) reporting under the Corporate Sustainability Reporting Directive (CSRD), with a specific focus on E4: biodiversity and ecosystems. In this demonstration, we will present THRIVE’s four modules and show how the tool delivers actionable insights to help companies reduce negative impacts on biodiversity and ecosystems.

PV03 Public-Private collaboration: examples and best practices

Thursday 7 May, 10h00-11h00, Room Joffre F

Biodiversity monitoring of restoration measures on German golf courses: Implementing a BACI framework through academic–private collaboration

Sandra ROJAS-BOTERO, Claudia Buchhart, Tim Diekötter, Norbert Hölzel, Alexandra-Marie Klein, Anna Klopstock, Jens Schaper, Pia Tappe, Judith Trunschke, Fredericke Velbert, Jörg Vowinckel-Ewald & Johannes Kollmann

Abstract: Golf courses represent a large share of private land in temperate Europe, and their non-playable areas have substantial potential for biodiversity conservation and restoration. Yet, biodiversity monitoring is lacking in these systems, resulting in knowledge gaps about the potential and effectiveness of restoration measures and hindering private-sector engagement in improved management. Addressing these gaps is essential for effective restoration based on evidence-to-action pathways. Thus, the project GolfBiodivers developed and implemented a biodiversity monitoring scheme for German golf courses, focusing on low-input grasslands with restoration potential. The approach has a Before-After-Control-Impact (BACI) design to quantify restoration outcomes through baseline assessments, restoration implementation, and monitoring; vegetation, soil, wild bees, butterflies, and landscape are included in the scheme. Site selection and monitoring protocols are coordinated to ensure data comparability and scalability. The project operates through collaboration of four universities and the German Golf Association (DGV). The researchers focus on study design, field methods, data quality, and statistical analysis, while the DGV coordinates communication with the participating golf courses and supports the consolidation of restoration measures. Early baseline results indicate similar ecological conditions between control and impact sites prior to restoration, with moderate to high species richness across sites, as a precondition for BACI application. This work shows how coordinated monitoring on golf courses can address data gaps across Europe, support the implementation of informed restoration practice on private land, and provide a transferable framework linking local biodiversity assessments to national and continental biodiversity monitoring schemes.

Imerys' and Patrinat's Integrated System for Biodiversity Data Production and Global Dissemination

Lina ROBLES, Santiago Forero

Abstract: Imerys, a specialist in industrial minerals, drives its ambition of reinforcing rehabilitation and preservation of nature, while also contributing to global knowledge on biodiversity through rigorous, science-backed systems for

data collection and transparent sharing. Sites conduct mandatory and voluntary wildlife surveys to establish ecological baselines and assess long-term biodiversity evolution. Specialized indicators and assessment tools (IQE, BIRS, PERSICAIRE, ECOVAL) are also deployed to continuously measure ecological quality, functionality, and impacts, ensuring data-driven management and restoration. Results are transparently shared with scientific communities. Inspired by the data diffusion engagement that Imerys undertakes since 2018 to share species occurrence data from French sites, the company has decided to scale-up and has recently started to carry out voluntary wildlife surveys and monitoring in sites all over the world and publish data to the GBIF. This process is governed by internal guidelines and specifications notes and uses a dedicated template for diffusion to structure recordings according to international Darwin Core standards, ensuring data quality and global interoperability. This data production and sharing process is carried out in partnership with Patrinat, whose rigor and expertise are key to guaranteeing the quality and global interoperability of data. This joint talk (Imerys and Patrinat) will detail the entire 'source-to-public' data system through the testimony of this company-science collaboration, addressing: why Imerys produces and shares this data, the methodologies and tools involved, how the partnership reinforces these objectives, and the key lessons learned. Alternatively, this talk could focus on the process of collecting, standardising and sharing data to GBIF, which could be classified under the theme of 'Data Management: Standardising and sharing surveys and data through GBIF and OBIS".

From project to policy: How BIODIVoltaïque bridges private data and national biodiversity monitoring

Nicolas HETTE-TRONQUART, Hervé Lelièvre, Evan Coulet, Thomas Eglin, Julie Fraix, Jérémie Schuhmann, Cheyenne Ziadi

Abstract: Private companies generate large amounts of biodiversity data as part of environmental impact assessments (EIA), but the data remain largely unexploited beyond the scale of the project. The main challenge lies in the multitude of protocols used to collect the data, making them incomparable. In collaboration with trade unions representing the solar energy sector, the French Biodiversity Agency and the Agency for Ecological Transition have led BIODIVoltaïque, a project dedicated to harmonising the sampling and monitoring protocols deployed for EIAs. BIODIVoltaïque has produced a toolkit of harmonised protocols for 13 ecological entities most commonly concerned by solar photovoltaic farms. The toolkit is accompanied by an analytical framework providing guidance for future data analysis. A key issue was to propose a sampling design that allows for "Before-After, Control-Impact" cross-comparisons, while keeping costs as low as possible for companies. The chosen approach is based on the idea of using the French biodiversity monitoring data as a control point. The validity of the comparisons is ensured by the fact that most of the protocols in the

toolkit are those of the French biodiversity monitoring program. On top of facilitating EIAs, the protocols in the BIODIVoltaïque toolkit will also allow data generated by private companies to be directly integrated into the national monitoring program. To our knowledge, BIODIVoltaïque is the first project of its kind at the European level and could be inspiring and be easily adapted to other Member States or other private sectors, such as transportation.

PV04 What's new out there? Innovations for biodiversity monitoring

Thursday 7 May, 11h30-12h30, Room Joffre F

Advancing impact assessments: estimating wildlife populations using Distance Surface Modeling with camera traps

Noémie CAPPELLE

Abstract: Assessing the impacts of infrastructure on wildlife remains challenging, particularly due to difficulties in estimating population size and density across large spatial scales. Many environmental impact assessments lack robust baseline data, which can lead to underestimated risks and insufficient mitigation measures. To address these limitations, we present a methodological framework based on Camera Trap Distance Sampling (CTDS) combined with Distance Surface Modeling (DSM) to estimate animal density from camera trap data. The approach relies on large-scale camera deployments and detection distance data to model detection functions and derive spatially explicit density estimates. We implement a Bayesian spatial modeling framework incorporating environmental covariates to predict species density across heterogeneous landscapes. Spatial autocorrelation is explicitly accounted for using a Stochastic Partial Differential Equation (SPDE) approach, allowing for robust inference at large scales. To support impact assessment applications, we integrate distance-based response functions that model changes in animal density in relation to proximity to infrastructure. This enables the identification of zones of influence and the quantification of potential population-level effects. This non-invasive approach is particularly well suited to terrestrial mammal species, especially those that are difficult to monitor through individual identification. It remains broadly applicable to other terrestrial and semi-terrestrial taxa. By combining statistical rigor with operational feasibility, this framework improves the reliability of impact assessments and supports evidence-based decision-making in conservation planning, particularly in regulated contexts such as European environmental policy.

Pollen composition as a sentinel of environmental health

Floriane CARRON, Antoine Gekière, Denis Lebailly, Quentin Meekers, Maria-Guadalupe Diaz, Julien P. Ponchart, Maryse Vanderplanck, Bach Kim Nguyen

Abstract: Understanding pollinator exposure to environmental stressors is key for biodiversity conservation. For over ten years, BeeOdiversity has monitored plant diversity and chemical contamination across 130+ sites annually in 35+ countries using pollen from honeybees. These datasets provide insights across temporal and spatial scales into floral resource use and exposure to pesticides and trace metals. Through the BeeOmetrics project (European Innovation Council-funded), wild bee nesting devices ("BeeÔtels") are tested as standardized biomonitoring tools. Pollen provisions collected in nesting tubes are analyzed to identify floral resources (DNA-based methods) and quantify chemical contaminants. In 2024, 50 BeeÔtels were deployed across European agricultural and peri-urban landscapes, expanding to 200 units in 2025, supported by a participatory monitoring protocol involving field partners. Soil and plant samples within bee foraging ranges are also analyzed, enabling the comparison of direct environmental contamination with indirect exposure measured in pollen provisions. Early results demonstrate the potential of wild bee pollen provisions as integrative environmental indicators and their complementarity with honeybee pollen, eDNA, and soil analyses, offering scalable tools for global biomonitoring.

eDNA for Marine Biodiversity Monitoring: Advantages of Long-Read Metabarcoding

Emilie DELPUECH, Maeva Leitwein, Maxime Lambert, Chloé Bellanger

Abstract: Environmental DNA (eDNA) has emerged as a game changer tool for marine biodiversity. Over the past decade, advances in sampling strategies and molecular workflows have expanded its applications, yet methodological standardization and taxonomic resolution remain limiting factors for policy-relevant implementation. Here, we compare two marine eDNA filtration systems : a triple-pump filtration setup using Waterra filters and a torpedo-based in situ filtration device equipped with enclosed membrane filters to evaluate sampling efficiency, field deployment and constraints across coastal environments. We further assess short-read metabarcoding (Illumina sequencing) versus long-read metabarcoding (Oxford Nanopore sequencing), integrating dedicated bioinformatic pipelines tailored to each approach. While short-read sequencing relies on well-established workflows, long-read sequencing improves taxonomic resolution and assignment accuracy. Long-reads also enable the detection of closely related species and provide access to haplotype-level variation within genetically diverse taxa. Our findings highlight the added value of long-read approaches for policymakers requiring high taxonomic resolution and high-confidence species identification.

From Genomics to Metrics: Building Scalable Biodiversity Data Pipelines for the Private Sector

Theo SERIVICHYASWAT, Tom van der Valk, Bilal Sharid

Abstract: Biodiversity is increasingly becoming a measurable requirement for companies operating in infrastructure, energy, forestry, mining, and land-use development. With emerging regulations such as the EU Nature Restoration Regulation, expanding ESG expectations, and new market mechanisms such as Nature Credits, the private sector faces an urgent need for biodiversity monitoring methods that are scalable, auditable, and decision-ready. However, current biodiversity assessments often rely on fragmented field surveys, limited taxonomic resolution, and reporting formats that are difficult to standardize across projects and time. In this talk, we present an approach to enabling biodiversity monitoring for the private sector using genome-wide environmental DNA (eDNA) metagenomics combined with automated bioinformatic analysis and structured reporting tools. We describe methods for integrating sampling metadata, sequencing outputs, and ecological interpretation into reproducible pipelines that can generate standardized biodiversity indicators across sites. We highlight how such approaches can support biodiversity baselines, detect ecosystem change over time, and provide transparent evidence for restoration progress and conservation outcomes. Finally, we discuss how biodiversity data products can be designed to meet private-sector requirements for traceability, quality assurance, comparability, and regulatory alignment. We also explore how robust genomic biodiversity monitoring can strengthen credibility and verification frameworks for emerging Nature Credit systems by improving monitoring, reporting, and validation (MRV). By bridging high-throughput genomics with user-friendly reporting frameworks, GenomeVault aims to help industry stakeholders move from biodiversity "data collection" to measurable, nature-positive decision-making.

PS01 Posters

Innovative Biodiversity Monitoring: A Nature Tech Approach to Strengthen Biodiversity Action Plan Performance in the Energy Sector

Camille CABANNE

Abstract: Following its commitments to manage and enhance biodiversity in its operating sites, TotalEnergies aims to facilitate the deployment of Biodiversity Action Plans (BAPs) whilst ensuring their effectiveness. Achieving this requires rigorous biodiversity baseline studies and large-scale monitoring across the Company's site portfolio. To support this effort, a standardized and science-based approach is needed to rapidly, cost-effectively and reliably design site-specific biodiversity monitoring. This innovative approach based on cutting-edge technology combines non-invasive data collection methods, automated analyses and tailored metrics to characterize the 'state' of biodiversity and track change over time, increasingly referred to as 'Nature Tech'. In 2024/25, TotalEnergies conducted a pilot study on four sites to test and compare this approach against traditional expert-led biodiversity surveys conducted previously. Remote sensing tools were applied for habitat classification, followed by in situ data collection using imagery (ground-level cameras, camera traps and drones), passive acoustic (acoustic and ultrasonic recorders) and environmental DNA (eDNA) sampling. These data were then analyzed using machine learning models for species identification, with subsequent expert validation. The study confirmed the relevance of using Nature Tech as a standardized approach to develop and inform indicators for assessing BAP performance. Furthermore, biodiversity monitoring supported by Nature Tech enables near real-time visualization and interpretation of results through dedicated dashboards. These tools can be used not only for routine monitoring but also for identifying biodiversity impacts arising from diverse pressures, thereby providing robust support for more informed decision-making.

DNA as a tool for biodiversity monitoring: aligning science and stakeholder needs

Maeva LEITWEIN, Emilie Delpuech, Maxime Lambert, Chloé Bellanger

Abstract: Various anthropogenic pressures, such as the destruction of natural environments and the over-exploitation of resources, have led to a drastic decline in biodiversity at all scales, impacting the evolutionary potential of species. With biodiversity loss becoming a global concern, stakeholders from policy-makers to conservationists increasingly demand accurate and actionable data for decision-making. Through LDgenX, a genomic analysis and expertise consultancy run by two PhDs in genetics and bioinformatics, we study DNA to study, monitor, and protect biodiversity. Protecting ecosystems and the species that populate them without integrating the underlying evolutionary dynamics is no longer enough to protect biodiversity. Certain measures that have a directly positive effect on demography (repopulation, translocation) can, on the other hand, negatively affect the evolution of populations by causing losses of genetic diversity and/or local adaptations. This is why we are highlighting the use of genetic markers (SNPs) for better monitoring of populations and ecosystems. To address these issues, we are implementing several approaches: (i) population genetics via high-throughput sequencing and in-depth analysis of identified markers; (ii) selection of traits of interest and study of cross-breeding plans to improve aquaculture or restocking populations; and (iii) environmental DNA (eDNA) for a better description of biodiversity, via sequencing of long DNA fragments. This non-invasive technique provides a snapshot of ecosystem composition in real-time. By using genomic data, conservation managers can

make informed decisions and develop more effective management strategies. In this way, genomic expertise promises to play an increasingly important role in protecting populations and ecosystems.

PS02 Posters

Evaluating Ecological Innovation Through an Integrated Monitoring Framework for Nature Inclusive Offshore Wind

Ingmar JANSE

Abstract: The Ecowende project at Hollandse Kust West positions ecological integrity as a core design constraint for offshore wind development. As a consortium led by major energy companies, Ecowende aims to demonstrate approaches for developing large scale renewable energy infrastructure that could contribute to improved ecological conditions. The project integrates a suite of ecological innovations, including nature enhancing foundation designs, bird friendly turbine configurations, low impact installation techniques that reduce acoustic disturbance, and ecological enhancement structures such as tree reefs and other artificial habitats intended to stimulate benthic and fish community development. A cornerstone of the project is its comprehensive, multi year ecological monitoring program. This program combines traditional ecological surveys with advanced sensing technologies, including passive acoustics, radar, underwater video, and autonomous drone based observations. These methods are complemented by measurements of bathymetric, hydrodynamic and biogeochemical parameters to characterize ecosystem functioning before, during, and after construction. Within this monitoring framework, environmental DNA (eDNA) plays a pivotal role. eDNA sampling detects marine taxa through genetic traces in seawater, using both targeted assays for sensitive detection of species of concern and community level metabarcoding to track biodiversity patterns across trophic groups. This non-invasive approach enables tracking of rare or cryptic species, quantifying community responses to habitat modification, and linking biological signals to physical and acoustic observations. Through this ecology first design and its rigorous monitoring strategy, Ecowende seeks not only to mitigate ecological impacts but to actively enhance marine biodiversity, setting a precedent for future offshore wind developments in the North Sea.

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Theme: Monitoring Governance — Organisational solutions for improving existing structures

GV03 Integrating indigenous & local knowledge in biodiversity monitoring

Tuesday 5 May, 11h30-12h30, Room Sully 2
Chair: Quentin Groom

Description: This session explores how Indigenous and local knowledge can be meaningfully and ethically integrated into biodiversity monitoring, and invites contributions that reflect diverse perspectives and experiences. We welcome abstracts that examine the complementary strengths of Indigenous knowledge systems and scientific approaches, including long-term, place-based observations, community-led monitoring, and novel indicators of change. Topics may also address governance, data sovereignty, consent, and equitable partnerships, as well as methodological innovation and co-production of knowledge. The session aims to inspire open, constructive dialogue on inclusive, resilient, and socially grounded approaches to biodiversity monitoring.

More Species than People: Biodiversity monitoring with a small island community

Quentin GROOM, Sofie Meeus, Jodey Peyton, Ajhermae White, and Catherine Wensink

Abstract: Montserrat is a small Caribbean island of fewer than 5,000 inhabitants, yet it harbours more endemic species than many northern European countries. Its ecosystems range from elfin montane forest and wet highland vegetation to orchid-rich dry forest and turtle-nesting beaches. An active volcano renders much of the island inaccessible, and tropical storms regularly disrupt both ecological and social systems. In this context, biodiversity monitoring is not only a technical challenge, but a social one. Over four years, we have worked with the National Trust of Montserrat, the Department of Environment, and the UK Overseas Territories Conservation Forum to strengthen local biodiversity knowledge and monitoring capacity. Together we re-established a national herbarium, reestablished permanent vegetation plots, documented medicinal plant knowledge, supported environmental education, promoted native species, and developed a GBIF-hosted data portal to enhance visibility while supporting local data stewardship. The island holds far more species than there are people to monitor them. Many taxa are difficult to identify, and new records continue to emerge. Although ecological knowledge is embedded in daily life, what is locally familiar is not always recognised as scientifically or conservation-relevant. Integrating local knowledge therefore depends not only on methods, but on asking the right questions and co-defining priorities. Our experience highlights issues of governance, trust, and data sovereignty. External support is essential, yet the manner in which it is provided determines whether it builds meaningful long-term capacity or perpetuates dependency on outside experts rather than ‘home-grown’. Employment, cultural identity, and national pride matter as much locally as scientific outputs do internationally. For researchers and funders, the lesson is clear: inclusive, resilient biodiversity monitoring in small, species-rich communities must be inclusive, co-produced, grounded in mutual respect, and aligned with local aspirations from the outset.

