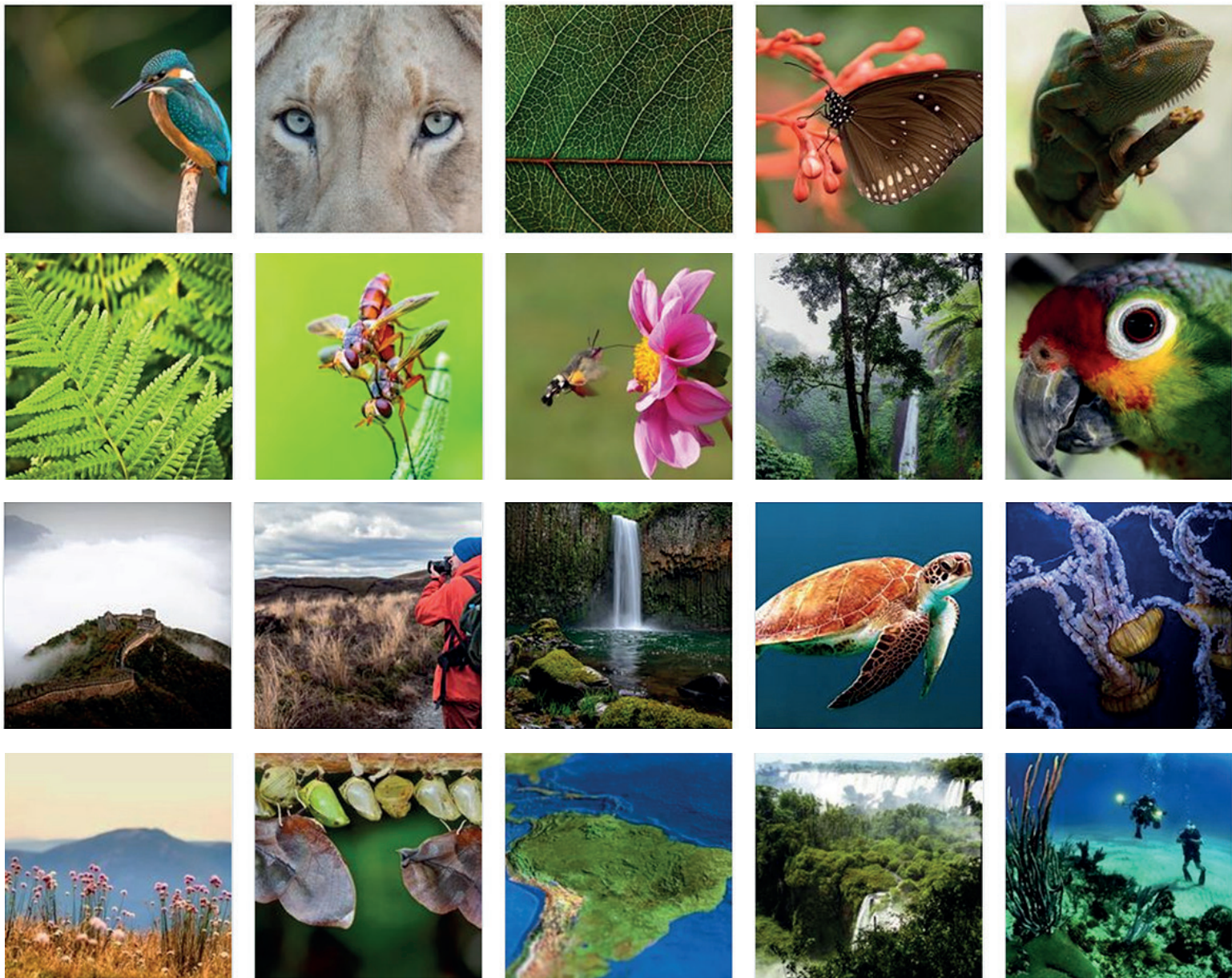


GEO BON OPEN SCIENCE CONFERENCE & ALL HANDS MEETING 2020

06–10 July 2020, 100 % VIRTUAL



Book of Abstracts

Keynote 1

IPBES: Science and evidence for biodiversity policy and action

Anne Larigauderie

Executive Secretary of IPBES

This talk will start by a presentation of the achievements of the Intergovernmental Science-Policy Platform for Biodiversity (IPBES) during its first work programme, starting with the release of its first assessment, on Pollinators, Pollination and Food Production in 2016, and culminating with the release of the first IPBES Global Assessment of Biodiversity and Ecosystem Services in 2019. The talk will highlight some of the findings of the IPBES Global Assessment, including trends in the contributions of nature to people over the past 50 years, direct and indirect causes of biodiversity loss, and progress against the Aichi Biodiversity Targets, and some of the Sustainable Development Goals, ending with options for action. The talk will then briefly present the new IPBES work programme up to 2030, and its three new topics, and end with considerations regarding GEO BON, and the need to establish an operational global observing system for biodiversity to support the implementation of the post 2020 Global Biodiversity Framework.

Keynote 2

Securing Critical Natural Capital: Science and Policy Frontiers for Essential Ecosystem Service Variables

Rebecca Chaplin-Kramer

Stanford University, USA

As governments, business, and lending institutions are increasingly considering investments in natural capital as one strategy to meet their operational and development goals sustainably, the importance of accurate, accessible information on ecosystem services has never been greater. However, many ecosystem services are highly localized, requiring high-resolution and contextually specific information—which has hindered the delivery of this information at the pace and scale at which it is needed. To meet the demand for global, standardized data on ecosystem services, while still retaining representation of their fine-scale socio-ecological processes, a new approach is warranted. Integrating the Essential Biodiversity Variables into ecosystem service modeling and the evolving framework for Essential Ecosystem Service Variables provides a path forward. With satellites scanning every meter of the planet every few days, a rich array of social media delineating human behavior and activity, and high-speed computing capable of metabolizing terabytes of data in minutes, we are poised to harness the information age to advance the reliability, relevance, and readiness of ecosystem service data.

Essential biodiversity and ecosystem service variables for the ocean

William W. L. Cheung

Institute for the Oceans and Fisheries, The University of British Columbia