Bolstering biodiversity conservation through the safeguarding and inventorying of local knowledge in France

Justine RIVES

Abstract: The IPBES Global Assessment (2019) describes biodiversity conservation, effective management, and sustainable use as depending on the development of “robust and inclusive decision-making processes that facilitate the positive contributions of indigenous peoples and local communities to sustainability by incorporating locally-attuned management systems and indigenous and local knowledge” (see {B6, D5}). Improving the existing structures of biodiversity conservation therefore implies integrating indigenous and local knowledge (ILK) in biodiversity governance. In its Stratégie Nationale Biodiversité 2030 (France’s NBSAP), the French Ministry of Ecological Transition has outlined a call for the preliminary drafting of a plan to safeguard and inventory traditional and vernacular knowledge of biodiversity. The French National Museum of Natural History is working towards the SILK Biodiversity project (Safeguard and Inventory of Local Knowledge — SISaL Biodiversité : sauvegarde et inventaire des savoirs locaux), which aims to provide better knowledge and understanding of biodiversity-related ILK to attempt providing an answer to the question: how can the integration of ILK in biodiversity monitoring contribute to improving its governance and conservation? In a context of eroding biodiversity, knowledge systems, and modes of transmission, along with diminishing resilience and adaptability, the SILK Biodiversity project is designed to confront these interlinked losses with a transdisciplinary approach rooted in conservation anthropology. The inventorying process of local knowledge in the French context aims to provide a better understanding of the diversity of forms, uses, and meanings of ILK so as to plan their safeguard as adequately as possible, keeping in mind their potential direct and indirect contributions to biodiversity conservation.

Transformative change in biodiversity monitoring

Carol GARZON LOPEZ, Bellis, L.M., Castillo, C., Nadim, T., Rocchini D., Van Meerbeek, K., Stokland, H., Turnhout, E., Gold, M, Beaulieu, A.

Abstract: Despite advances in biodiversity agreements and monitoring, the world is facing a dramatic loss, a 73% decline in wildlife populations over the past 50 years, ultimately endangering the future of life on Earth. In addition to the biodiversity crisis, we face climate change and the loss of cultural diversity. Biodiversity monitoring guides policy-making, financial decisions, and

conservation actions that shape the future of both people and nature. However, the current global approach to monitoring hampers these processes by failing to account and connect with regional and local knowledges. In this talk we want to share the ideas we presented in a recent paper1 where we tackle the role of environmental sciences in reinforcing inequalities in the ways of knowing, organizing, and doing, by creating narratives about global patterns of biodiversity, organizing biodiversity within a dominant classification system, and structuring the foundations of what counts as knowledge and who produces it. We suggest six strategies to address these issues and harness the potential of transformative change (i.e. system-wide shift in views, structures, and practices). In our strategies, we propose a shift in perspective by opening space for transformative change through the exploration of shared values, using relations as the unit of analysis to track the state and changes in biodiversity across plural visions of nature. To shift practices, we propose using citizen science to create and circulate knowledge, including adopting plural approaches to our understanding of space and time. Finally, to change structures, we propose transformative biodiversity governance that seeks to place justice at the center by integrating local efforts, as well as improvements to knowledge infrastructures that allow questioning of whose nature? whose rights? and explores who should be involved in biodiversity monitoring, including institutions, stakeholders, and technologies.

CCHF risk in rural northern Spain: the role of local knowledge and landscape change

Juan VALDEZ, Almudena Mari Saez

Abstract: This presentation examines the articulation between local actors, veterinarians and clinical professionals in the context of wildlife management and exposure to ticks in rural areas of Castilla y León, Spain. This region accounts for around 70% of reported cases of Crimean Congo haemorrhagic fever (CCHF), despite persistent uncertainties regarding the ecology of the vector and the conditions of its transmission. Based on ongoing ethnographic fieldwork using qualitative research, including interviews with livestock farmers, veterinarians and hunters, the study explores how these actors perceive ticks and the emergence of CCHF, and how they interpret risk in relation to concrete environmental transformations. Particular attention is given to the abandonment of grazing, shrub clearance and traditional agricultural practices, as well as the expansion of wild ungulate populations such as wild boar and deer. These changes increase vegetation density and modify patterns of animal circulation, creating favourable conditions for tick adaptation and human exposure. Risk is therefore linked to specific places and practices within the landscape. This multispecies anthropological study explores how situated knowledge is produced through everyday experience and how it relates to concerns about environmental changes. It further shows that such knowledge is not exclusive to scientific

experts, but is continuously co-produced through dialogue among clinical and veterinary experts, livestock herders and hunters, thereby shaping interpretations of risk. This study argues that prevention policies must be built and informed by local knowledge, including scientists, health professionals and rural actors, as CCHF risk is also linked to the abandonment of traditional practices.

Indigenous-led conservation of ancestral Amazonian land and culture - The Nii Nete case in Peru

Lena DEN BOER, Eleazar López Maynas & Julio Emanuel Casper Sánchez

Abstract: The Shipibo-Conibo community of Santa Clara, in the Ucayali region (approximately 200 families), bought 3200 hectares of rainforest. Their aim with this land is to protect their ancestral ecosystem and build a new community named Nii Nete (or "World of Trees" in the Shipibo language), where they can recover ancestral knowledge and cultural traditions. Nii Nete invites volunteers, eco-tourists, and scientists to collaborate, support their vision, and exchange knowledge and culture. If they succeed in doing so, the government has promised them an expansion of the acreage, resulting in a total area of over 10000 hectares. To reach their goal, the community will go through the following steps: 1. Creating an ecological and spatial inventory of the current terrain. This includes terrestrial and freshwater monitoring of the diverse microclimates and biodiversity. The expected forest types are primary forest, degraded primary forest, and secondary forest. 2. Building 10 huts for residents and volunteers, a small medical center, and clearing walking trails around the area. 3. Write a statement on the settlement and activities to the government to seal the land expansion deal. 4. Start a reforestation program for degraded areas and design the agroforestry systems. Develop art sales programs for women. Expand the residential area with housing and a carpentry workplace. 5. Long-term: expand volunteer and eco-tourism programs. Build a school. Employ residents of the surrounding communities at the farm, school, and tourism facilities. We are working on the first step together, and to reach the next, we need help with public policy and funding for monitoring, as well as professional monitoring training, tools, and knowledge development for the community. They want to learn about good examples, get to know role models, and identify organizations and funds that can provide them with advice and resources. I am interested in a talk or a poster, depending on suitability.

GV01 Biodiversity monitoring approaches and challenges

Tuesday 5 May, 16h30-17h30, Room Sully 2

Designing Flexible and Statistically Robust Biodiversity Monitoring Programmes: The Swedish NILS Programme

Henrik HEDENÅS

Abstract: Designing statistically robust biodiversity monitoring programmes is challenging when habitats are rare and spatially clustered. At national scale, complete field inventories are often infeasible, and maps alone cannot provide statistically valid estimates. Instead, national-scale monitoring requires probability-based sampling to enable unbiased estimation of habitat area, condition and change. The National Inventories of Landscapes in Sweden (NILS) illustrates how such programmes can be designed. It is a nationwide monitoring programme focusing on habitats underrepresented in other programmes. It was developed to accommodate multiple habitat types within a common statistical design. Today, NILS integrates multiple habitat inventories, Grasslands, Deciduous Forests, Alpine areas, Sea Shores and Wetlands. The design consists of a hierarchical two-phase approach combining remote sensing and field inventory. The sampling frame is a national 1 × 1 km grid. Tracts are selected using coordinated spatially balanced sampling to ensure coverage across environmental gradients. Within selected tracts, 10 m radius plots are classified using aerial imagery, auxiliary geospatial information or satellite-based predictive models, depending on the inventory. These classifications define strata guiding random selection for field inventory. Plots without focal habitats are excluded from field visits but retained as zero observations, preserving unbiased estimation. This increases efficiency while maintaining statistical rigour. The framework is scalable and adaptable: new habitats, monitoring questions or restoration follow-up can be integrated without redefining the sampling frame, and it enables robust estimates of status and change over time. The NILS case demonstrates transferable design principles for building flexible, cost-efficient and statistically robust biodiversity monitoring programmes across multiple habitats.

Balancing open access and sensitive observations – the Swedish case

Mark MARISSINK

Abstract: The Swedish Species Observation System (Artportalen) is the largest national data set within GBIF, at about 118 million occurrences. Yet in reality the number of observations in the system is even higher – a number of observations marked as sensitive either by the reporters or through criteria cannot be shared openly. Access to species observation data is an important asset in spatial planning, forestry, nature conservation and similar activities. Much of this information is provided voluntarily by enthusiasts through citizen science. However, they are not willing to share information if they see a risk for abuse that might cause danger to the species (or, in extreme cases, harm to the observer). Therefore, it is important to balance data access with a precautionary approach in order not to lose reporters. Similarly, observation data provided by researchers or certain monitoring frameworks may face challenges if shared completely openly. In this short presentation I will present some of the challenges we face in making as much as possible of the data as accessible as possible. I will talk about the biological, technical, administrative, legislative and relational considerations that we have taken into account in order to make species observation data available while avoiding harming the species and losing the confidence of the citizen science reporters.

Understanding long-term plant diversity changes in Europe

Ute JANDT, The Motivate consortium. Stephan Kambach, Helge Bruelheide, Manuele Bazzichetto, Michael Glaser, Borja Jimenez-Alfaro, Milan Chytrý, Franz Essl, Klara Friesová, Johannes Hähn, Tracy Hruska, Florian Jansen, Ilona Knollová, Roger Norum, Alicia Valdez, Alicia Acosta, Francesco Sabatini, Marta Carboni

Abstract: The MOTIVATE project (motivate-biodiversity.eu) brings together approaches from vegetation science, biodiversity modelling, remote sensing, and anthropogeography to complement the monitoring of European plant diversity. The project will support standardized, policy-relevant reporting for habitat conservation, using and promoting time series data on vegetation resurveys of the ReSurveyEurope database. As a part of this framework, we present our recent analysis of 55,975 vegetation plots that were resurveyed over the past century across all major European habitat types. Beside the high degree of specificity, with regard to the identity and changes in habitat types, we showed that local species richness and phylogenetic diversity frequently increased, especially in dynamic systems such as disturbed wetlands and forests undergoing succession, and declined in habitat types characterized by specialists. Functional evenness decreased across most habitat types, indicating biotic homogenization. Red List species showed mixed trajectories, with gains in early-successional stages and losses in stable grasslands and forests. Habitat-specific species pools remained mostly stable and only increased in grasslands that were neither affected by succession or perturbation and sparsely vegetated habitat types undergoing succession. These insights and the methods that produced them provide a pathway to i) harmonize reports under the EU Habitat Directive, ii) develop habitat-specific management options to counteract succession or perturbation and, iii) identify data gaps in space and habitat types in Europe for future monitoring efforts in Europe.

Towards an Integrated Biodiversity Monitoring Framework for Agricultural Systems

Joana CANELAS, Cesare Di Girolamo-Neto, Ana Farinha, Margarida Palma, Ameli Kirse, Martina Clausen, Adham Ashton-Butt, David Noble, Luis Figueroa, Daniel Dalton, Ilja Svetnik, Vanessa Berger, Asef Darvishi, Michael Schirrmann, Paul

Jarick, Katarzyna Zawalińska, Julia Tsybulska, Adrianna Wojciechowska, Vitaliy Krupin, Dragan Chobanov, Tiffany Jedrecka, George Muscatt, Nicky Petkov, Anna Gamero, Alena Klvaňová, Robert Griffiths, David Fidler, Christoph Scherber, Nils Borchard

Abstract: Agricultural land covers nearly half of global habitable land, representing a major driver of global biodiversity change. A robust biodiversity monitoring system is essential to assess biodiversity trends and inform more sustainable agricultural practices and policies. Yet, biodiversity monitoring still lacks data consistency, taxonomic and geographical coverage. To address these gaps, we conducted a systematic literature review of farmland biodiversity indicators for habitats, soils, insects and birds, identifying 176 distinct indicators. These were matched to Essential Biodiversity Variables (EBV) and evaluated by a panel of experts on five quality criteria: relevance, spatial scalability, temporal dynamics, data availability, and methods standardisation. Results show that biodiversity indicators generally scored high for relevance and spatial scalability, but presented major limitations in data availability and methods standardisation, impairing their ability to capture temporal dynamics across all EBV classes and biodiversity groups. Only Species Population metrics present a good standardisation and, along with birds and habitat metrics, good temporal dynamics. Considering their evaluation, we selected 26 high performing indicators to inform a comprehensive, robust and cost effective biodiversity monitoring system for agroecological systems. These offer a balanced coverage of EBV classes and taxonomic groups, combining traditional with advanced technological methods for biodiversity monitoring, such as remote sensing and DNA based approaches. To strengthen interoperability, the selected indicators were compared to relevant European policies and integrated with the Europa BON framework, resulting in a harmonised and policy relevant set of 29 indicators. This integrated farmland biodiversity monitoring framework offers a scalable and scientifically robust foundation for a results-based CAP, enhancing understanding of biodiversity change in agroecological systems.

GV02 PANEL Collaboration & transnational networks of monitoring schemes

Wednesday 6 May, 16h30-17h30, Room Barthez

Chairs: Aino LIPSANEN, Michele BRESADOLA, Hugo RIVERA, David EICHENBERG, Jan-Erik PETERSEN, Dag ENDERSEN

Description: Putting Europe's biodiversity on the path to recovery by 2030 requires solid monitoring data to detect Europe-wide biodiversity change. However, most of the biodiversity monitoring is carried out within Member States, by various organizations and networks, leading to fragmentation and limited data availability. Making most out of existing data requires transnational collaboration, from co-designing governance models to harmonizing methods and integrating monitoring results. This session discusses pathways to strengthen transnational networks of monitoring schemes and highlights approaches and findings from topical projects, initiatives and partnerships across Europe.

Biodiversa+ Partnership: connecting national systems and supporting collaboration

Michele BRESADOLA

Abstract: Achieving Europe's biodiversity recovery targets requires coordinated, high-quality monitoring systems capable of capturing change across national borders. While most biodiversity monitoring efforts are currently developed and organized at national level, increasing policy demands, including EU biodiversity legislation and international reporting obligations like the CBD, highlight the need for stronger transnational collaboration, improved data interoperability, and more coherent governance approaches. Biodiversa+, the European Biodiversity Partnership, contributes to this transition by supporting the alignment of national biodiversity monitoring and research efforts across Europe. Through its work on monitoring and data, Biodiversa+ facilitates coordination among Member States, promotes the development of common frameworks and approaches, and fosters dialogue between policy, research, and operational communities. In particular, the partnership aims to help countries better organize their national monitoring systems while enabling their integration into a broader European context. This presentation will show how Biodiversa+ addresses key challenges discussed in this panel session and how it positions itself in the biodiversity monitoring landscape. It will highlight ongoing activities that support transnational cooperation, such as the co-development of national coordination centers, engagement with national authorities, and collaboration with European initiatives and infrastructures. By reflecting on lessons learned, the presentation will contribute to the broader discussion on how European initiatives can effectively support Member States in strengthening biodiversity monitoring, increasing data availability and usability, and moving towards a more connected and resilient European monitoring landscape.

GV04 WORKSHOP How to design Biodiversity monitoring programs

Thursday 7 May, 9h00-11h00, Room Sully 2
Chairs: Mona Naeslund and Guillermo Aguilera Núñez
Contributors: Henrik Hednås, Laura Sutcliffe, Dirk Lindemann, Andrea Hagyo

Description: How do you build biodiversity monitoring programmes that are representative, scalable, and truly useful for policy, especially across regions and countries? This interactive workshop explores the key design choices behind effective monitoring: from stratification and sampling bias, to harmonising methods across borders, balancing cost, accuracy, and coverage, and turning data into clear, policy-relevant indicators. Through live questions and shared experiences, participants will reflect on common challenges, trade-offs, and solutions for biodiversity monitoring in Europe and beyond.

GV05 Linking local, national, regional, global monitoring networks

Thursday 7 May, 11h30-12h30, Room Sully 2
Chairs: Andrew Rodrigues and Niels

Description: Effective biodiversity monitoring depends on strong connections between local initiatives and national, regional, and global frameworks. This session explores how monitoring networks can be better aligned across scales to ensure that locally collected data contribute meaningfully to national reporting and global assessments. We will discuss interoperability, shared standards, data flows, and governance mechanisms that enable coordination and mutual benefit. Through practical examples, the session will highlight opportunities and challenges in building a coherent, multi-level biodiversity monitoring landscape that supports both local action and global policy needs.

From Pixels to Policy: SenseForest's Pan-European Test of Remote Sensing for Forest Conservation

Jesper Erenskjold MOESLUND, Risto Heikkinen, Topi Tanhuanpää

Abstract: Forests face unprecedented pressure from climate and land-use changes, driving biodiversity loss—yet monitoring their ecological condition remains slow, inconsistent, and resource-intensive. The Biodiver-sa+ pilot project SenseForest aims to change this by identifying key forest habitat condition indicators that can be reliably measured using remote sensing, enabling scalable, cost-effective, and standardized monitoring across Europe. Over three years, this pan-European collaboration (spanning 10+ countries, 4+ forest habitat types, and 3+ biogeographic regions) will: 1. Review and prioritize existing indicators used in forest habitat reporting, focusing on forest landscapes (including edges, glades, and natural elements). 2. Field-test the most promising indicators across countries and habitats, assessing their feasibility for remote sensing applications. 3. Deliver actionable recommendations for EU countries' nature planning, reporting, and local management, empowering them to integrate remote sensing into routine monitoring. Why attend this talk? • Discover how cutting-edge remote sensing is being tested to transform forest conservation, making monitoring faster, cheaper, and more precise. • Learn from cross-border collaboration in action, with insights from 10+ EU countries and realworld case studies. • Explore how these tools can support policy goals, from the EU Biodiversity Strategy to local na-ture restoration efforts. This project isn't just about data—it's about equipping managers with the tools to monitor and protect forests more effectively. Join us to explore how SenseForest will reshape the future of forest monitoring—turning data into action for conservation!"

Harmonising biodiversity monitoring schemes in Catalonia, from an opportunistic to a comprehensive approach

Gloria CASABELLA-HERRERO, Martí Franch, Mireia Fuertes, Gemma Gual, Artur Lluent, David Martí, Helena Ramírez, Sergi Herrando

Abstract: The need for a mapping of the biodiversity monitoring landscape to foster harmonization of the ongoing initiatives and its methodologies, avoid duplicated efforts, and assess monitoring gaps is a shared problematic across borders and scales. Aiming to provide a cohesive and comprehensive solution to this challenge in Catalonia, the Catalan Observatory of Natural Heritage and Biodiversity created the project 'Harmonizing Biodiversity Monitoring in Catalonia' (in short, HARMON). HARMON aims at identifying all the monitoring programs and schemes that analyse changes in the natural heritage over time and centralizing them into a single monitoring metadata database. The database is currently focused on species and habitats monitoring information about methodologies, distributions, targeted EBVs and involved actors, mapping the current Catalan monitoring landscape and identifying key stakeholders who are responsible for data generation and integration. This mapping exercise does not only allow to strategically mobilize and harmonize essential monitoring information, but it also creates a monitoring community supporting public policy. HARMON enables constructive dialogues on inclusive, resilient and socially grounded approaches for biodiversity monitoring. The community, which includes scientists, managers, technicians and policy makers, is actively involved in shaping the proposals for biodiversity monitoring from field data to analysis, highlighting local knowledge and enabling participation of sovereign entities at Catalan scale, while also aligning with available European standards and initiatives.

EC-steered biodiversity monitoring schemes and applications relevant for agriculture

Andrea HAGYO, Momtchil Iordanov, Jon Skoien, Renate Koeble, Talie Musavi, Linda See, Theo Larcher, Matteo Marcantonio, Simona Bosco, Rajasekaran Murugan, Rui Catarino, Jean Michel Terres, Marijn Van der Velde

Abstract: Agriculture is one of the human activities most directly interacting with nature, having a significant impact on biodiversity while also relying on biophysical processes. Biodiversity monitoring at EU-level is essential to tracking policy impact and performance related to EU biodiversity objectives. Monitoring biodiversity together with agricultural land use and management is important to provide evidence on both negative and positive impacts of farming in the context of the EU Nature Restoration Regulation and the Common Agricultural Policy. It underpins scientific advice to stimulate transition to biodiversity-positive farming. The European Commission initiated several monitoring schemes targeted at biodiversity or proxies of biodiversity and ecosystem services in the European Union over the last two decades. These include the Land Use/Cover Area Survey (LUCAS) modules on soil biodiversity, grassland and landscape features and the Environmental Monitoring of Biodiversity in Agricultural Landscapes (EMBAL). These schemes record data on both biodiversity and agricultural land use and management; however, for reliable policy assessment, additional data integration is needed. We provide an overview of these monitoring initiatives, their objectives, variables collected, the locations of the observations, and data availability. We present an innovative data sharing solution to enhance data accessibility. We illustrate with examples the challenges and opportunities to integrate data from these and other types of monitoring schemes (e.g. European Vegetation Archive, Pan-European Common Bird Monitoring Scheme). Biodiversity is a multidimensional issue so effective monitoring requires integrating data from multiple disciplines across scales ranging from the local to the EU level. Our overview provides insights on how to increase monitoring and analytical potential through data sharing and synergies between monitoring schemes by design (e.g. co-locations, protocols).

A 10-Year Framework for Biodiversity Monitoring in Georgia's Protected Areas

Guram CHKHIKVISHVILI

Abstract: Georgia has developed a strategic 10-year framework to institutionalize biodiversity monitoring across its Protected Areas, establishing a systemic, policy-driven approach to conservation management. This presentation outlines the evolution of the national monitoring programme, with a focus on the evidence-based selection of priority species and habitats according to both ecological significance and national policy requirements. Monitoring is currently led by specialized research organizations; however, a central strategic objective is ensuring long-term sustainability through structured capacity building. Protected Area rangers are actively integrated into fieldwork, enabling the continuous transfer of technical expertise. Central to this transition is the adoption of the SMART (Spatial Monitoring and Reporting Tool) platform, which has substantially improved data collection, standardization, and reporting workflows. Finally, we examine the governance structures that enable the integration of local field data into national decision-making processes. By aligning technical methodologies with long-term strategic goals, Georgia’s experience demonstrates a practical and replicable pathway for creating a cohesive monitoring network. This model highlights how decentralized data collection can be successfully harmonized

within a national governance framework to support informed environmental policy and sustainable management.

Optimising and integrating biodiversity monitoring data

Lisa NORTON

Abstract: Investments in biodiversity monitoring need to target key areas for transformational change, be co-ordinated at country, EU and global levels and be as cost-efficient as possible. I will talk through the continuing evolution of monitoring approaches in the UK and links with EU monitoring programmes, discussing some of the key issues around integrating and co-ordinating monitoring approaches. Key areas will include; the importance of monitoring biodiversity across agro-ecosystems as well as in protected areas, integration of monitoring approaches at different scales, from eDNA to field survey to remotely sensed data, the relevance of who and how the data is collected, integration of monitoring programmes across countries, governments, research bodies and NGO's and the need for co-ordinated cost-effective and efficient programmes for evidence provision. In this regard, I will draw attention to the Knowledge Exchange Networks which will be part of the Science Service for Biodiversity being launched late 2027. The UK Centre for Ecology and Hydrology (UKCEH) is the primary UK terrestrial (including freshwater) monitoring research institute in the UK with responsibility for many national monitoring programmes including national Countryside Surveys (field surveys) which have been in place since 1978, the UKCEH Land Cover Maps (Satellite mapping) since 1990. UKCEH also host the data from the National Biodiversity Network containing over 300 million records held since 2000.

PS01 Posters

A Bioregional Partnership Approach to Address Biodiversity Challenges in Ireland's South East

Andrew MADIGAN, Emer Kearney, Dean McDonnell, Sarah Prosser, David Ryan

Abstract: Global biodiversity loss has reached an unprecedented crisis, mirrored by severe declines in Ireland. Ireland's 4th National Biodiversity Action Plan (NBAP) highlights the urgent need for coordinated, effective action. In collaboration with Bioregioning South East Ireland (BioSEI), this research proposes a novel, holistic approach to biodiversity rejuvenation through landscape-scale restoration, adapted for implementation by public bodies and biodiversity-focused organisations in the South East (SE) of Ireland. The project adopts a regional, evidence-based approach — integrating qualitative and quantitative data—to inform strategic, long-term whole of society, whole of government approach (NBAP Objective 1). Central to this BioSEI-designed model is treating the SE as a single bioregion: a biogeographically and culturally coherent area defined primarily by watershed boundaries, topography, and shared ecological and social characteristics. The SE bioregion is primarily shaped by the catchments of the Barrow, Nore, Suir and Blackwater rivers, alongside coastal catchments draining from the Comeragh Mountains. It encompasses multiple counties across Leinster and Munster, including the surrounding seascape of Waterford. Landscape restoration within this bioregion will be guided by a Four Returns (4R) framework, delivering benefits for (i) nature and habitats, (ii) society, (iii) inspiration and cultural connection, and (iv) financial sustainability. Through sustained collaboration with key stakeholders (e.g. EPA, NPWS, NBDC and Local Authorities), the project will explore how this framework can inform regional, bioregion-based policy and governance models that move beyond administrative boundaries. This innovative approach has the potential to position Ireland as a leader in integrated biodiversity restoration, supporting resilient ecosystems and communities for future generations.

Private finance and Nature-based Solutions: can a blueprint for intermediation bridge the gap?

Mark VAN NIEUWSTADT, Janneke Horsten, John Garvey

Abstract: The successful implementation of Nature-based Solutions (NbS) inevitably depends on highly context-specific approaches. However, this intrinsic specificity hinders the inclusion of Nature Positive solutions (N+) in risk assessments that financial institutions typically use for their decision-making. Despite various attempts over the past decades, NbS are still rarely financed with private funds. To address this financing gap, the BIOFIN-EU project aims to define Biodiversity-Finance (BIOFIN) intermediary functions that facilitate alignment between financial requirements and local ecological realities. A literature review was conducted to define the core functions of BIOFIN intermediation from a financial perspective. This framework was validated through comparison against real-world examples of (potential) intermediaries to assess current capacity to perform these functions. The role of intermediary is widely acknowledged in finance, but due to lack of an overarching framework, intermediation usually remains a one-off solution. Many organisations exist that were not established with the aim of performing BIOFIN intermediating functions, but which do have the potential to fulfil that role. A blueprint describing intermediating functions and the core characteristics of intermediaries offers a promising opportunity to facilitate private investment in NbS. Our initial analysis suggests increased effectiveness when intermediaries are allocated a combination of functions.

The Catalan Biodiversity Observatory : from data to decisions

Lluís BROTONS, Casabella, G., Herrando, S., et al.

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.

Biodiversa+ BiodivPond Monitoring Pilot

Jonáš GAIGR, LEMMENS Pieter, BALDUCCIO Nadia, BRENNAN Georgina, BRESADOLA Michele, BRYS Rein, BUCAK ONAY Tuba, COHEN Ariel, EVERTS Teun, FRANKOVIĆ Matija, HAMIDOVIC Daniela, HILPOLD Andreas, HUIKKONEN Ida-Maria , IVANOVA Teodor, KRIŠTOFOVÁ Eva , LAMBRECHTS Sam, LONKILA Kirsi-Marja, MATZNER Orna, MILSTEIN Dana, MOENS Michael, NEMCEK Vladimir, PAKKASMAA Susanna, PALMROOS Ida , POCTA Jan, RODIC Petra, SANCHEV Radoslav, SEEBER Julia, ŠIBÍK Jozef, ŠIBÍKOVÁ Mária, ŠÍBLOVÁ Zuzana, SMEELE Simeon Quirinus, SNÅRE Henna, SVITKOVÁ Ivana, SVITOK Marek, TOLONEN Kimmo, VLADIMIROVA Tanya, ZADRAVEC Mladen

Abstract: BiodivPond (2026–2028), supported by Biodiversa+, is a pilot initiative titled “Biodiversity monitoring of ponds: evaluating the applicability of novel methods and identification of obstacles to wide use.” It addresses the need for standardised, transnational monitoring of European pond ecosystems by testing emerging technologies against traditional surveys. In spring 2026, contributors will implement a unified protocol across at least six ponds each, using traditional sampling, environmental DNA (eDNA), and passive acoustic monitoring to survey amphibians, fish, macro-invertebrates, and bats, while assessing local environmental conditions. The project will also pilot a citizen science scheme across 500 additional ponds, focusing on amphibians, fish, and macro-invertebrates through participatory eDNA collection and environmental assessments. To ensure transparency, BiodivPond will deliver a shared, open-access digital repository for all genomic and acoustic data, metadata, and species records by the project’s end. The initiative will operationalise data workflows via transferable pipelines to integrate eDNA and acoustic outputs into national and international biodiversity frameworks. Interactive dashboards and visualisation tools will provide stakeholders and the public with accessible species distribution data. By evaluating these methodologies, BiodivPond seeks to identify and mitigate obstacles to the widespread adoption of modern biodiversity monitoring frameworks across Europe.

PS02 Posters

Innovation in monitoring: mycorrhizas for national-level ecosystem assessment

Ellie WILDING, Carrie Andrew, Martin Bidartondo, Jill Kowal, Tom Weeks, Laura Martinez Suz

Abstract: Environmental monitoring programmes are increasingly expected to assess ecosystem condition and function, not only biodiversity. Yet one of the most influential drivers of terrestrial ecosystem processes - mycorrhizal fungi - remain largely absent from most monitoring frameworks despite their fundamental role in plant productivity, nutrient cycling, and soil carbon dynamics. This presentation highlights work undertaken by the Royal Botanic Gardens, Kew as part of the UK Government's Natural Capital and Ecosystem Assessment (NCEA) programme, which is generating the first large-scale baseline dataset on mycorrhizal fungi across England. Within this national monitoring programme, soil samples collected through environmental surveys are analysed to characterise mycorrhizal communities and link belowground fungal biodiversity with broader measurements of soil condition, vegetation, and ecosystem function. By integrating mycorrhizal data with other environmental variables measured across the NCEA network, this work demonstrates how belowground biodiversity can contribute to indicators of ecosystem health and resilience. The presentation will outline how mycorrhizal monitoring can complement existing approaches to habitat condition assessment, support land use planning and strengthen natural capital assessments. Finally, the talk will consider practical methods developed to incorporate fungal indicators into operational monitoring programmes, including standardisation, interpretation, and integration into policy-relevant frameworks. Together, this work illustrates how large-scale national monitoring initiatives such as NCEA can help close critical gaps in terrestrial ecosystem assessment by linking belowground biodiversity with ecosystem function.

Study and monitoring of biodiversity in France: Feedbacks on special efforts gathering Research and Policy communities

Olivier NORVEZ

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: 1) Map out the skills and willingness at the national level to address the "who's doing what" ; 2) Create a mailing list for the community ; 3) List current projects, tools (Virtual research environment, biodiversity monitoring frameworks) and networks from French research and biodiversity policies communities and links with international related initiatives; 4) Broaden the scope and move beyond the focus on occurrence data (strengthen the AI, satellite and genetic dimensions, and integrate these communities) ; 5) Explore the functioning of other networks such as the Knowledge-Action hub of the One Health community or the French Barcode of Life node ; 6) Beware of the voluntary nature of the network, and avoid redundancy with currently existing initiatives.

Indigenous-led conservation of ancestral Amazonian land and culture - The Nii Nete case in Peru

Lena DEN BOER, Eleazar López Maynas & Julio Emanuel Casper Sánchez

Abstract: The Shipibo-Conibo community of Santa Clara, in the Ucayali region (approximately 200 families), bought 3200 hectares of rainforest. Their aim with this land is to protect their ancestral ecosystem and build a new community named Nii Nete (or "World of Trees" in the Shipibo language), where they can recover ancestral knowledge and cultural traditions. Nii Nete invites volunteers, eco-tourists, and scientists to collaborate, support their vision, and exchange knowledge and culture. If they succeed in doing so, the government has promised them an expansion of the acreage, resulting in a total area of over 10000 hectares. To reach their goal, the community will go through the following steps: 1. Creating an ecological and spatial inventory of the current terrain. This includes terrestrial and freshwater monitoring of the diverse microclimates and biodiversity. The expected forest types are primary forest, degraded primary forest, and secondary forest. 2. Building 10 huts for residents and volunteers, a small medical center, and clearing walking trails around the area. 3. Write a statement on the settlement and activities to the government to seal the land expansion

deal. 4. Start a reforestation program for degraded areas and design the agroforestry systems. Develop art sales programs for women. Expand the residential area with housing and a carpentry workplace. 5. Long-term: expand volunteer and eco-tourism programs. Build a school. Employ residents of the surrounding communities at the farm, school, and tourism facilities. We are working on the first step together, and to reach the next, we need help with public policy and funding for monitoring, as well as professional monitoring training, tools, and knowledge development for the community. They want to learn about good examples, get to know role models, and identify organizations and funds that can provide them with advice and resources. I am interested in a talk or a poster, depending on suitability.

EBOCC piloting – need for Member State input

Päivi SIRKIÄ, Kari Lahti, Aino Juslén, Kristian Meissner, Johannes Stahl, Hugo Rivera

Abstract: The Preparatory Action Project for EU Biodiversity Observation Coordination Centre (EBOCC) builds on Horizon 2020 EuropaBON recommendations. It aims to improve coordination of biodiversity monitoring and data flows across ecosystems. The project explores pathways to streamline workflows, reduce duplication, and lower administrative burden for Member States. It also promotes FAIR (Findable, Accessible, Interoperable, Reusable) principles through close collaboration with the European Commission, national authorities, and stakeholders. EBOCC focuses on diagnosing Member State needs, fostering exchange of good practices, and delivering harmonised and interoperable data flows. It supports policy-relevant indicators and strengthens capacity across key actors. The current pilot phase covers six thematic areas: terrestrial habitats, freshwater benthic invertebrates, freshwater habitats, marine mammals, seagrass habitats, and pollinators. Building on earlier activities and existing knowledge, a key early task in piloting is to map biodiversity monitoring actors and responsibilities, existing monitoring data, data flows for reporting, and monitoring methods and field protocols. This work will identify gaps, overlaps, and bottlenecks. It will also support the design of data flow and governance frameworks and the performance analysis of monitoring methods. In addition, an online collection of monitoring methods will be developed. The results will identify critical gaps and areas where co-creative development of harmonised protocols and new approaches provide the greatest benefits. To support this work, a large survey targeting EU Member States will be launched in spring 2026. Responses will require input from multiple experts in most countries. This poster invites discussion with BioMonWeek participants on related national or international initiatives and aims to raise awareness of the upcoming survey and encourage broad participation.

Animal sensor networks: building a scientific basis for researchers, policy makers and nature managers

Veronique ADRIAENSSENS, Jim Casaer, Peter Desmet, Tanja Milotic, Eric Stienen, Pieter-Jan Verhelst, Stijn Van Onsem

Abstract: With INBO (Research Institute Nature and Forest, Flanders, Belgium), we are participating in research projects on animal sensor networks that allows us to address various needs in the aquatic and terrestrial areas by cost-effective monitoring. Through these advanced monitoring techniques such as camera traps, fish tracking and bird tracking embedded in well-structured surveys and supported by experts managing data flows, we develop a scientific basis for both research, policy makers and nature managers: (1) it encourages university students and researchers to address specific scientific research questions, building on a well-developed monitoring network (2) it allows policy makers to test policy scenarios and impacts of implementation of measures (3) it supports nature managers to address specific needs for conservation and restoration. These networks are developed in open science environments which encourages exchange at the European as well as regional level by researchers, policy experts and nature managers.

BioMonWeek 2026
The European Conference for Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: Capacity-building in monitoring — Training, tools and knowledge development

CP04 WORKSHOP What jobs and skills for biodiversity monitoring in the future

Tuesday 5 May, 16h30-17h30, Room Sully 1
Chair: Suzon Bedu

Description: What will be your job like in 10 years? What are the skills we will need? What younger generations will bring to monitor biodiversity in the future? Come and join us in this interactive session to shape the future of our daily workdays!

CP07 Capacity building with genetic tools

Tuesday 5 May, 16h30-17h30, Room Joffre F

Democratizing environmental DNA: Simple, Scalable Tools for Monitoring Critical Habitats

Patrick NICHOLS

Abstract: Environmental DNA (eDNA) has transformed biomonitoring, but widespread adoption, especially by non-specialists, is often limited by complex, costly, and equipment-dependent protocols. Building genuine monitoring capacity requires methods that are scientifically robust yet accessible, scalable, and transferable. Our research across marine and freshwater ecosystems demonstrates how simplified eDNA workflows can empower community practitioners. A central focus is the validation and application of passive eDNA samplers (PEDS): simple cotton substrates that eliminate the need for resource-intensive active water filtration. In the remote Papahānaumokuākea National Marine Sanctuary, PEDS were compared with traditional filtration for detecting the nuisance macroalga Chondria tumulosa. Despite their simplicity, PEDS achieved comparable detection probabilities while greatly reducing fieldwork complexity, enabling rapid, large-scale deployment by teams with limited training and equipment. These tools are now being adapted for freshwater monitoring. PEDS are particularly suited for under-ice collection of aquatic eDNA to monitor endangered Saimaa ringed seals (Pusa hispida saimensis) and Eurasian otters (Lutra lutra) during winter, when traditional surveys are largely unfeasible. This approach provides a non-invasive method for mapping critical winter habitats. To further reduce barriers, the workflow integrates rapid DNA extraction and portable Nanopore sequencing platforms. Streamlining the process from collection to sequencing lowers both technical and financial barriers to routine biomonitoring. Standardized, low-cost protocols will allow these approaches to be incorporated into existing monitoring programs by professionals, conservation managers, and citizen scientists. Broad adoption can empower local stakeholders to conduct robust eDNA monitoring, fostering a more inclusive and resilient approach to biodiversity observation.