Marine ecosystems have been impacted by human activities, including overfishing, habitat destruction, climate change and pollution. These impacts are altering ecosystem functions, goods and services deemed vital to human communities. There are urgent calls, such as through the Intergovernmental Platform on Biodiversity and Ecosystem Services, for engaging in societal pathways that will lead us to 'positive' futures in which these ocean challenges can be met. Development of such pathways require knowledge about the past and current capacity of the ocean to support biodiversity, maintain ecosystem functions and services, as well as projections of how such capacity would be altered under scenarios of global changes. Here, using fisheries as an example, I illustrate how a candidate set of essential biodiversity and ecosystem service variables for the ocean, with global coverages, can be used to track past changes and explore the consequences of climate and societal changes. These candidate sets of essential variables for the ocean have also been applied to project the futures of fisheries-related ecosystem functions and services using integrated ocean models under scenarios of global change and policy options. These examples highlight the importance and utilities of developing interconnected essential biodiversity and ecosystem services variables that are harmonized across the ocean. They also underscore the need to build data and modelling infrastructure to facilitate the use of these variables in exploring sustainable ocean development pathways.

Keynote – EBV & EESV Development

What monitoring invasive species has taught us about governing biodiversity knowledge

Melodie A. McGeoch

Monash University / Australia

Biodiversity governance is what holds the relevant actions, research, expertise, policy and institutions together as we work towards a common goal. GEO BON and Essential Biodiversity Variables (EBVs) have played a significant role over the last decade developing the concepts, tools and networks to span the boundaries of otherwise sometimes disconnected thinking and activity on biodiversity and how best to govern it. As a test case, monitoring biological invasions has posed opportunities and challenges to implementing GEO BON's vision to improve the quality, quantity and usefulness of biodiversity data. From a biodiversity perspective, biological invasions are a theoretically well-understood, species populations problem and one with substantial policy traction. Nonetheless, the many hurdles encountered in the process of implementing EBVs for invasion monitoring may provide more general insights on the work needed to support the Post-2020 Biodiversity Framework. I'll provide an overview of progress on invasion monitoring for the purpose of national and global reporting, examine what some of the more general emergent messages might be, and how these could guide the tasks for GEO BON in the coming decade.