Mobilising Ethical Dialogue Methods in the Co-Design of Biodiversity Analysis Tools (BMD)

Tami WOOLDRIDGE, Christopher Ellis, Wojcieh Mroz Emma Bush, Monica Vidal, Eva Alonso Vizcaino, Niels Raes, Stella Koprinkova, Louise Hendrickx, Julian Oeser, Joaquin Lopez, Marina Skunca, Peter Hollingsworth

Abstract: Vast amounts of biodiversity data are available to monitor species and habitats, and link biodiversity trends with pressures and drivers. These data will rapidly increase as new monitoring technologies such as eDNA, camera traps and audio detection are mainstreamed. The biodiversity data space is challenging to navigate and is not optimally designed towards delivering policy objectives. Improved availability, accessibility and harmonisation of biodiversity data would support conservation practitioners in monitoring, decision-making, implementation and reporting under key policies such as the EU Nature Directives. Working towards this goal Biodiversity Meets Data (BMD) brings together existing innovations to create a Single Access Point (SAP) to high-throughput biodiversity data, monitoring and analyses. An intuitive SAP, and underpinning Biodiversity Analysis Tools (BATs), requires the integration of many knowledge sources and user perspectives throughout all stages of the project. Co-design of the SAP and BATs with stakeholders (site managers, practitioners, decision makers) is an ongoing practice that has fostered collaboration among the project's teams and across the stakeholder landscape to ensure that the tools being designed best meet the needs of those anticipated to use them. In this presentation, we will share the principles (design thinking, ethical dialogue) and methods (interactive workshops) that are being used in BMD's co-design activities. We will give an overview of our findings from one strand of co-design in BMD: the User Story Workshops which invited stakeholders to work together to explore their biodiversity monitoring needs and how the BATs might address these. We will reflect on the approaches that we have found to support effective co-design, which are relevant for practitioners working collaboratively to improve biodiversity monitoring and conservation.

Co-Creation to Strengthen the Science-Policy Interface: Opportunities and Challenges in Genetic Indicator Monitoring

Christina Ritzl VEJLGAARD, Theunissen, E., Lundmark, C., Leus, K., Geue, J. C., & Hvilsom, C.

Abstract: Translating scientific advances into policy practice goes beyond knowledge transfer—it demands cross-disciplinary and cross-organizational collaboration. Genetic diversity monitoring exemplifies this challenge: under the Convention on Biodiversity (CBD) in the Kunming-Montreal Global Biodiversity

Framework,, countries must now report on genetic diversity indicators, yet bridging science and practice remains difficult. The EU Biodiversa+ GINAMO project (Genetic Indicators for Nature Monitoring) supports this transition in five European countries—Belgium, Sweden, France, Italy, and Norway—focusing on Target 4 indicators (populations with Ne > 500 and maintained populations). GINAMO's approach centers on co-creation, engaging stakeholders early to develop context-specific, sustainable solutions. To assess country-specific needs and challenges, GINAMO organized stakeholder workshops in each partner country. These workshops—part of an ongoing co-creation process—helped identify capacities and gaps, guiding collaborative development of reporting workflows. Co-creation in GINAMO operates on two levels: externally with national stakeholders and internally among 30+ researchers across six work packages. While co-creation enhances research relevance and societal impact, it demands skills beyond traditional scientific training, such as facilitation, communication, and iterative engagement. A critical challenge is preparedness: researchers must understand and anticipate co-creation's complexities before engaging. This presentation reflects on GINAMO's experiences, highlighting challenges and offering practical recommendations to help research teams navigate co-creation—both with stakeholders and in interdisciplinary research collaborations.

The Ne500 genetic indicator in species with diverse life history strategies: best estimation practices from DNA data and operationalisation

Myriam HEUERTZ, Marie-Gabrielle Harribey, Laura Martinez Anton, Joachim Mergeay, Anja Westram, Xiatong Cai, Julia Geue, Frédéric Raspail, Peter Galbusera, Sean Hoban, Alexander Kopatz, Linda Laikre, Gernot Segelbacher, Cristiano Vernesi, Christina Hvilsom, Yvan Le Bras, Joost Raeymaekers, Myriam Heuertz, Pauline Garnier-Géré

Abstract: Genetic diversity (GD) is the basis for long-term survival, adaptation and resilience of populations. Effective population size, Ne, is a genetic parameter that impacts the rate of random genetic drift, inbreeding, and adaptive potential and is therefore highly useful for monitoring GD, understanding evolutionary processes and designing conservation strategies. Indicator A.4 of the Kunming-Montreal Global Biodiversity Framework, "The proportion of populations within species with an effective population size > 500" (Ne500), allows monitoring GD through Ne assessment based on genetic (DNA) or proxy data. To provide conservation practitioners with best practices to estimate Ne from genetic data in a variety of species, we applied a framework to categorise species based on life-history traits (LHT) pertaining to longevity and reproductive strategies. We selected DNA datasets from 18 European species spread across the main LHT categories and computed Ne and other population genetic metrics for 195 populations. Ne estimates displayed a large variation across LHT categories,

including populations with Ne below and above 500. Ne was negatively correlated with population-specific divergence across a large proportion of LHT categories and was on average higher in core populations than in marginal populations. We discuss the interpretation of the obtained Ne estimates for the calculation of the Ne500 indicator and highlight the practical challenges of reliably estimating Ne in natural populations, particularly when spatial and age structures interact. To provide conservation practitioners with a practical tool to calculate Ne and the Ne500 indicator, we operationalised our scripts into FAIR workflows under Galaxy Ecology. The workflows are currently being enhanced to perform population delimitation based on genetic clusters and to control the effect of genomic data quality on Ne estimates. They will be tested by conservation practitioners for feedback to further improve them.

Pladias - database of the distribution of vascular plants

Karol MARHOLD, Adam Kantor

Abstract: Pladias (Plant Diversity Analysis and Synthesis Centre) was a project funded by the Czech Science Foundation in 2014–2018. It integrated research capacities dealing with the diversity of temperate flora and vegetation from Masaryk University (Brno), Institute of Botany of The Czech Academy of Sciences and the University of South Bohemia in České Budějovice, in cooperation with many external specialists. An extensive database of critically revised data on Czech flora and vegetation, available at this web portal, was created as an infrastructure to support research within this project. It is continuously updated also after the end of the Pladias project in collaboration with the Czech Botanical Society. In 2024, a version of this software was also installed in the Slovak Republic by the Plant Sciences and Biodiversity Centre of the Slovak Academy of Sciences, with initial support from a grant awarded by GBIF. The Slovak version of Pladias is continuously growing, and currently it provides more than 3,500,000 observation records on the distribution of vascular plants in Slovakia. The databases focus on native and naturalized flora occurring in the Czech Republic and Slovakia. Cultivated plants are not within the scope of the databases, although the most commonly cultivated crops and woody plants are included.

CP09 WORKSHOP Standardising and sharing survey and monitoring data through GBIF

Wednesday 6 May, 9h00-11h00, Room Barthez

Chairs: Kate Ingenloff and Salza Palpurina

Description: The data clinic will provide participants with an opportunity to learn how to standardise their survey and monitoring data using Darwin Core (https://dwc.tdwg.org) and sharing their standardised data through GBIF (https://www.gbif.org). The session will include a brief introduction to these topics followed by a data mapping demonstration with an example dataset specifically addressing some of the more difficult aspects of the process associated with complex survey data. Bring your own data—our clinic wraps up with a hands-on session where you can work directly with organisers and peers to model your SAM data at its best.

CP06 Capacity needs and availability for species identification and naming

Wednesday 6 May, 16h30-17h30, Room Joffre G

Description: Accurate species identification and stable naming are fundamental to biodiversity monitoring, research, and policy. This session focuses on current capacity for species identification and taxonomy, and where critical gaps remain. We will examine the distribution of expertise, training needs, and access to collections, reference materials, and digital tools. The discussion will address how capacity constraints affect data quality and monitoring outcomes, and explore practical pathways to strengthen taxonomic expertise and ensure a robust foundation for biodiversity knowledge and conservation action.

Machine Listening as a Capacity-Building Tool for European Bat Monitoring

Leonie BAIER, Burooj Ghani, Dan Stowell, Vincent Kalkman

Abstract: Monitoring global biodiversity depends on accurate species identification, yet taxonomic expertise remains unevenly distributed. Bat monitoring highlights this challenge; because bats are nocturnal and cryptic, acoustic monitoring is the primary tool for study. However, their ultrasonic calls are shaped more by behavioral function than by species-specific traits, leading to significant acoustic overlap. As a result, few experts can reliably identify species from recordings, creating analytical bottlenecks and limiting the detection of population trends in the face of habitat loss and insect declines. Machine listening, the use of artificial intelligence (AI) to interpret sound, offers a powerful way to address these constraints. By combining deep learning with expert-validated data, AI can support species-level classification, reduce bottlenecks, and expand monitoring coverage. Robust models, however, depend on high-quality annotated datasets. In practice, training data are imbalanced: common species are well represented, while rare or cryptic taxa remain underrepresented. Many recordings carry “weak labels,” naming only a single species per clip and omitting background vocalizations, whereas “strong labels” provide precise information about when a species vocalizes within a clip, often enabling more reliable and generalizable models. Within the EU-funded project MAMBO (Modern Approaches to the Monitoring of Biodiversity), we develop and

benchmark AI-based sound recognition tools for European bats while addressing these structural challenges. Our approach combines expert-curated datasets, standardized labeling practices, and integration with open infrastructures such as the sound repository Xeno-canto. By pooling annotated recordings across borders, we aim to reduce geographic and taxonomic blind spots and build transparent, reusable tools that scale rather than replace taxonomic expertise, strengthening biodiversity monitoring across Europe.

An analysis of the supply of taxonomists and the demand for their services in Europe

Sofie MEEUS, Quentin Groom, Melanie De Nolf, Lina M. Estupinan-Suarez

Abstract: Taxonomic expertise is essential for conservation, ecological research, and the implementation of environmental policy. Yet the field faces persistent challenges, collectively termed the “taxonomic impediment”, including insufficient human capacity, uneven taxonomic coverage, and weak alignment with policy needs. We conducted a meta-research analysis of European taxonomic capacity using an open and reproducible workflow built on data from OpenAlex, Wikidata, and GBIF. We identified over 31,000 taxonomic authors affiliated with European institutions and profiled their taxonomic scope, institutional base, and geographic distribution. We compared this supply of expertise with indicative demands arising from biodiversity-related policies, including European and global policy drivers. Our analysis reveals significant mismatches between capacity and need, particularly for underrepresented groups such as fungi, algae, and some invertebrates. We argue that the supply and demand for taxonomy are often disconnected due to institutional inertia, historical biases, and weak feedback from policy. This work highlights the importance of expert taxonomists, but identifies the lack of integration of the profession with other disciplines as a bigger issue than the absolute number of taxonomists.

Building taxonomic capacity for soil meiofauna in Europe: the SoilMATs training model

Edoardo MASSA, Karin Hohberg, Miloslav Devetter, Iasmi Stathi, Roberto Guidetti

Abstract: The biodiversity crisis is paralleled by a persistent taxonomic impediment, particularly severe for soil meiofauna, where species identification and taxonomy are limited by a shortage of specialists and insufficient transfer of expertise. This is especially relevant for neglected limno-terrestrial groups such as Tardigrada, Rotifera, and Nematoda, which are important for biodiversity assessment and soil monitoring. Soil Meiofauna Advanced Taxonomy school (SoilMATs) was established as satellite project of TETTRIs to address these gaps through a structured European training programme. SoilMATs combined online preparation, synchronous teaching, field sampling, and hands-on activities. Expert

taxonomists first trained five Future Local Trainers, who then contributed to the practical training of 20 selected scholars. The open European call received 84 applications, revealing a strong demand for advanced taxonomic training across countries and career stages. Training activities in Italy, Germany, and the Czech Republic focused on integrative identification workflows combining morphology, advanced microscopy, and molecular approaches. Beyond direct training, the programme generated longer-term impacts: some scholars returned to partner laboratories to strengthen their skills, others accessed research opportunities enabled by the expertise gained, and an international network of support and knowledge exchange developed among trainers and trainees. In parallel, SoilMATs is developing a practical syllabus to support future self-directed learning in taxonomically relevant morphology and terminology. SoilMATs shows that targeted, practice-oriented training can strengthen taxonomic capacity for understudied groups while supporting biodiversity monitoring, experience sharing, and long-term knowledge transfer across Europe.

Reference Collections as Infrastructure for Long-Term Biodiversity Monitoring and Taxonomy Capacity Building: Lessons from the ARCADE project

Tatiana MOREIRA PINHAL, Hugo Gaspar, Eduardo Marabuto, Francisco Gil, Martim Baptista, Albano Soares, Hugo Silva, Cristina Rufino, Luena Marques, Carla Rego, Mário Boieiro, Alperen Yayla, Renata Santos, Zeynep Ladin Cosgun, João Birg, Guilherme Melo, Olga Ameixa, Helena Castro, Catarina Almeida, Márcia Santos, Luís Bonifácio, Ana Afonso, José Manuel Grosso-Silva, Roberto A. Keller, Dora Aguin Pombo, Paulo Alexandre Vieira Borges, Patrícia Garcia Pereira, João Loureiro, Sílvia Castro

Abstract: The ARCADE (Aligning Reference Collections with tAxonomic Development Efforts for pollinator conservation in Portugal), a 3PP of the TETTRIs project, tackles a critical bottleneck in biodiversity monitoring: the need for accessible, standardised, and taxonomically rigorous reference collections. Focusing on bees, hoverflies, and butterflies across Portugal, the project bolstered the taxonomic infrastructure essential for future conservation and restoration strategies, aligning with Article 10 of the EU Nature Restoration Regulation. Through an integrative approach, ARCADE combined species- and specimen-level indexing, systematic taxonomic revisions, and gap analyses with targeted efforts across eight collections from eight institutions. All records were digitised into searchable databases using Darwin Core standards, significantly enhancing data accessibility and interoperability. By the project's conclusion, these curated collections comprised 57,256 bees, 11,346 hoverflies, and 33,319 butterflies, covering 79%, 31%, and 100% of the respective species known to Portugal. Furthermore, strategic field surveys added 12,851 bee and 960 hoverfly specimens, alongside targeted sampling of underrepresented butterflies, effectively filling critical gaps in under-sampled regions and taxa. Findings

emphasise that monitoring readiness depends as much on curated physical archives and shared data standards as on field methodology and taxonomic training. ARCADE engaged eight institutions and over 60 participants and ultimately provided a scalable model for monitoring capacity through accurate digitisation and taxonomic validation. By bridging the gap between museum collections and FAIR-by-design standards, ARCADE established a robust national taxonomic baseline and a dynamic legacy for voucher-based pollinator conservation. Crucially, the project established national standards for safeguarding reference collections and provides the essential foundation for long-term monitoring.

CP08 WORKSHOP Boosting science-industry partnerships for underwater biodiversity monitoring

Thursday 7 May, 9h00-10h00, Room Sully 1
Chairs: Alice Guittard, Louise Forsblom, Renato Mendes, Alexandra Zachariadou, Kostal Proios
Description: This dynamic workshop aims at bringing together scientists, industry leaders, innovators, and policymakers to explore how stronger knowledge-sharing and other forms of collaboration can accelerate breakthroughs and innovation uptake in underwater biodiversity mapping and monitoring. Through interactive discussion and real-world examples, participants will uncover what makes science-industry collaborations truly work—while identifying the gaps still holding us back. From cutting-edge technologies to smart knowledge-transfer models, this session seeks to spark fresh ideas, new partnerships, and actionable pathways to support marine biodiversity protection and restoration. Join us to co-shape tomorrow's ocean solutions.

CP02 Monitoring training, and experience sharing

Thursday 7 May, 11h30-12h30, Room Rondelet

From Data to Dialogue: Transforming Biodiversity Monitoring into Societal Engagement

Kathrin HELSPER

Abstract: Effective biodiversity monitoring depends not only on robust scientific methods but also on how the resulting data are communicated to society. Monitoring initiatives generate rich information about ecosystems and species, yet without clear translation into accessible and emotionally resonant narratives, these insights often remain confined to academic or technical spaces. When communicated effectively, biodiversity data can foster public understanding, connection, and stewardship, helping to bridge the gap between scientific knowledge and societal action. This presentation explores innovative communication and engagement strategies developed within the WildLIVE! project, a large-scale citizen science initiative focused on wildlife monitoring and AI-assisted biodiversity research. Drawing on experience across digital platforms, museum-based outreach, and creative science communication, we demonstrate how diverse approaches can effectively reach both targeted citizen scientist communities and broader public audiences. Central to our work is the principle of “closing the loop” between research and society — ensuring that scientific outcomes are returned to the public in meaningful and engaging forms. Beyond traditional outreach, WildLIVE integrates artistic storytelling and visualization to translate biodiversity research into emotionally resonant formats that foster ecological literacy and personal connection. Throughout the presentation, practical lessons and transferable strategies are shared for researchers seeking to strengthen public engagement and maximize the societal impact of biodiversity monitoring.

Building local capacity for invasive species monitoring through OneSTOP Living Labs

Laura ABRAHAM, Groom Quentin, Bayliss Helen, Franklin Alex, Green Sian, Delva Soria, Hendrickx Louise, Vicente Joana R., Vale Cândida, Malta-Pinto Eva, Jauni Miia, Poimala Anna, Preda Cristina, Gavrilescu Carla, Rozylowicz Laurentiu, Memedemin Daniyar, Patrascu Lucian, Dehnen-Schmutz Katharina

Abstract: Effective biodiversity monitoring depends not only on advanced technologies, but on the capacity of local actors to apply, interpret and sustain monitoring efforts over time. We present the Living Lab approach developed within the Horizon Europe OneSTOP project (OneBiosecurity Systems and Technology for People, Places and Pathways), which focuses on strengthening local and regional capacities to monitor invasive alien species across Europe. OneSTOP uses five Living Labs across diverse bioclimatic and socio-economic European regions in Romania, the UK, Finland, Portugal and Belgium. These Living Labs function as real-world learning environments that connect science, society and practice, enabling the co-development of monitoring tools and shared knowledge through practice-led iterative feedback. Invasive alien species represent a major driver of biodiversity loss and impose significant economic costs, requiring early detection and coordinated monitoring that extends beyond expert-led systems. Within each Living Lab, local stakeholders, including authorities, NGOs, civil society organisations and researchers, are actively involved in co-designing and testing monitoring approaches. Capacity building is embedded through participatory workshops and continuous feedback, ensuring that tools are accessible, context-appropriate and usable beyond the project lifetime. The Living Labs support the deployment and evaluation of complementary monitoring methods, including air-DNA, computer vision, iEcology approaches and citizen science initiatives such as Sentinel Gardens, enhancing detection capability while fostering local ownership of monitoring processes. By integrating technological innovation with learning and institutional engagement, the OneSTOP Living Labs demonstrate how capacity building can transform biodiversity monitoring systems into resilient, locally grounded practices that strengthen Europe’s ability to detect, prioritise and respond to invasive alien species.

OCEANIS: Structuring the monitoring–knowledge–action continuum in ocean initiatives

Lina MTWANA NORDLUND

Abstract: Effective ocean monitoring requires more than sustained observations; it depends on coherent systems that connect measurements to data stewardship, analysis, usable products, and societal uptake. Despite major advances in marine observing infrastructures, many initiatives still face challenges in translating monitoring outputs into decision-relevant knowledge. This points to the need for operational frameworks that embed monitoring within the broader knowledge-to-action system. We present OCEANIS, a framework that structures ocean initiatives across eight interconnected domains: exploration of knowledge needs, societal relevance, observations and data collection, data management, analysis and modelling, data products, communication, and evaluation. Rather than treating monitoring as an isolated technical component, OCEANIS positions observations within a dynamic architecture where societal priorities guide monitoring design, data stewardship ensures interoperability and accessibility, analytical processes transform observations into indicators and assessments, and communication and evaluation enable uptake and adaptive improvement. The framework is operationalized through a multidimensional Spiderweb schema that visualizes system balance across domains and supports diagnosis, planning, and coordination. This allows initiatives to identify structural gaps, such as strong observational capacity but limited pathways to decision-support products or stakeholder engagement. By linking monitoring activities to the full knowledge–action continuum, OCEANIS provides a transferable approach for strengthening the effectiveness and societal impact of ocean observing and assessment systems across scales. The framework supports more integrated, adaptive, and outcome-oriented monitoring aligned with evolving policy and sustainability needs.

Developing European capacity and infrastructure for DNA based monitoring

Andy NISBET, Tiina Laamanen

Abstract: DNA based monitoring and genomics have the potential to provide powerful tools to observe and track biodiversity across space and time. To realise this potential, we need to build technical capacity and infrastructure including harmonised protocols and standards, curated and taxonomically sound reference data bases, robust metadata standards aligned with FAIR data orinciples, and open data repositories. Equally important are the institutional infrastructure and human capacity. Clear governance and legal frameworks will support data use, ethical and legal compliance, and sustainable funding. This should happen as a collaboration of stakeholders from research, policy, regulation and monitoring practitioners. Our talk will present current developments and European initiatives in this field including: Biodiversity Genomics Europe's work to develop tools, capacity, and communities of practice for DNA barcoding and whole genome sequencing. The example of the UK Barcode of Life project will illustrate progress with improvements to reference databases. The importance of national policy and governance will be discussed with reference to the Finnish roadmap for environmental DNA. This sets out a shared vision and action plan to deliver coordinated infrastructure, capacity building and funding at the national scale. Finally, we will discuss the importance of join up across the community using the examples of the UK DNA Working Group and the newly established eDNA Europe society. Note - This could be part of a group of talks on DNA capacity building or on infrastructure development for emerging monitoring technologies.

How to integrate genetic diversity into monitoring

Gernot SEGELBACHER, Hvilsom Christina, Eklom Robert , O'Brien David, Fischer Martin

Abstract: Genetic diversity is one of the three main components of biodiversity. It provides the foundation necessary for long-term survival, adaptation, and resilience not only for individuals, but also for populations, species, and entire ecosystems. If we want to preserve the whole entity of biodiversity, we need to assess the changes in genetic diversity that are occurring. Recent studies found that genetic diversity is declining on a global scale, but often data are missing. Monitoring genetic diversity across different time points is a first step to gain insight into the extent to which populations or species might be at risk, to guide conservation action and to provide evidence for solutions. However, current biodiversity monitoring is mostly focusing on species, and the monitoring of genetic diversity within species has often been neglected. The Kunming Montreal Global Biodiversity Framework includes diversity indicators and the 196 signatory nations of the Convention on Biological Diversity are requested to report on them. To help reporting we have produced IUCN Guidelines that 1) provide a number of steps to be considered when developing monitoring projects and 2) list criteria which should be evaluated for selecting species for any monitoring programme. We will showcase examples from different countries on genetic diversity

monitoring programmes, highlighting different approaches, and availability of resources and DNA/non-DNA data.

PS01 Posters

French capacity building for the implementation of the European pollinator monitoring scheme

Xavier HOUARD, Andréa Barraux

Abstract: The European Nature Restoration Regulation (ENR) aims to reverse the decline of pollinators by 2030 and achieve satisfactory population levels. This obligation is accompanied by a monitoring method based on a standardized protocol developed at the European level, the European Union Pollinator Monitoring Scheme (EU PoMS). This protocol aims to assess the abundance and diversity of pollinating insect species within each Member State and to measure population trends up to 2050. Furthermore, the measured indicators will allow for the evaluation of the success of the restoration measures implemented under the Nature Restoration Regulation. At the national level in France, the deployment of EU-PoMS is part of the National Plan for Pollinating Insects and Pollination (2021-2026), led by the government. It also falls within the framework of the National Terrestrial Biodiversity Monitoring Program, as outlined in the Master Plan for Terrestrial Biodiversity Monitoring. Currently in France, identification skills are very limited, or even nonexistent in some areas, and assessments are primarily carried out by volunteers outside of their professional hours. Such a situation would not be sustainable when deploying a protocol of the scale of EU-PoMS, and funding dedicated training for the identification of bees, hoverflies, butterflies, and moths is essential. The "EU-PoMS Skills Development" project aims to structure French efforts to establish knowledge bases and develop approaches to pollinator monitoring through two coherent objectives: 1) the educational and technical coordination (instructional design) of the network of organizations involved in knowledge and scientific monitoring of pollinating insects; 2) the technical and scientific training of the network of operators in the ability to identify pollinating insects (parataxonomic knowledge).

FEdA – Research Initiative for the Conservation of Biodiversity

Julian TAFFNER

Abstract: The Research Initiative for the Conservation of Biodiversity (German acronym: FEdA) is a nationwide program funded by the German Ministry of Research, Technology and Space (BMFTR). Consisting of over 40 transdisciplinary projects, FEdA brings together scientists with stakeholders from civil society, business, and politics to jointly develop systemic solutions and practical guidelines to combat the biodiversity crisis. Our work focuses on three areas of

action: 1) assessing biodiversity using innovative methods, 2) understanding the causes and consequences of biodiversity loss, and 3) developing systemic solutions and portfolios of measures. The individual projects are supported by the FEdA Central Coordination Office, which works to disseminate research results to relevant stakeholders and engages the public to spread awareness and knowledge about biodiversity loss and possible actions for its reversal, for example in the form of policy briefs for decision-makers as well as action weeks and a traveling exhibition for laypeople. In addition, we support accompanying research such as the Faktencheck Artenvielfalt (published in 2024) and KIBA-D, which is developing an AI workflow to continuously monitor the state of biodiversity in Germany.

PS02 Posters

Activating Europe's Marine Biodiversity Data for the Digital Twin of the Ocean: The DTO-BioFlow Approach

Carlijn KOOLE, Christina Pavloudi, Christos Arvanitidis, Lise Cronne, Marialetizia Mari, Tamires Davi de Godoi, Julie Abergas-Arteza, Neil Holdsworth, Cristina Huertas, Frederic Leclercq, Inés Martinez Bustamante, Oonagh McMeel, Carlota Muñiz, Matthias Obst, Sara Pittonet, Andrei Roncea, Ioulia Santi, Maria Teresa Spedicato, Nathalie Tonné and Klaas Deneudt

Abstract: The Ocean and its biodiversity are essential to life. Protecting biodiversity is one objective of the Horizon Europe Mission Restore our Ocean and Waters, supporting the EU Green Deal, the EU Biodiversity 2030 Strategy and the Ocean Pact. The EU Digital Twin of the Ocean (DTO), a Mission enabler, will integrate observations and advanced digital infrastructures to explore potential scenarios, inform evidence-based policy, and deliver societal benefits. Central to this is a robust biodiversity component. Despite myriad actors collecting biodiversity data, and the development of cost-effective monitoring tools, much marine biodiversity data remains inaccessible. The Horizon Europe-funded DTO-BioFlow project is changing this. Since September 2023, DTO-BioFlow has been working to increase the volume and quality of marine biodiversity data in European data infrastructures and the EU DTO by (i) creating data flows from existing monitoring networks to EMODnet and the EU DTO (ii) building capacity among data providers through training and financial support, (iii) developing Demonstrator Use-Cases that address real-world marine environmental management challenges, and (iv) mobilising the community to share and use marine biodiversity data and digital resources through outreach and engagement. A first "Barriers Playbook" identified barriers to enabling data to flow into the pathways developed within DTO-BioFlow. Two Data Calls to data holders resulted in 18 grant winners supporting the ingestion of previously inaccessible

biodiversity data. A Blueprint was produced specifying dataflows for several novel biodiversity data types. Data pipelines to EMODnet are ongoing, with direct connections to the EU DTO underway for key European-level repositories, including the European Tracking Network, Ocean Biodiversity Information System, and EcoTaxa. DTO-BioFlow is generating good practices for activating biodiversity data flows and integrating this into digital twin frameworks.

BioMonWeek 2026

The European Conference for Biodiversity Monitoring

4-8 May 2026
Montpellier

Theme: eDNA cross-realm theme

eDNA01 General overview of the methodology and key method aspects

Wednesday 6 May, 9h00-10h00, Room Auditorium
Chair: Florian Leese

Applications and Limitations of Environmental DNA in Biodiversity inventories and monitorings

Johan MICHAUX

Abstract: Environmental DNA (eDNA) has emerged as a powerful, non-invasive tool for biodiversity monitoring , based on the recovery of genetic material from environmental matrices (water, soil, air) or biological traces such as hair, feces, saliva, and mucus. Advances in molecular technologies, particularly Next Generation Sequencing (NGS) and digital PCR (dPCR), have substantially improved species detection across diverse ecosystems. Metabarcoding coupled with NGS enables high-throughput and comprehensive biodiversity inventories and monitoring from a wide range of substrates, including water, soil, air, leaf surfaces, spider webs, and hair traps. These approaches allow the simultaneous detection of multiple taxonomic groups (insects, fish, amphibians, reptiles, birds, and mammals) in both aquatic and terrestrial environments. In parallel, dPCR provides highly sensitive and targeted detection of specific taxa by quantifying minute amounts of DNA, making it particularly suitable for rare, elusive, or low-abundance species, as well as invasive taxa and pathogens. In this presentation, I will highlight case studies conducted in our laboratory on the monitoring of several species of conservation concern, including the European wildcat, European beaver, Eurasian lynx, European otter, grey wolf, and Pyrenean desman. I will demonstrate how non-invasive sampling combined with eDNA analyses supports investigations of population genetics (e.g., hybridization, genetic diversity, and structure) and the assessment of anthropogenic impacts such as habitat fragmentation. Additionally, these approaches enable the study of ecological interactions, diet, pathogens, vectors, and microbiomes. Despite its major advantages, eDNA analysis presents limitations related to DNA degradation, environmental variability, and detection uncertainties. Therefore, I will also explain how a careful interpretation and integration with traditional ecological expertise remain essential.

Empowering large-scale marine biodiversity monitoring using autonomous eDNA samplers on ships of opportunity

Sofie DERYCKE, Cornelis I, Vanhollebeke J, Carneiro A, Marques P, Martins A, Pape D, Hostens K

Abstract: Effective conservation and management of our seas and oceans require adequate spatiotemporal resolution of biological data. Environmental DNA (eDNA) is an innovative, non-invasive monitoring method that uses DNA molecules released by organisms into the seawater. eDNA detects a wide range of Essential Biodiversity Variables and is suitable for autonomous sample collection. Moreover, eDNA samplers mounted on ships of opportunity offer significant geographic expansion of environmental sampling and bring technical benefits (continuous power supply, onboard wifi system for sampling and real-time communication, no risk of losing equipment). As such, scalable biodiversity monitoring becomes feasible. To demonstrate this, we mounted an autonomous eDNA sampler on a coastal fishing vessel. The full sample cycle (bleaching, filtering water, adding preservative) can be monitored in real time. The study area was divided into 5 × 5 km grid cells, and the sampler filtered 1 L of seawater per grid. During two trips in the North Sea, 28 samples were successfully collected. Metadata for each sample (time stamps, geographical coordinates, filtered water volume) were linked to the catch data of the vessel. The 12S eDNA metabarcoding data detected all fishes caught during the shrimp fishery (mainly flatfishes), as well as commercial pelagic fishes. An optimized version of the sampler with 45 filters will be used to monitor the Belgian part of the North Sea in spring 2026. Together, these pilot studies demonstrate the feasibility of large-scale eDNA data collection using ships of opportunity, extending biodiversity monitoring beyond national monitoring programs to include the high seas.

Accuracy of occurrence and abundance estimates from insect metabarcoding

Ela IWASZKIEWICZ-EGGEBRECHT, Fredrik Ronquist, Emma Granqvist

Abstract: DNA metabarcoding of bulk insect samples enables efficient, large-scale biodiversity assessment, but quantitative accuracy is influenced by biological traits (e.g. body size, sclerotization) and methodological choices, including destructive (homogenization) versus non-destructive (mild lysis) extraction and the use of spike-in controls. How these factors jointly affect abundance estimation remains unclear. We assessed metabarcoding accuracy using 4,749 bulk samples from a national insect monitoring program processed with mild lysis, of which 856 were also homogenized for direct treatment comparison. Six biological spike-ins (foreign insects) were added to all samples, and two synthetic spike-ins (artificial DNA fragments) to homogenized samples. Additionally, all specimens in 15 samples were individually barcoded to provide independent reference data on species presence and abundance. We evaluated treatment-specific detection biases, the performance of spike-ins for calibration, and overall abundance accuracy. Both treatments recovered most species but showed consistent, taxon-specific biases. Mild lysis favored small and soft-bodied taxa, whereas homogenization increased recovery of large or heavily sclerotized taxa. Biological spike-ins substantially reduced variance in read counts per specimen, particularly in homogenized samples, while synthetic spike-ins contributed little to abundance calibration. Bayesian calibration using the

best-fitting biological spike-in curve produced accurate abundance estimates (±1 individual) for 78.9% of species occurrences. Our results show that metabarcoding can yield reliable abundance estimates when appropriate calibration is applied. While mild lysis and homogenization introduce different detection biases, homogenization combined with biological spike-ins provides the most consistent quantitative performance for abundance estimation.

Towards a quantitative interpretation of lake fish eDNA metabarcoding surveys: the relative importance of sampling, laboratory and data analyses strategies

Jonas BYLEMANS, Vautier Marine, Baudoin Jean-Marc, Guillard Jean, Goulon Chloé, Logez Maxime, Raymond Jean-Claude, Domaizon Isabelle

Abstract: Analyses of environmental DNA (eDNA), i.e. DNA obtained from environmental samples, has been shown to be highly promising tool for biomonitoring fish communities. The ability to obtain quantitative estimates, especially for eDNA metabarcoding surveys, remains debatable but numerous recent efforts have been undertaken to enhance the quantitative nature of eDNA metabarcoding surveys. Comparative studies assessing the impact of different sampling and metabarcoding strategies on the quantitative interpretation of eDNA metabarcoding surveys are, however currently lacking. We implemented two common sampling strategies in two natural lakes and six approaches for a more quantitative interpretation of eDNA metabarcoding data. Metabarcoding estimates of eDNA concentrations were correlated against standard gillnet fishing estimates of species' abundance and biomass, absolute eDNA quantifications for five target species, and the allometrically scaled abundance. Results showed that a spatially integrated sampling strategy and the use of internal standards to convert read counts to eDNA concentrations increases the probability of detecting positive correlations between eDNA concentrations and species' abundance and biomass estimates and increases model predictive performance. To our knowledge we provide the first comparative study to determine the optimal strategies to move toward a quantitative interpretation of fish eDNA metabarcoding surveys which is essential for a routine implementation of eDNA metabarcoding surveys to assess the ecological state of freshwater ecosystems within the European Water Framework Directive.

eDNA signals improve local predictions of fish abundances in Mediterranean coastal ecosystems

David MOUILLOT

Abstract: Predicting marine species distribution and abundance is essential for effective conservation and management. Yet, it remains challenging in data-limited regions where traditional biodiversity surveys are logistically or financially constrained. Combining underwater visual census and eDNA fish sampling across the northwestern Mediterranean Sea, we tested a novel modelling framework that uses eDNA metabarcoding sequences to complement socio-environmental covariates in predicting species-specific local abundances. The eDNA-derived community proxies revealed ecological gradients complementary to visual census data, helping to distinguish sites dominated by coastal demersal fishes versus offshore predators, territorial reef fishes versus mobile dispersers, and benthic versus pelagic species. Using joint Species Distribution Models (jSDMs), within the Hierarchical Modelling of Species Communities (HMSC) framework, we compared the predictive performance of models based solely on socio-environmental covariates with those that additionally incorporated eDNA-based information. Including eDNA information significantly improved model fit for 16 out of 26 species, including the endangered dusky grouper (Epinephelus marginatus), and contributed to one-third of explained variance in species local abundances on average. Synthesis and applications. This study demonstrates that integrating eDNA metabarcoding data into species distribution models can improve fish abundance predictions, especially for site-attached and reef-associated species. This approach provides a scalable and cost-effective tool for monitoring, impact assessment, spatial planning, and adaptive management of marine resources.

eDNA02 Upscaling biodiversity monitoring cases

Wednesday 6 May, 10h00-11h00, Room Auditorium
Chair: Joanna WARWICK-DUGDALE

Airborne eDNA for large-scale historical biodiversity monitoring

Bea Angelica ANDERSSON

Abstract: Biodiversity loss threatens ecosystems and human well-being, making accurate, large-scale monitoring crucial. Environmental DNA (eDNA) has enabled species detection from substrates such as water, without the need for direct observation. Lately, airborne eDNA has been showing promise for tracking organisms from insects to mammals in terrestrial ecosystems. Conventional biodiversity assessments are often labor-intensive and limited in scope, leaving gaps in our understanding of ecosystem response to environmental change. In our research, we demonstrate that airborne eDNA can detect organisms across the tree of life, quantify changes in abundance congruent with traditional monitoring, and reveal land-use induced regional decline of diversity in a northern boreal ecosystem over decades. By analyzing weekly archived aerosol filters from two large scale air filtering stations in Sweden, we reconstruct temporal relative abundance data for tens of thousands of species using non-targeted shotgun sequencing. Further, using weather data for air-flow modelling and trajectory analysis, we estimate eDNA source areas for species of interest allowing us to detect distribution changes. Previously, large scale analyses of ecosystem changes, targeting all types of organisms, has been prohibitively expensive and difficult to attempt. By using archived air samples from preexisting facilities (that exist in many European countries), our approach provides a method of unified, ecosystem-scale biodiversity surveillance spanning decades, enabling historical biodiversity monitoring without the need for new sampling. At this conference, we hope to share our method and results with interested parties, and to discuss ways of developing this novel approach for accurate biodiversity monitoring.