The InSiGHTS framework for modelling species' Area of Habitat

Carlo Rondinini

Sapienza University / Italy

InSiGHTS (Integrated Scenarios of Global Habitat for Terrestrial Species) is a modelling framework that enables the estimation, monitoring and projection of species' Area of Habitat (AOH), i.e., the habitat available to a species within its range. InSiGHTS combines three components: (1) a climate-envelope model, used for projecting climatically suitable space; (2) assumptions on species' response to climate change, used to infer potential range gains and losses following changes in climate suitability; and (3) a habitat suitability model to estimate the AOH. All three components of the framework are flexible in terms of data input and processing. InSiGHTS has been applied in a variety of contexts to assess the indirect effects of alternative pathways of socio-economic development, exerted through changes in climate and land use, on mammal habitat, populations and extinction risk. Based on InSiGHTS projections, known sustainability pathways reduce impacts on mammal diversity, but are insufficient to halt declines.

Panel discussion on BON Development

The Global Coral Reef Monitoring Network – the thematic BON for coral reefs

David Obura

CORDIO East Africa and GCRMN Regional coordinator for the Western Indian Ocean

Four years from the last GEOBON Open Science Conference in 2016, conditions for coral reefs have worsened, with the 3rd global bleaching event spanning three years from 2015-2017 touching almost all coral reef regions around the world. 2020 was anticipated as a ‘bumper policy year’ for the biodiversity and climate nexus, but the global attention has been diverted by another global nexus crisis, the Covid-19 pandemic. With this as a backdrop, the Global Coral Reef Monitoring Network (GCRMN) adopted a new Implementation and Governance Plan in January 2019, incorporating standards and principles from the Essential Biodiversity and Ocean Variable (EBV/EOV) frameworks.

The principal task of the GCRMN in 2020 is to produce the first global update of coral reef status since 2008. The GCRMN community contributed 195 datasets from 75 countries. These datasets included more than 1,7500,000 observations of 23 different variables recorded from more than 100,000 transects. Long-term time series data (>15 years) were provided from almost 700 different sites around the world. The report will be produced in the second half of 2020. With both climate and biodiversity Conferences of Parties delayed to 2021, the timing of the report will be perfect to strengthen global commitments to stay within the safe climate boundary of 1.5-2°C and to adopt strong goals and targets of the new Global Biodiversity Framework (GBF) for 2021-2030 to achieve no net loss of biodiversity. In this regard, the GCRMN’s parent body, the International Coral Reef Initiative, submitted recommendations to the Open Ended Working Group on the GBF, including recommended metrics for coral reefs in the indicator framework of the GBF for monitoring target and goal attainment.

A number of additional threads are in motion relevant to establishing the GCRMN as a thematic BON or OOS, including:

- strengthening protocols, standards and data platforms, as well as of metadata and data sharing agreements, to facilitate aggregation, sharing and multiplying the use of data from a global, or set of coherent regional, datasets;
- establishing formal procedures for contribution of GCRMN data into the Biodiversity Indicators Partnership and related platforms for international reporting on biodiversity policies, as well as for global standard reporting indices such as the IUCN Red List of Threatened Species and the Red List of Ecosystems;
- establishing regional processes to address data contributor and networking needs, including returning individual and shared data to contributors and local to national users, adding value to contributors;
- establishing complementary monitoring and data aggregation for social and economic data.

Biodiversity Observation Networks are People Networks

Aletta Bonn

Helmholtz-Centre for Environmental Research – UFZ / German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Often the development of observation networks is approached from a data centric point of view and a technological angle. Data records, however, are collected and observation schemes are run by people. By organisations of different interests, aims and capacities. Recognising, welcoming and embracing this diversity of actors provides the basis for developing strong and societal relevant BONs. As the majority of biodiversity observations are recorded by volunteers and citizen scientists, BONs can build on a long history bridging the science-practice-policy interface. Drawing on our recent work and experience in the sMon network, a community of experts from German federal and national state agencies, natural history societies, museums and science institutes, this talk will discuss how joint working and learning, while keeping distinct identities and profiles, and applying novel statistical tools as well as providing trusted data management and infrastructures can provide a baseline to develop resilient joint biodiversity observation networks.

The Design and Operation of China Biodiversity Observation Network

Haigen XU

Nanjing Institute of Environmental Sciences, Ministry of Ecology and Environment, Nanjing 210042, China

The China Biodiversity Observation Network (China BON) was developed and operated under the auspices of the Ministry of Ecology and Environment. The network consists of four components, i.e. bird monitoring network, amphibian monitoring network, butterfly monitoring network and mammal monitoring network. The first two networks were initiated in 2011 and the last two networks were initiated in 2016. Guidelines for the selection of monitoring sites, line and point transects, field survey of species and habitats were developed. Currently, 749 monitoring sites were applied for monitoring with more than ten thousand line transects and point transects. Challenges in designing and operating a long-term monitoring network were discussed, including goals and indicator species of monitoring, funding strategies, human resources, data analysis and sharing.

Communities of practice for supporting multiscale decision making in a megadiverse country

Maria Cecilia Londoño

Humboldt Institute / Colombia

The Colombia Biodiversity Observation Network, BON COLOMBIA, has been established since 2015 and is led by the Humboldt Institute. The BON COLOMBIA has focused on building communities of practice represented by multiple and diverse stakeholders that take different decisions at different scales across the national territory. These communities of practice are the core and more important element of the network, and around them a digital infrastructure is built to connect a multiscale decision making platform. BON COLOMBIA has developed a structure that allows it to integrate its work to thematic BON`s and working groups in GEOBON, providing an example of the bottom-up approach of the network.

The Circumpolar Biodiversity Monitoring Programme – The Arctic BON; Monitoring and reporting changes in Arctic Biodiversity and ecosystems

Tom Christensen, Cathy Coon, Tom Barry

Aarhus University / Denmark

Arctic biodiversity faces increasing threats from a variety of anthropogenic stressors including, chemical pollutants and climate change. The Conservation of Arctic Flora and Fauna (CAFF) is the biodiversity Working Group of the Arctic Council and the primary objective of CAFF's Circumpolar Biodiversity Monitoring Programme, CBMP, is to provide early detection of changes in biodiversity and ecosystems and to coordinate ongoing monitoring that can be used to inform decision makers to mitigate further degradation of Arctic biodiversity.

The CBMP is formally recognized as a regional GEO BON. CBMP, is an adaptive and question driven ecosystem based biodiversity monitoring programme. This ecosystem-based approach integrates information across ecosystems, species, and their interactions, and lends itself to monitoring central biotic aspects called Focal Ecosystem Components (FECs). Changes in FECs status likely indicate changes in the overall environment.

The release of the CBMP State of Arctic Biodiversity Reports demonstrates how cooperative efforts to monitor and report on biodiversity can both help identify status and trends, as well as identify vital gaps in monitoring.

This session will present the CBMP and discuss lessons learned and challenges.

EBV to support National Reporting on Aichi Targets in AFRICA (The case for Kenya)

Lucy Waruingi

Executive Director, African Conservation Centre. Nairobi. KENYA

Monitoring biodiversity and observing and documenting changes in an organised and coherent infrastructure is a major contributor towards the objectives of the CBD Strategic Plan 2011–2020 which states that “by 2050, biodiversity is valued, conserved, restored and wisely used, maintaining ecosystem services, sustaining a healthy planet and delivering benefits essential for all people”

In Africa, Terrestrial and marine ecosystems and their biodiversity underpin economic growth, sustainable development and human wellbeing. However, we are facing severe degradation leading to the decline or loss in biodiversity and the impairment or disruption of ecosystem functions and services, thus threatening Africa’s ability to realize the African Union Agenda 2063 goals and the 2030 Agenda for Sustainable Development and its Sustainable Development Goals.

One key challenge hindering effective approaches to biodiversity conservation is the lack of credible and easily accessible information to support decision makers, practitioners and other stakeholders to improve their strategies and ecosystem management policies and practice. With the upcoming post 2020 biodiversity target, its time to look at the gaps that continue to hinder progress and the opportunity to use Essential Biodiversity Variables as a foundation to streamline monitoring and reporting on the status of Africa’s biodiversity. We look into examples from Kenya and the key recommendations to move this agenda forward in order to realise The Africa We Want, a continent whose biodiversity is ecologically healthy, diverse and resilient in support the region’s development objectives and well-being of its people.