Patterns, conservation challenges and monitoring of fungal biodiversity at continental scale : first results from a large-scale study in european pine forests

Franck RICHARD, Bazan G, Bellanger J.-M., Blažević A, de-Miguel S, Glen Dierickx, Kadi-Bennane S, Kozłowska M, Krah F, Krisai-Greilhuber I, Loizides M, Mallet L, Marcon E, Mešić A, Mezaour N, Richter F, Rinaldi A, Ruszkiewicz-Michalska M, Vizzini A, Zervakis GI, Heilmann-Clausen J, Gross A, Kauserud A

Abstract: Across Europe, pine forests are among the most extended and most threatened ecosystems by global change, particularly in the Mediterranean region, where endemic pine species face unprecedented risks of local extinction. Ecologically, pines interact with a wide range of fungi, both functionally and taxonomically. On their roots, these plants obligatorily associate with ectomycorrhizal fungi, which receive carbon from their photosynthetic hosts and, in exchange, provide water and nutrients. Aboveground, living and dead plant material sustains a high diversity of parasites and decomposers that, in turn, play crucial roles in biogeochemical cycles. At the continental scale, almost nothing is known about anthropogenic impacts on fungal diversity patterns in European forests, and there is an urgent need to document and understand the drivers of the distribution of this biota to anticipate the consequences of the current human-induced pressures on ecosystems. This is a major concern of the BiodivMon FUNDIVE program (2024-2027), which investigates fungal biodiversity patterns across Europe. Here, we present the first results from a large sampling of European soils, deadwood and air samples collected in three pine-dominated ecosystems (P. sylvestris, P. cembra, P. nigra). Using a standardized eDNA-metabarcoding approach applied to 2,500 samples collected by 70 collaborators from 25 EU countries as well as from Ukraine, Cyprus and Algeria, we detected more than 35,000 fungal operational taxonomic units. This study provides the first comprehensive overview of fungal diversity in pine forests across Europe and is intended to serve as a powerful diagnostic tool for assessing multi-scale conservation challenges and perspectives for fungi in Europe.

From stratified soil eDNA sampling to soil food web predictions in space

Wilfried THUILLER

Abstract: Our understanding of the factors shaping the distribution of soil organisms remains fragmented, largely limited to specific taxonomic groups. This knowledge gap hampers our ability to identify the drivers structuring entire soil multitrophic networks, critical components of ecosystem functioning. To address this challenge, we implemented a large-scale soil biodiversity monitoring program across the French Alps, now extended to the Pyrenees and Corsica. Using environmental DNA (eDNA) from over 400 soil samples, we developed a semi-automated pipeline to transform raw eDNA data into ecologically meaningful trophic groups, representative of the soil food web. Our analyses reveal significant spatial variation in the structure of soil multitrophic networks, both between and within habitats along mountain gradients. Notably, trophic group abundance shifts from fungal-dominated to bacterial-dominated feeding channels when moving from forests to grasslands, reflecting distinct ecosystem processes. Forest soil networks exhibit stronger spatial structuring, only partially explained by abiotic conditions, while grassland networks are more strongly influenced by plant community composition and soil properties. To further advance predictive modeling, we leveraged Earth Observation Foundation (EOF) models, deep learning models pre-trained on extensive remote sensing datasets, to generate embeddings summarizing earth observation images. By integrating these embeddings, we demonstrate that remote sensing data can substantially improve the prediction of multi-trophic soil biodiversity, particularly in regions lacking detailed in-situ measurements. Ultimately, our work bridges critical gaps in soil biodiversity research by combining cutting-edge molecular and remote sensing technologies. These insights not only deepen our understanding of soil ecosystem dynamics but also pave the way for more robust, scalable approaches to monitoring and conserving biodiversity in a changing world.

eDNA Reveals Mammal Diversity and Connectivity Across Portuguese Landscapes

Sara PARDAL

Abstract: Environmental DNA (eDNA) provides a non-invasive method for detecting mammals across diverse habitats, enabling robust biodiversity assessments in both managed and natural systems. This study compares mammalian detections from three eDNA surveys in Portugal: (a) forestry and conservation areas in Arouca; (b) a proposed protected area; and (c) an ecological corridor beneath a highway. Across all sites, eDNA metabarcoding revealed consistent patterns of mammalian occurrence and habitat use, highlighting its value for conservation monitoring. Samples were collected from multiple substrates (air, vegetation, surface swabs) and analyzed using vertebrate-targeted 12S rRNA metabarcoding. In Arouca, 19 species were detected, including stone marten (Martes foina), red fox (Vulpes vulpes), European hedgehog (Erinaceus europaeus), greater white-toothed shrew (Crocidura russula), and Eurasian otter (Lutra lutra). Mammals occurred across production and conservation zones, with higher richness in undisturbed areas. In the proposed protected area, 13 taxa were identified across varied habitats, including European badger (Meles meles), Iberian hare (Lepus granatensis), and red squirrel (Sciurus vulgaris). Elusive species such as European polecat (Mustela putorius) and grey long-eared bat (Plecotus austriacus) highlighted the sensitivity of airborne and surface eDNA. The corridor study detected 20 species, including Cabrera's vole (Microtus cabrerae), Egyptian mongoose (Herpestes ichneumon), and common genet (Genetta genetta), confirming functional connectivity. Species of concern included Plecotus austriacus (Near Threatened) and European rabbit (Oryctolagus cuniculus, Endangered). Overall, eDNA effectively characterizes mammalian communities across management gradients and connectivity structures, supporting landscape-level conservation planning.

Microalgae biomonitoring in freshwater: new opportunities offered by massive DNA metabarcoding datasets

Frédéric RIMET

Abstract: Diatoms are a group of microalgae used worldwide to assess the ecological integrity of freshwater ecosystems through microscopic observations. Over the past decade, the emergence of DNA metabarcoding as an alternative for assessing diatom biodiversity has provided access to large and robust molecular datasets. This methodology provides molecular information that makes it possible to easily integrate the evolutionary perspective into ecology and facilitates the investigation of ecological processes shaping freshwater diatom communities. We present two examples to illustrate this potential. The first concerns speciation and the environmental factors involved in this process. We showed that preferences for nutrients and organic matter exhibit a phylogenetic signal between species and genera. This finding has implications for the development of assessment tools, as robust pollution assessments do not necessarily require a fine taxonomic resolution, we even recommend the opposite. In contrast, we detected a signal of climate at the infraspecific level, enabling the possibility to monitor biological invasions potentially linked to climate change. The second example concerns geographical dispersal. Using null model approaches and analyses of taxonomic and phylogenetic turnover, we showed that lowland alpine lakes experience significant biotic homogenization, unlike remote high-altitude lakes from the same area. This pattern can be explained by the numerous exchanges occurring among lowland lakes, either through wildlife (e.g., birds and invasive species) or human activities. Overall, these examples demonstrate that traditional diatom-based biotic indices used to assess freshwater quality can be effectively complemented by innovative tools addressing additional ecological questions relevant to environmental management.

eDNA03 Integrating eDNA methods into policies, focus on indicators

Wednesday 6 May, 11h30-12h30, Room Auditorium
Chair: Pedro Junger

Testing environmental DNA on the established WFD/MSFD indicator 'Plankton Lifeforms' with two decades of coastal marine biodiversity data.

Joanna WARWICK-DUGDALE, Clare Ostle; Hanneloor Heynderickx; Michael Cunliffe

Abstract: Reliable and efficient plankton monitoring is vital in assessing the status of marine pelagic habitats and food webs. Characterisation of plankton communities via environmental DNA (eDNA) may provide scalable biodiversity information, however inherent differences between eDNA and standardised microscopy are non-trivial and can complicate the application of eDNA to established monitoring indicators. Challenges include incomplete DNA reference databases, restriction to relative abundance values derived from eDNA community profiling (i.e. metabarcoding), divergent taxonomies between data types, and size-related resolution differences (i.e. microscopy cannot resolve picoeukaryotes beyond high taxonomic levels). Here we compared a 20-year time series of eDNA plankton samples from the Western Channel Observatory coastal Station L4 and a co-sampled microscopy dataset. Consensus between microscopy and eDNA-based biodiversity was assessed, and stability with different analytical methods evaluated. Additionally, two test datasets of 'eDNA Plankton Lifeforms' were generated towards the WFD/MSFD indicator 'Change in plankton communities: PH1/FW5'. Two different strategies were adopted, and different numbers of unique biological DNA sequences were retained (i.e. Amplicon Sequence Variants; ASVs; total: 2980). Course-grained survey with assignment of plankton taxa into five high-level groups (i.e. Diatoms; Dinoflagellates; Coccolithophores; Flagellates; Ciliates) yielded 1096 ASVs. Fine-grained survey with taxonomic assignment, filtration, and relative abundance via AphiaIDs (i.e. World Register of Marine Species PIDs) listed in the Plankton Lifeform Extraction Tool (PLET) master list yielded 2063 ASVs. Calculation of lifeform pairs and Kendall statistics illustrate how data type and processing strategy affect indicator outputs. Long-term patterns in seasonal diversity appeared more congruent between microscopy and eDNA data than changes in plankton diversity between years.

Measuring the state of aquatic environments using eDNA— upscaling spatial resolution of biotic indices

Rosetta BLACKMAN, Luca Carraro, François Keck, Florian Altermatt

Abstract: Aquatic macroinvertebrates, including many aquatic insect orders, are a diverse and ecologically relevant organismal group, yet strongly affected by anthropogenic activities. As many of these taxa are highly sensitive to environmental change, they offer a particularly good early warning system for human-induced change, thus leading to their intense monitoring. In aquatic ecosystems there is a plethora of biotic monitoring or biomonitoring approaches with more than 300 assessment methods reported for freshwater taxa alone. Ultimately, monitoring of aquatic macroinvertebrates is used to calculate ecological indices describing the state of aquatic systems. Many of the methods and indices used are not only hard to compare, but especially difficult to scale in time and space. Novel DNA-based approaches to measure the state and change of aquatic environments now offer unprecedented opportunities, also for possible integration towards commonly applicable indices. Here, we demonstrate a proof-of concept for spatially upscaling ecological indices based on environmental DNA, demonstrating how integration of these novel molecular approaches with hydrological models allows an accurate evaluation at the catchment scale.

Paving the way for DNA based WFD monitoring of phytoplankton and phytobenthos in Slovakia

Ondrej VARGOVČÍK, Lucia Kováčová, Dana Fidlerová, Balázs Tibor Kunkli, Katalin Nagy, Judit Knisz, Emre Keskin, Zuzana Velická, Gabriela Horváthová, Marianna Cíchová

Abstract: Implementation of DNA metabarcoding into ecological assessments of freshwaters under WFD still requires intercalibration with the methods established locally. As part of Slovakia's involvement in Joint Danube Survey 5, we evaluated the local capacity for DNA based monitoring of phytoplankton and phytobenthos. We analysed 17 samples of benthic biofilm and 36 of filtered riverine eDNA, collected from Danube and its tributaries, in parallel with the main JDS5 samples. DNA was extracted using harmonised protocols, and the same pool of rbcL, 18S, 23S, 12S amplicon libraries was sequenced on three competitor platforms. Preliminary analyses focused on diatoms using DADA2 pipeline and Diat.barcode database, and were compared with outcomes from the established identification via light microscopy. The primary sequencing platform yielded ~150k rbcL reads per sample and adequate coverage for other markers. The diatom rbcL dataset contained 1009 ESVs, of which 246 lacked species assignment and additional 309 lacked even genus assignment. Although per-sample species richness was ~1.7x higher in metabarcoding than microscopy, the overall richness was 183 and 222 species, respectively. The two methods found 46 common genera (plus 9 and 20 unique, respectively) and several dominant species showed similar occurrence patterns. However, relative abundances and community composition differed substantially, partly due to DNA copy-number

and cell biovolume effects, requiring further correction factors (e.g. Melosira varians). These findings highlight both the feasibility and the current limitations of DNA-based assessment of phytobenthos and phytoplankton in Slovakia. The work provides a basis for comparison with lead JDS5 laboratories and among sequencing platforms, and it identifies priority steps—parallel analyses, filling reference databases, data curation, understanding intraspecific diversity—needed for future integration of metabarcoding into national WFD monitoring.

Ectomycorrhizal indicators of soil carbon: a proof of concept for integrating fungal community data into landscape monitoring

Robert BARBER

Abstract: Below-ground fungal communities play a central role in soil carbon cycling, yet they remain largely absent from biodiversity monitoring frameworks. We tested whether DNA-identified ectomycorrhizal communities can function as fine-scale biological indicators of soil carbon stocks, providing resolution that conventional habitat or soil-type classifications cannot. Across 189 plots in a single temperate woodland landscape, we sequenced over 3,500 live ectomycorrhizal root tips, recorded morphological foraging traits, and paired fungal community data with in situ soil carbon measurements. Working within one landscape controlled for the climatic and biogeographic variation that confounds broad-scale studies. Community composition and hyphal presence — rather than diversity or abundance — were the strongest predictors of soil carbon after accounting for soil chemistry, topography, and vegetation. Crucially, composition effects reversed after environmental correction, demonstrating that fungal community structure carries independent information beyond habitat type. Indicator analysis identified specific taxa, notably Russula ochroleuca and Lactarius tabidus, as reliable markers of carbon-rich soils at finer resolution than standard forest classifications. These findings provide a proof of concept for incorporating molecular fungal data into ecosystem monitoring. Single indicator species could complement existing carbon assessment approaches, offering high-resolution predictions where conventional predictors lack precision. As these indicator taxa are detectable via bulk soil eDNA, the approach has clear potential for integration into scalable monitoring networks.

eDNA04 Mixed session - upcoming methodologies, outlook on eDNA society

Wednesday 6 May, 16h30-17h30, Room Auditorium
Chair: Tiina Laamanen

MetaPlantCode: METAPLANTCODE – Harmonizing plant metabarcoding pipelines in Europe

Birgit GEMEINHOLZER, Stephanie J Swenson, Hugo de Boer, Dag Endresen, Quentin Mauvisseau, Niels Raes, Barbara Gravendeel, Sydney Wizenberg, João Queirós, Panagiotis Madesis, Ioanna Karamichali, Fotis Psomopoulos, Nikolaos Pechlivanis, Rui Figueira, Maria M. Romeiras, Pedro Arsénio, Pedro Beja, Paulo Celio Alves, Vanessa Mata, Eugeni Belda, Auguste Gardette, Eric Chenin, Edi Prifti, Jean-Daniel Zucker, Youcef Sklab, Mihael Cristin Ichim, Ancuta Cristina Raclariu-Manolica, Patrick Ruch, Emilie Pasche, Donat Agosti, Daniel Lundin, Olaf Banki

Abstract: Currently, ~2 out of 5 plant species are threatened with extinction. Plant loss will also affect other groups of organisms and the environment in ways that are not yet understood, as plants have important functional dependencies in complex organism networks. METAPLANTCODE presents a unique collaborative and transnational approach to test, optimize, harmonize and recommend best practices for plant metabarcoding for samples with varying degrees of species complexity, contamination and DNA degradation using case studies across Europe. The METAPLANTCODE project aims to test and optimize pan-European case studies on metabarcoding, provide best practice recommendations, optimize analysis pipelines for species identification, and create easy-to-use reference databases. The project will identify and specify gaps, publish best practice documents on FAIR data publishing of plant metabarcode data to GBIF and the INSDC databases, and implement ELIXIR-compatible multimodal DL models in novel tools for stand-alone metabarcoding analyses using different data sources. The project will enhance species identification accuracy through GBIF records and metadata and map regional, national, and international botanical taxonomic checklists, red lists, and floras to the Catalogue of Life (COL) through COL ChecklistBank. Furthermore, taxonomic and floristic literature will be semantically enriched with new entity recognition and relationship extraction modules to support the enhanced identification of species via domain-specific descriptive/phenotypic features. An interface will be provided to link taxonomic names to treatments, identify homonyms and synonyms, and facilitate the conversion and annotation of flora, red lists, and ecological treatments. All METAPLANTCODE products will be FAIR+. Stakeholder engagement, training, and outreach efforts are planned to ensure that plant metabarcoding becomes a routine standard for biodiversity monitoring in Europe and beyond in the future.