Session: Ecosystem Functions

Oral presentations

Incorporating ecosystem functional diversity into geographic conservation priorities using remotely-sensed Ecosystem Functional Types

Alcaraz-Segura, Domingo (1); Cazorla, Beatriz P. (2); Cabello, Javier (2); Peñas, Julio (1); Garcillán, Pedro P. (3); Reyes, Andrés (2)

1: University of Granada, Spain; 2: University of Almería, Spain; 3: CIBNOR, Mexico

Conservation biology needs to set geographic conservation priorities not only based on species composition or ecosystem structure, but also on the functional dimensions of biodiversity. However, assessing functional diversity is still challenging at the regional scale. Here, we propose the use of Ecosystem Functional Types (EFTs), defined as patches of the land surface that share similar dynamics of matter and energy exchanges between the biota and the physical environment, to incorporate ecosystem functional diversity in the design of representative protected area networks. As a proof of case, we applied the EFT approach in Baja California Peninsula (Mexico): 1) to characterize the regional heterogeneity of ecosystem functional diversity; 2) to prioritize new protected area candidates based on EFTs richness and rarity; and 3) to explore whether such EFT-based geographic priorities are consistent, complementary, or both with previous independent assessments mainly focused on biodiversity structure and composition. EFTs were identified using three key functional attributes derived from the seasonal dynamics of the MODIS Enhanced Vegetation Index (EVI): annual mean (surrogate of primary production), seasonal coefficient of variation (descriptor of seasonality), and date of maximum EVI (indicator of phenology). EFT-based conservation priorities highlighted 26% of the Peninsula under extreme or high priority. By comparing EFT-based priorities with traditional assessments, we were able to reinforce the importance for functional diversity of already prioritized areas. But more importantly, we showed that traditional prioritization methods did not identify the full range of important areas for ecosystem functional diversity and tended to better capture areas of high EFT rarity than areas of high EFT richness. In practice, EFT-based geographic conservation priorities represent a feasible new approach to long-established ones based on the compositional (e.g., species richness) and structural characterization of biodiversity (e.g., vegetation types), but also to the more recent functional approaches based on species functional traits.

Assessing the role of ecosystem functioning and dynamics to support model-assisted monitoring of biodiversity

Arenas-Castro, Salvador (1,2); Adrián Regos (2,3); João F. Gonçalves (2); Domingo Alcaraz-Segura (4,5); Ivone Martins (2,6); Joaquim Alonso (1,2); João Honrado (2,6)

1: Instituto Politécnico de Viana do Castelo. Escola Superior de Tecnologia e Gestão, Viana do Castelo, Portugal; 2: CIBIO-InBIO—Centro de Investigação em Biodiversidade e Recursos Genéticos, Laboratório Associado, Universidade do Porto, Portugal; 3: Departamento de Zooloxía, Xenética e Antropoloxía Física, Universidade de Santiago de Compostela, Spain; 4: Department of Botany and Inter-University Institute for Earth System Research, University of Granada, Spain; 5: Andalusian Center for the Assessment and Monitoring of Global Change (CAESCG), University of Almería, Spain; 6: Faculdade de Ciências, Universidade do Porto, Portugal

Global biodiversity and ecosystem functioning are undergoing profound and intense changes worldwide. These environmental changes greatly impact both the distribution and the abundance of species, resulting in the depletion or loss of key communities and ecosystems functions. Thus, both ‘species distribution’ and ‘population abundance’ are widely used as essential biodiversity variables (EBVs) to monitor environmental changes. Conversely, the ecosystem functioning – that involves several socio-ecological processes driving the exchange of matter and energy – is key for species and their population dynamics. In this context, ecosystem functioning attributes (EFAs), derived from time series of satellite images, are being also considered as candidate EBVs (in the Ecosystem Function – EF group). EFAs are known to inform on spatial and temporal dynamics affecting species distribution and abundance patterns, being recently evaluated as predictors in species distribution and abundance models (SDMs). Despite the increasing role of the remotely sensed EFAs as predictors in SDMs, the performance of EFAs can be context-dependent and scale-dependent. Thus, much more needs to be investigated regarding how data quality and scale-related factors or life-history traits affect this role. In this sense, we explored and assessed the spatiotemporal features of EFAs in different contexts, facing different data quality (e.g. different sources or methods of data collection: standardized scientific data vs. citizen data) across spatiotemporal scales (i.e. extent and resolution), and multiple species traits (differing in taxonomic, degree of habitat specialization, or temporal coverage). Based on different EFA-SDM applications, we illustrated the importance of issues related to the scale of analysis, the life-history traits of species, the temporal and thematic data quality, and the spatial uncertainty, when using EFAs as essential biodiversity variables in biodiversity modelling and monitoring.