Metagenomic approaches for DNA-based monitoring of benthic invertebrate communities

Martijn CALLENS, Marianne Lolivier, Tom Moens, Sofie Derycke

Abstract: DNA-based methods are increasingly applied for biodiversity assessments and ecological monitoring, especially for organism groups that are difficult to detect or identify morphologically. Metabarcoding is currently the most established DNA-based method for determining species composition and relative abundance, and can provide advantages for biodiversity monitoring due to a higher sensitivity and time- and cost effectiveness. However, one drawback of metabarcoding is PCR bias, caused by between-species variation in the amplification efficiency of a marker gene. Within the Biodiversa+ project DNASense we have developed a PCR-free method for DNA-based monitoring of macrobenthos- and meiofaunal communities. The method we developed allows for an easy generation of whole-genome reference data for a large number of species. This reference data can then be used to classify sequences originating from DNA extracts of invertebrate samples. Results from samples collected for macrobenthos monitoring showed that our method outperformed metabarcoding for estimating species biomass, allowing for a better alignment with morphology-based monitoring data. Furthermore, these results can be obtained with sequencing depths similar to metabarcoding. The method is sequencing-platform independent and produces comparable results between Illumina- and nanopore data, allowing flexibility and a short timeframe between sampling and the generation of results on community composition.

Bat guano uncovers ecological processes and ecosystem health

Orianne TOURNAYRE

Abstract: Traditional biodiversity assessments, though effective, often focus on single groups, lack scalability, and require intensive logistics. In this study, we used bats as natural, and wide-ranging samplers of biodiversity, capturing a snapshot of ecosystem complexity through trophic aggregation. Each insect a bat consumes carries not only its own DNA but also DNA of its own food source and associated microorganisms. Thus, using bat guano offers a unique and non-invasive approach for multi-taxon biodiversity monitoring and ecosystem health assessment. We collected guano from two bat species (Rhinolophus hipposideros and Eptesicus serotinus) in 18 colonies spanning three European bioclimatic zones (temperate oceanic, humid continental, and Mediterranean). Synchronous sampling occurred monthly from May to September over two consecutive years. Using multi-marker metabarcoding, we identified DNA from plants, arthropods, and fungi. This was complemented by metagenomic analyses of the associated viral communities. This yielded over 5 000 insects, 4 000 fungal, and 1 000 plant OTUs, including invasive and pest species, along with numerous viruses (mainly insect-associated), some impacting pollinators or crops. Together, these data enabled comprehensive analyses of climate effects on species diversity, community composition and the reconstruction of ecological networks, demonstrating that bat-based biomonitoring can offer a powerful lens into ecosystem health across space and time under ongoing global changes.

eDNA-Europe : Establishing a European eDNA society

Florian Altermatt, Karolina Bacela-Spychalska, Pedro Beja, Manuela Coci, Isabelle DOMAIZON, Marija Gligora Udovič, Pascal Hablützel, Pete Hollingsworth, Belma Kalamujić Stroil, Jasmina Kamberović, Panagiotis Kasapidis, Lori Lawson Handley, Florian Leese, Kristian Meissner, Massimiliano Molari, Fabrice Not, Thorsten Stoeck & Bettina Thalinger

Abstract: Environmental DNA (eDNA) and molecular methods (such as metabarcoding, metagenomics and metatranscriptomics) are becoming critically important tools for assessing biodiversity and evaluating ecosystem status. In parallel, current and upcoming policy frameworks are in need of these methods to support regulatory monitoring and help predicting future conditions under environmental change. A key challenge is the absence of a shared European roadmap and a coordinated planning framework for eDNA, leading to fragmented development and implementation across stakeholders, and hindering convergence on common approaches. Establishing a formal organizational framework can catalyze research and technological advances across sectors (research, industry, policy and society) and ensure effective operational transfer to public policies. Here, we present eDNA-Europe, a European society advancing Environmental DNA (eDNA) research and implementation, fostering knowledge exchange, supporting cooperation and skills development, and acting as a link between science and society. Upon completing its ongoing founding process, the society aims to a) build a European community of eDNA researchers and stakeholders, b) connect the European eDNA community with wider national, regional and global initiatives, c) promote technological advancement and share research findings and best practices, and d) facilitate mainstreaming of eDNA methods into policy and practice. By introducing this initiative at the BioMonWeek congress, we hope to garner the support of researchers, industry partners and policy makers working across terrestrial, freshwater, and marine ecosystems, to establish eDNAEurope as a central hub for eDNA-based biodiversity monitoring in Europe.

eDNA05 Conservation-related eDNA applications

Thursday 7 May, 9h00-10h00, Room Joffre F
Chair: Emilie Boulanger

Genome-wide eDNA Metagenomics for Detection and Population-Level Monitoring of Marine Invasive Species

Nedine KACHORNNAMSONG, Theo Serivichyaswat, Tom van der Valk, Muhammad Bilal Sharif

Abstract: Marine invasive alien species pose a major threat to biodiversity, fisheries, and coastal infrastructure. Effective management requires early detection and continuous monitoring, yet traditional approaches often rely on visual surveys or targeted assays that can miss cryptic or early-stage invasions. We have developed a genome-wide environmental DNA (eDNA) metagenomic workflow designed to enable comprehensive biodiversity monitoring from environmental samples. Unlike metabarcoding methods that rely on a limited number of genetic markers, genome-wide metagenomics captures DNA fragments from across entire genomes, allowing simultaneous detection of diverse taxa while preserving genetic variation for deeper analysis. Using marine water samples from the Danish North Sea as a case study, we demonstrate how genome-wide eDNA metagenomics can detect invasive species and recover population-level genetic signals directly from environmental samples. For example, genomic variation within environmental DNA enabled confirmation of the presence and genetic origin of the invasive comb jelly Mnemiopsis leidyi. These results highlight how genome-wide eDNA metagenomics can move beyond presence/absence detection toward population-level insights, supporting improved early detection, tracking of invasion dynamics, and evidence-based management of marine ecosystems.

A nuclear – DNA enrichment-based capture method (Hyrad) to advance marine eDNA population genomics

Stéphanie MANEL, Faure Nadia

Abstract: Traditional population genetics approaches require sampling tissue from individuals, which is often challenging in aquatic environments. Filtering water allows researchers to collect environmental DNA (eDNA), genetic material shed by organisms into their surroundings. Unlike approaches targeting a single DNA barcode, we recently developed a new genomic approach, HyRAD, that enables the capture of multiple nuclear DNA fragments present in the eDNA samples, making it possible to study intraspecific genetic diversity and population structure. This approach was first successfully developed using the common fog (Rana temporaria) in freshwater ponds. We have recently extended the method to the common bottlenose Dolphin (Tursiops truncatus) in a marine environment. In this talk we will introduce the new method from its origin in ancient DNA to its first application to the common frog. We will then present preliminary results on the bottlenose dolphin to illustrate its potential for studying population genomics of marine ecosystems.

Isothermal amplification as a tool for real-time eDNA monitoring in freshwater environments: example of the Natterjack toad (Epidalea calamita)

Abigaël CHIEUX

Abstract: Environmental DNA approaches have become a powerful complement to traditional biomonitoring methods, enabling the detection and tracking of target species across time and space to assess biodiversity and support ecosystem management. Access to timely and accurate data on the presence, distribution, and diversity of species, particularly those with elevated conservation status or key ecological roles, is essential for effective management decisions, particularly for freshwater ecosystems. Current eDNA workflows remain costly, laboratory-dependent, and time-consuming, limiting their applicability in low-resources settings or remote areas. Metabarcoding of eDNA relies on expensive sequencing technologies, and delivery time of results can take up to several months, while qPCR analysis still requires several hours of processing. Overcoming these limitations requires the development of portable, affordable, and rapid tools that can deliver real-time monitoring results directly in the field. Here, we present our ongoing work toward a fully field-deployable sequencing-free eDNA approach for monitoring freshwater biodiversity. We have developed and validated two isothermal amplification-based approaches: (i) Recombinase Polymerase Amplification (RPA) and (ii) Loop-mediated Isothermal Amplification (LAMP) for the detection of the Natterjack toad (Epidalea calamita). Through an in-situ species detection protocol, both methods bypass the sample conservation step typically required for eDNA studies. It enables rapid and real-time results without the need for sterile laboratory and bioinformatics analysis, making it accessible to non-experts. We will present the methodological development, current advances, and field-testing outcomes of these tools. We will also discuss their broader potential for scaling-up biodiversity monitoring efforts.

Beyond species detection: eDNA metabarcoding and community science unveil genetic diversity patterns and habitat fragmentation in fish communities

Till-Hendrik MACHER, Lina Frank, Andreas Uth, Bastian Haag, Lars Meitner, Siri Wetzel, Henrik Krehenwinkel

Abstract: Stream ecosystems are highly diverse and provide essential ecosystem services, yet they are undergoing unprecedented biodiversity loss. While such declines are typically assessed using species abundance and richness, genetic diversity, an essential component of biodiversity, remains largely underrepresented. Genetic diversity is particularly important in stream ecosystems, which depend on longitudinal connectivity to maintain migratory pathways and population exchange in fish communities. Conventional fish monitoring methods lack the resolution to detect genetic effects of habitat fragmentation, whereas environmental DNA (eDNA) metabarcoding offers a non-invasive alternative, though it is usually limited to qualitative species inventories. Importantly, eDNA metabarcoding is based on the detection of genetic variants, usually to differentiate species, but potentially also enabling the assessment of intraspecific variation. Here, we conducted a proof-of-concept study along the River Ruwer (Germany), which is divided into upstream and downstream sections by a historical waterfall. Using fine scale eDNA metabarcoding along the entire river, complemented by electrofishing data and a citizen science eDNA dataset, we assessed spatial patterns in species composition and genetic diversity. Overall, we detected 18 fish species with a total of 159 exact sequence variants (ESVs). Both species richness (rho=-0.94, p=7.6e-23) and genetic diversity (rho=-0.88, p=8.1e-17) decreased significantly along the watercourse, with distinct upstream and downstream communities separated by the waterfall. Only four of sixteen species occurred in both sections, and upstream populations showed reduced genetic diversity with unique variants indicating long term isolation. Our results demonstrate that fish eDNA metabarcoding can reveal genetic isolation patterns at the population level that remain undetected by conventional monitoring approaches.

BioMonWeek
2026
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4-8 May 2026
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EU-funded projects — participation and contributions

ACT NOW

Project page: https: //cordis.europa.eu/project/id/101060072
Website: https: //www.actnow-project.eu/

AI4WildLIVE

Website: https: //www.feda.bio/en/projects/biodivki/ai4wildlive/

- Posters: **PS01**: AI4WildLIVE: Integrating AI, Citizen Science, and Data Infrastructure for Global Biodiversity Monitoring

AlpsLife

Website: https: //www.alpine-space.eu/project/alpslife/

ANERIS

Project page: https: //cordis.europa.eu/project/id/101094924/news
Website: https: //aneris.eu/

- Talk: **MR12**: Consolidating the Operational Marine Biology Network. The ANERIS project

AquaBioSens

Project page: https: //cordis.europa.eu/project/id/101135432
Website: https: //www.aquabiosens.eu/

- Talk: **FR04**: New ways to evaluate freshwater biodiversity using periphyton genomics

AURORA

Project page: https: //cordis.europa.eu/project/id/101157643
Website: https: //www.auroraclima.eu/

- Talk: **DT07:** AURORA - A Shiny app designed to create Darwin Core Archives from messy biodiversity datasets

B Cubed

Project page: https: //cordis.europa.eu/project/id/101059592
Website: https: //b-cubed.eu/

- Talk: **DT01**: Operationalizing Biodiversity Data Cubes for Open Science and Informed Policy, **MM03**: An Extended Biodiversity Data Cube: Integration of Multi-Spectral Imagary, **DT01**: Optimising the Habitats Directive top-down assessment and bottom-up reporting in Europe

Bcoming

Project page: https: //cordis.europa.eu/project/id/101059483
Website: https: //bcoming.eu/en/

BEAGLE

Website: https: //projectbeagle.eu/

BeeOImpact

Project page: https: //cordis.europa.eu/project/id/190123465

BeeOmetrics

Project page: https: //cordis.europa.eu/project/id/101159322
Website: https: //beeometrics.com/

- Talk: **PV08**: Pollen composition as a sentinel of environmental health

BENCHMARKS

Project page: https: //cordis.europa.eu/project/id/101091010
Website: https: //soilhealthbenchmarks.eu/

BGE

Project page: https: //cordis.europa.eu/project/id/101059492
Website: https: //biodiversitygenomics.eu/

BGEPlus

Website: https: //biodiversitygenomics.eu/2026/02/16/bgeplus-selected-for-funding/

BICIKL

Project page: https: //cordis.europa.eu/project/id/101007492
Website: https: //bicikl-project.eu/

- Talk: **DT08**: Biodiversity Knowledge Hub Bridging RIs, Aggregators & Communities: Past, Present & Future

BIG PICTURE

Website: https: //www.biodiversa.eu/2024/04/15/big_picture/

BioAgora, Monitoring KEN

Website: https: //bioagora.eu/

Bioboost+

Website: https: //www.biodiversa.eu/2024/04/15/bioboost/

- Talk: **MM03:** Boosting biodiversity monitoring using novel approaches

BIO-CAPITAL

Website: https: //bio-capital.eu/

BIOcean5D

Project page: https: //cordis.europa.eu/project/id/101059915
Website: https: //biocean5d.org/

BIOCONSENT

Project page: https: //www.biodiversa.eu/2022/10/11/bioconsent/
Website: https: //www.bioconsent.eu/

BioDiMoBot

Project page: https: //cordis.europa.eu/project/id/101181363
Website: https: //www.biodimobot.eu/

- Talk: **PV06**: BioDiMoBot: Autonomous Robotic Monitoring for Aquatic Biodiversity - A Science-Industry Partnership

BiodivCrEW

Website: https: //www.eurosite.org/life-biodiv-crew/

Biodiversa+ Pilots

Website: https: //www.biodiversa.eu/biodiversity-monitoring/pilots/

BIODIVERSEA

Website: https: //www.metsa.fi/en/project/biodiversea-eng/

Biodiversity Meets Data

Project page: https: //cordis.europa.eu/project/id/101181294
Website: https: //bmd-project.eu/

- Talk: **DT01**: Biodiversity Meets Data: A data cubing engine for analysis- and modelling-ready data in biodiversity monitoring , **CP07**: Mobilising Ethical Dialogue Methods in the Co-Design of Biodiversity Analysis Tools (BMD), **TR05**: High-throughput biodiversity monitoring and Biodiversity Analysis Tools in support of the EU Nature Directives, **DT08**: Biodiversity Knowledge

Hub Bridging RIs, Aggregators & Communities: Past, Present & Future, **DT05**: Harmonising policy relevant species data with Catalogue of Life

BiodivPaysanne

Website: https: //life-biodivpaysanne.fr/en/home-page/

BiodivPond

Project page:
https: //www.biodiversa.eu/biodiversity-monitoring/pilots/biodivpond/
Website: https: //biodivpond.github.io/

- Posters: **PS01**: Biodiversa+ BiodivPond Monitoring Pilot

BioDT

Project page: https: //cordis.europa.eu/project/id/101057437
Website: https: //biodt.eu/

BioEcoOcean

Project page: https: //cordis.europa.eu/project/id/101136748
Website: https: //bioecoocean.org/

BIOFIN-EU

Project page: https: //cordis.europa.eu/project/id/101135476
Website: https: //biofin-project.eu/

- Posters: **PS01**: Private finance and Nature-based Solutions: can a blueprint for intermediation bridge the gap?

BioGeoSea

Project page: https: //cordis.europa.eu/project/id/101216427
Website: https: //biogeosea.eu/

BioMonI

Project page: https: //www.biodiversa.eu/2024/04/15/biomoni/
Website: https: //biomoni.github.io/BioMonI/index.html

- Posters: **PS01**: BioMonI - Biodiversity monitoring of island ecosystems: a spotlight on biodiversity hotspots

BioMonitor4CAP

Project page: https: //cordis.europa.eu/project/id/101081964
Website: https: //biomonitor4cap.eu/en/

BirdWatch

Project page: https: //cordis.europa.eu/project/id/101082634
Website: https: //birdwatch-europe.org/

Blue4Green

Website: https: //blue4green.org/

Buffer+

Website: https: //bufferplus.nweurope.eu/

CAMBioMed

Project page: https: //www.biodiversa.eu/2024/04/15/cambiomed/
Website: https: //cambiomed-biodiversa.com/

- Talk: **MM03**: Boosting biodiversity monitoring using novel approaches

CINNEPHILIA

Project page: https: //cordis.europa.eu/project/id/101104596

- Talk: **MR07**: Computational methods for monitoring Nephrops norvegicus populations

CIRCHIVE

Project page: https: //cordis.europa.eu/project/id/101082081
Website: https: //circhive.eu/

CLEVER

Website: https: //clever-project.eu/

CoCo

Project page: https: //cordis.europa.eu/project/id/101181958
Website: https: //cocoproject.eu/en

CoForFunc

Project page: https: //www.biodiversa.eu/2024/04/15/coforfunc/
Website: https: //coforfunc.eu/

- Talk: **TR03**: CoForFunc- Toward a biome-scale monitoring of the Congo basin FORest FUNCtional composition

ConNaturLIFE Ukraine

Project page: https://webgate.ec.europa.eu/life/publicWebsite/project/LIFE23-PRE-CZ-ConNaturLIFE-Ukraine-101148569/conservation-of-natural-heritage-for-life-in-ukraine
Website: https://epl.org.ua/en/about-us-posts/zberezhennya-pryrodnoyi-spadshhyny-dlya-life-v-ukrayini/

ConservES

Project page: https://www.biodiversa.eu/2023/04/19/conserves/

- Talk: **TR08**: CoForFunc- Toward a biome-scale monitoring of the Congo basin FORest FUNCtional composition

CONTRAST

Project page: https://cordis.europa.eu/project/id/101135037
Website: https://www.contrastproject.eu/

- Talk: **MR01**: Metagenomic approaches for DNA-based monitoring of benthic invertebrate communities

COOP4CBD

Project page: https://cordis.europa.eu/project/id/101081778
Website: https://coop4cbd.eu/

COOP4SAFE

Website: https://www.openbordersforbears.com/

Copernicus Marine Service

Website: https://marine.copernicus.eu/

COST

Website: https://www.cost.eu/

- Talk: **DT07**: How a camera trap data standard enabled an ecosystem of interoperable tools,

DarCo

Project page: https://www.biodiversa.eu/2023/04/19/darco/
Website: https://www.iret.cnr.it/en/progetto/darco-en/

- Talk: **FR06**: Groundwater Biodiversity Monitoring in Switzerland: from Case Study to Upscaling

DIABOLO

Project page: https: //cordis.europa.eu/project/id/633464
Website: https: //diabolo-project.eu/

DIGI4ECO

Project page: https: //cordis.europa.eu/project/id/101112883/en
Website: https: //digi4eco.eu/

DiSSCo

Project page: https: //cordis.europa.eu/project/id/101130121
Website: https: //www.dissco.eu/

- Talk: **DT08**: From Physical Specimens to Digital Intelligence: Navigating the Interoperability Landscape with DiSSCo
- Booth: NextBON: From Methods to a Shared Blueprint for European Biodiversity Monitoring

DiverSea

Project page: https: //cordis.europa.eu/project/id/101082004
Website: https: //www.ntnu.edu/diversea

- Posters: **PS02**: Co-producing Marine Knowledge through Blue Citizen Science for Biodiversity Monitoring

DNAquaIMG

Project page: https: //www.biodiversa.eu/2024/04/15/dnaquaimg/
Website: https: //dnaquaimg.eu/

- Talk: **MM01**: Upscaling of DNA-based methods for aquatic biodiversity monitoring

DNASense

Project page: https: //www.biodiversa.eu/2024/04/15/dnasense/

- Talk: **MR01**: Metagenomic approaches for DNA-based monitoring of benthic invertebrate communities

DRYvER

Project page: https: //cordis.europa.eu/project/id/869226
Website: https: //www.dryver.eu/

DTO-BioFlow

Project page: https: //cordis.europa.eu/project/id/101112823
Website: https: //dto-bioflow.eu/

- Posters: **PS02**: Activating Europe’s Marine Biodiversity Data for the Digital Twin of the Ocean: The DTO-BioFlow Approach
- Talk: **MR07**: New observation systems using computer vision for dynamic assessments of marine biodiversity

eBMS

Website: https: //butterfly-monitoring.net/

- Talk: **PP01**: From volunteer transects to EU policy: how the eBMS network delivers indicators for the Nature Restoration Regulation

EBOCC

Project page:
https: //knowledge4policy.ec.europa.eu/news/proposal-eu-biodiversity-observation-coordination-centre-ebocc_en

- Posters: **PS02**: EBOCC piloting – need for Member State input

Eco2Adapt

Project page: https: //cordis.europa.eu/project/id/101059498
Website: https: //www.eco2adapt.eu/

EDITO

Project page: https: //cordis.europa.eu/project/id/101227771
Website: https: //www.edito.eu/

eDNAqua-Plan

Project page: https: //cordis.europa.eu/project/id/101112800
Website: https: //ednaquaplan.com/

- Talk: **PS01**: eDNAqua-Plan recommendations towards a future of federated, curated reference libraries and aligned eDNA (meta)data publishing infrastructure and practices, **MM01**: Upscaling of DNA-based methods for aquatic biodiversity monitoring, **DT03**: The digital ecosystem of eDNA data in Europe

ELIXIR

Website: https: //elixir-europe.org/

- Talk: **eDNA04:** MetaPlantCode: METAPLANTCODE – Harmonizing plant metabarcoding pipelines in Europe

EMBAL

Project page: https://data.jrc.ec.europa.eu/dataset/723355a8-e549-4691-9c0d-83ab7fc7a0c4

- Talk: **TR08**: Testing the EMBAL Methodology for Grassland Biodiversity Monitoring in Slovenia, **PP07**: European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL): a tested, in-situ methodology to deliver harmonized, EU-wide monitoring data **GV05**: EC-steered biodiversity monitoring schemes and applications relevant for agriculture

EMBRACE

Project page: https://www.biodiversa.eu/2025/04/08/embrace/

EMMA4EU

Website: https://www.emma4eu.eu/

EMPHATIC

Project page: https://www.biodiversa.eu/2024/04/15/emphatic/

- Talk: **MR06**: The EMPHATIC project: advancing non-invasive cetacean monitoring to support marine biodiversity conservation

Endangered Landscapes

Website: https://www.endangeredlandscapes.org/

Enetwild

Website: https://enetwild.com/

- Posters: **PS02**: Towards a continent-wide harmonised estimation of wildlife density: lessons learnt from a large-scale camera-trapping network

ESA Coastal Blue Carbon

Website: https://esa-coastal-blue-carbon.eu/

- Talk: **MM03**: Mapping, monitoring and enhancing BCEs biodiversity at large scale through the ESA Coastal Blue Carbon project.

EU PoMS

Project page:

https: //joint-research-centre.ec.europa.eu/jrc-news-and-updates/protecting-pollinators-new-eu-monitoring-scheme-safeguard-ecosystems-2024-10-21_en

- Posters: **PS01**: French capacity building for the implementation of the European pollinator monitoring scheme

EuroBirdPortal

Website: https: //www.eurobirdportal.org/ebp/en/about/

- Talk: **TR08**: The European Bird Census Council: 35 years monitoring changes in bird populations

EuRockfish

Project page: https: //www.biodiversa.eu/biodiversity-monitoring/pilots/eurockfish-pilot/

- Talk: **MR05**: Monitoring of rocky reef fish communities: A case study at the Euro-Mediterranean level.

EXPLORA

Project page: https: //cordis.europa.eu/project/id/101226908
Website: https: //explora-project.eu/

FIPbio

Website: https: //docs.gbif.org/freshwater-data-publishing-guide/en/

FUNDIVE

Website: https: //fun-dive.eu/en/home-2/

- Talk: **MM07**: FunDive: pan-European fungal monitoring enriched by structured citizen science engagement backed by molecular-based identification, **eDNA02**: Patterns, conservation challenges and monitoring of fungal biodiversity at continental scale: first results from a large-scale study in european pine forests

G4B

Project page: https: //www.biodiversa.eu/2023/04/19/g4b/
Website: https: //www.grass4b.com/_sub/

GenAI4Earth

Website:

https://fr.linkedin.com/posts/dataterraorg_english-in-first-comment-genai4earth-activity-7426644971509895170-zhR0

GENOA

Website: https://www.cost.eu/actions/CA23121/

GINAMO

Project page: https://www.biodiversa.eu/2024/04/15/ginamo/
Website: https://ginamo.org/

- Talk: **PP02**: GINAMO: Operationalising Genetic Diversity Indicators for Biodiversity Reporting and Monitoring, **CP07**: Co-Creation to Strengthen the Science-Policy Interface: Opportunities and Challenges in Genetic Indicator Monitoring

GoProFor

Website: https://www.lifegoprofor.eu/en/

GoProFor MED

Website: https://www.lifegoproformed.eu/

GUARDEN

Project page: https://cordis.europa.eu/project/id/101060693
Website: https://guarden.org/

GuardIAS

Project page: https://cordis.europa.eu/project/id/101181413
Website: https://guardias.eu/

- Talk: **MM03**: Boosting biodiversity monitoring using novel approaches

HiRAD

Project page: https://www.biodiversa.eu/2024/04/15/hirad/
Website: https://hirad.science/

IAS Pilot Biodiversa +

Project page: https://www.biodiversa.eu/biodiversity-monitoring/pilots/ias-pilot/

InfraFADA

Website: https://www.naturalsciences.be/en/science/research/biodiversity-in-a-changing-world/projects/infrafada

INTERCEDE

Website: https://intercede-project.eu/

LatViaNature

Website: https://latvianature.daba.gov.lv/en/

LeDNA

Project page: https://cordis.europa.eu/project/id/852621

- Posters: **PS02**: Connecting People, Experts and Satellites: An Integrated System for Invasive Species, Protected Plant Species and Remote Habitat Monitoring in Latvia

LUCAS Soil

Project page: https://esdac.jrc.ec.europa.eu/content/lucas-2022-topsoil-data

- Talk: **GV05**: EC-steered biodiversity monitoring schemes and applications relevant for agriculture

MAMBO

Project page: https://cordis.europa.eu/project/id/101060639
Website: https://www.mambo-project.eu/

- Talk: **CP06**: Machine Listening as a Capacity-Building Tool for European Bat Monitoring, **MM03**: Broadening the standardized retrieval of vegetation structure metrics from airborne laser scanning point clouds across Europe
- Booth: From Sensors to Open Biodiversity Data: AI-enabled Monitoring at Scale

MARCO-BOLO

Project page: https://cordis.europa.eu/project/id/101082021
Website: https://marcobolo-project.eu/

- Talk: **DT02**: A Dream of a Lean Marine Metadata Machine, **MM01**: From Raw Data to Indicators: eDNA-based Essential Variables for Marine Biodiversity Monitoring, **MR05**: From marine biodiversity data to action

Merlin

Project page: https: //cordis.europa.eu/project/id/101036337
Website: https: //project-merlin.eu/

MetaBug

Project page: https: //www.biodiversa.eu/biodiversity-monitoring/pilots/metabug/

MetaPlantCode

Project page: https: //www.biodiversa.eu/2024/04/15/metaplantcode/
Website: https: //metaplantcode.github.io/metaplantcode/

- Talk: **eDNA 04**: MetaPlantCode: METAPLANTCODE – Harmonizing plant metabarcoding pipelines in Europe, **DT05**: Connecting the dots: the essential role of taxonomic names to enable connecting monitoring data over time, space and existing knowledge.

MONIFUN

Project page: https: //cordis.europa.eu/project/id/101134991
Website: https: //www.monifun.eu/

- Posters: **PS01**: Advancing forest biodiversity and conservation monitoring in Europe: A Harmonised Indicator Framework; Authors: Iciar Alberdi, Nerea Oliveira et al.

More4Nature

Project page: https: //cordis.europa.eu/project/id/101133983
Website: https: //more4nature.eu/

- Talk: **PP06**: Public Involvement in Monitoring the Kunming–Montreal Global Biodiversity Framework in Denmark

MOTIVATE

Website: https: //motivate-biodiversity.eu/

- Talk: **GV01**: Understanding long-term plant diversity changes in Europe

MPA4Fish

Project page: https: //www.biodiversa.eu/2026/04/03/mpa4fish/

Natura.si

Website: https: //natura2000.gov.si/en/natura-2000/life-ip-natura-si/

NaturaConnect

Project page: https: //cordis.europa.eu/project/id/101060429
Website: https: //naturaconnect.eu/

NatureRestore

Website: https: //www.biodiversa.eu/2022/10/26/restore/

NECCTON

Project page: https: //cordis.europa.eu/project/id/101081273
Website: https: //neccton.eu/

- Talk: **MR05**: Monitoring marine biodiversity: a new ecosystem modelling framework

NEMESIS

Project page: https: //www.nemesis-soil.eu/
Website: https: //www.nemesis-project.eu/

Network Nature

Project page: https: //cordis.europa.eu/project/id/887396
Website: https: //networknature.eu/

NewLife4Bioislands

Project page:
https: //webgate.ec.europa.eu/life/publicWebsite/project/LIFE24-NAT-ES-NewLIFE4BioIslands-101216081/establishing-new-biodiversity-islands-in-degraded-land-to-reverse-native-pollinator-decline-improve-habitat-connectivity-and-restore-with-resilience
Website:
https: //www.creaf.cat/en/research/research-directory/new-life-4-bioislands

NextBON

Website:
https: //www.linkedin.com/posts/stelioskatsanevakis_nextbon-biodiversity-monitoring-activity-7417878749217632256-Yala

- Booth: NextBON: From Methods to a Shared Blueprint for European Biodiversity Monitoring

NorthDIVeRSITY

Website:
https://www.umu.se/en/research/projects/northdiversity-environmental-dna-edna-as-a-monitoring-tool-for-biodiversity-in-the-north/

OBAMA-NEXT

Project page: https://cordis.europa.eu/project/id/101081642
Website: https://obama-next.eu/

OBSGESSION

Project page: https://cordis.europa.eu/project/id/101134954
Website: https://obsgession.eu/

- Talk: **MM03**: Standardized algorithm benchmarking framework to advance production of RS-based Essential Biodiversity Variables

OneAquaHealth

Project page: https://cordis.europa.eu/project/id/101086521
Website: https://www.oneaquahealth.eu/

OneSTOP

Project page: https://cordis.europa.eu/project/id/101180559
Website: https://onestop-project.eu/

- Talk: **CP02**: Building local capacity for invasive species monitoring through OneSTOP Living Labs
- Booth: From Sensors to Open Biodiversity Data: AI-enabled Monitoring at Scale

OPRA

Website: https://dutpartnership.eu/projects/opra

P2F

Project page: https://cordis.europa.eu/project/id/101184070
Website: https://past2future.org/

PATHFINDER

Project page: https://cordis.europa.eu/project/id/101056907
Website: https://pathfinder-heu.eu/

PATHWAYS

Project page: https: //cordis.europa.eu/project/id/101000395
Website: https: //pathways-project.com/

PECBMS

Website: https: //pecbms.info/
- Talk: **TR08:** The European Bird Census Council: 35 years monitoring changes in bird populations

PHOENIX

Project page: https: //cordis.europa.eu/project/id/101037328
Website: https: //phoenix-horizon.eu/

Poctefa CONECTFOR

Website: https: //ari.ad/en/projects/conectfor

Priodiversity Life

Project page:
https: //webgate.ec.europa.eu/life/publicWebsite/project/LIFE22-IPN-FI-Priodiversity-LIFE-101104217/prioritized-actions-for-promoting-biodiversity-targets-in-finland
Website: https: //www.metsa.fi/en/project/priodiversity-eng/

PROSPECTIVE LIFE

Project page:
https: //webgate.ec.europa.eu/life/publicWebsite/project/LIFE22-IPN-CZ-PROSPECTIVE-LIFE-101104621/protect-species-actively-by-life

PYRENEES4CLIMA

Project page:
https: //webgate.ec.europa.eu/life/publicWebsite/project/LIFE22-IPC-ES-LIFE-PYRENEES4CLIMA-101104957/towards-a-climate-resilient-cross-border-mountain-community-in-the-pyrenees

Red list EU

Project page:

https: //environment.ec.europa.eu/topics/nature-and-biodiversity/european-red-list-threatened-species_en

REDRESS

Project page: https: //cordis.europa.eu/project/id/101135492
Website: https: //redress-project.eu/

RefBar

Project page: https: //cordis.europa.eu/project/id/101236590
Website: https: //www.refbar.com/

REMOVE_DISEASE

Project page: https: //www.biodiversa.eu/2022/10/25/remove_disease/

RESMED+

Website: https: //marcatgemari.cat/en/

RESPIN

Website: https: //respin-project.eu/

Restore4Carbon

Project page: https: //cordis.europa.eu/project/id/101056782
Website: https: //www.restore4cs.eu/

Restore4Life

Project page: https: //cordis.europa.eu/project/id/101112736
Website: https: //restore4life.eu/

Revisited

Rewet

Project page: https: //cordis.europa.eu/project/id/101056804
Website: https: //www.rewet-he.eu/

SEACLIM

Project page: https: //cordis.europa.eu/project/id/101180125
Website: https: //seaclim.eu/

SEAWATCH

Website: https: //sea-watch.org/en/

Seedforce

Website: https: //lifeseedforce.eu/en/

- Talk: **TR05:** Drone-based monitoring of threatened plant species on inaccessible cliffs: from manual census to AI-assisted plant detection within the LIFE Seedforce project

SELINA

Project page: https: //cordis.europa.eu/project/id/101060415
Website: https: //project-selina.eu/

SenseForest

Website: https: //www.biodiversa.eu/biodiversity-monitoring/pilots/senseforest/

- Talk: **GV05**: From Pixels to Policy: SenseForest's Pan-European Test of Remote Sensing for Forest Conservation

SONATA

Website: https: //sonata-nbs.com/

Sub-BioMon

Project page: https: //www.biodiversa.eu/2024/04/15/sub-biomon/
Website: https: //www.sub-biomon.net/

- Talks: TR05**: Developing approaches to monitor subterranean biodiversity in karst**

SUDOE FloRE

Website: https: //interreg-sudoe.eu/en/proyecto-interreg/flore/

SUNBIO

Project page: https: //cordis.europa.eu/project/id/101157493
Website: https: //sunbioproject.eu/

SUPERB

Project page: https: //cordis.europa.eu/project/id/101036849
Website: https: //forest-restoration.eu/

- Posters: **PS01**: Scalable, multi-taxon environmental DNA approaches to monitor above and belowground biodiversity assessment in relation to EU forest restoration.

Sustainable Wildlife

Project page:
https: //www.eeas.europa.eu/delegations/guyana/sustainable-wildlife-management-programme_en
Website:
https: //www.wcs.org/our-work/sustainable-wildlife-management-programme

TABMON

Project page: https: //www.biodiversa.eu/2024/04/15/tabmon/
Website: https: //tabmon-eu.nina.no/

TETTRIs

Project page: https: //cordis.europa.eu/project/id/101081903
Website: https: //tettris.eu/

- Talk: **MM07**: A feedback loop framework for flexible citizen science biodiversity monitoring, **CP06**: Reference Collections as Infrastructure for Long-Term Biodiversity Monitoring and Taxonomy Capacity Building: Lessons from the ARCADE project, **CP06** - Building taxonomic capacity for soil meiofauna in Europe: the SoilMATs training model
- Booth: TEOSS: Training the European Orthoptera Sound System – Building Capacity and Innovation in Bioacoustic Monitoring

TETTRIX

Website:
https: //cetaf.org/cetaf-secures-funding-for-new-horizon-europe-project-tettrix/

THRIVE

THUF

TickRisk

Website:

https: //anrs.fr/en/scientific-research/research-projects/tickrisk-understanding-and-preventing-crimean-congo-haemorrhagic-fever-in-europe/

TRANSITIONS

Website: https: //dutpartnership.eu/

TRANSPONDER

Project page: https: //www.biodiversa.eu/2024/04/15/transponder/
Website: https: //ecos.au.dk/en/researchconsultancy/themes/transponder

- Talk: **FR06**: The TRANSPONDER project: towards a standardized protocol for monitoring biodiversity in freshwater ponds across Europe

TU Rise

Website: https: //tus.ie/rdi/tu-rise/

TWIN2EXPAND

Project page: https: //cordis.europa.eu/project/id/101078890
Website: https: //twin2expand.surf.com.cy/

Upsurge

Project page: https: //cordis.europa.eu/project/id/101003818
Website: https: //upsurge-project.eu/

urbanLIFEcircles

Website: https: //finestcentre.eu/project/urban-life-circles/

UrbanOcean

Website: https: //www.biodiversa.eu/2026/04/03/urbanocean/

VISTA TICINO

Website:
https: //www.interreg-italiasvizzera.eu/wps/portal/site/interreg-italia-svizzera/DettaglioRedazionale/progetti/progetti-finanziati/vistaticino

WADER

Website: https: //lifewader.co.uk/

WatchReefFish

Website:
https: //www.blacksea-cbc.net/interreg-next-bsb-2021-2027/projects/bsb01105