Identification of ecosystem functional types in tropical drylands: a functional outlook for monitoring EBVs

Burbano Girón, Jaime (1); Estupiñan, Lina (2); Gans, Fabian (2); Mahecha, Miguel (2); Londoño, Maria Cecilia (1)

1: Instituto de Recursos Biológicos Alexander von Humboldt, Colombia; 2: Max Planck Institute for Biogeochemistry, Germany

Addressing functional variability under ecological transitions in highly transformed regions is critical for monitoring biodiversity changes. However, there is a lack in the evaluation of the seasonal dynamics of functional characteristics of tropical ecosystems, where most important biodiversity hotspots occur, but also where the largest losses in natural ecosystems and variability in climate change projections have been identified. Therefore, to focus on monitoring priorities, essential biodiversity variables (EBVs) accounting ecosystems functional types are a priority. This study aimed to identify and characterize EFTs in the Caribbean dry region of Colombia using five remote sensing ecosystem variables: NVDI, NPP, FPAR, LAI, and ETP. Variables were resampled from MODIS data at 1km resolution and accessed through the Earth System Data Lab (ESDL) from the ESA. EFTs were defined based on the identification of break-points in 8-day time series for the period 2001-2014 by applying the BFAST method. For each EFT, a set of 40 statistics were estimated for the period after the break-point. The most informative statistics ($R \geq 0.7$) characterizing each EFT were selected from the two first dimensions of a PCA applied in each EFT and for each variable analyzed. These statistics were proposed as monitoring indicators for functional ecosystem characteristics in each EFT. We found that most of EFTs for each variable did not agree, but the locations where the date in the break-point was coincident occurred mostly over the remanent tropical dry forest (TDF). Differences found in the EFTs proposed for each variable support the necessity to include multiple variables accounting different ecosystem processes to better characterize ecosystem heterogeneity and their responses to environmental change. Our results also supported local climatic and phenologic characteristics of the region, i.e., climatic variability, phenology, and water availability are less variable on TDF. Most relevant indicators for monitoring found were the time series mean values accounting ecosystems dynamics in terms of productivity, photosynthetically activity, and water use; the coefficient of variation accounting the seasonality of ecosystems processes, and the amplitude accounting phenology. These indicators characterizing EFTs were similar regarding other studies defining EFTs; therefore, they should be considered as robust measures of change in ecosystems functions.

Developing remotely sensed indicators for tree disease

Cavender-Bares, Jeannine; Pinto-Ledezma, Jesús; Juzwik, Jennifer

University of Minnesota, United States of America

Monitoring changes in biodiversity, including forest ecosystem integrity, is critical to meeting international biodiversity targets. Accurate and early detection of forest threats are key to effective management. Oaks (*Quercus*)—a major tree lineage in the Northern Hemisphere that comprise nearly 30% of forests in the US—are under threat from multiple pathogens. Oak wilt fungus *Bretziella fagacearum* is considered the most destructive threat to oaks in the US but can be controlled when detected early.

Current detection methods rely largely on aerial and ground-based surveys. Satellite in combination with airborne digital imagery has the potential for accurate and earlier detection of tree disease at much larger spatial scales. We are using two types of satellite data for forested regions in Minnesota and Wisconsin, including hyperspectral data at 30 m spatial resolution from DESIS sensor on the International Space Station and multi-spectral data at 1 m resolution from WorldView for the deciduous and mixed forest regions in Minnesota and Wisconsin, US. DESIS—the DLR Earth Sensing Imaging Spectrometer from the German Aerospace Center (DLR) is a spaceborne sensor with a spatial resolution of 30 m and is one of several precursors to NASA's Surface Biology and Geology (SBG) hyperspectral-thermal IR mission. We are combining satellite imagery collected at different spatial resolutions using data fusion algorithms to downscale hyperspectral imagery at 30 m spatial resolution to higher spatial resolution (<1 m) using multi-spectral imagery, yielding high spatial and spectral resolution data.

We are developing a mapping tool in collaboration with forest health specialists and practitioners, who manage oak wilt on public and private land. By the end of the project we will provide a mapping tool that can be applied to data sources that extend beyond DESIS, and we will work directly with our implementation partners to generate user-guided maps. These approaches can be applied to many kinds of tree diseases to monitor forest health and ecosystem integrity as part of biodiversity monitoring efforts globally.

Assessing Ecosystem Functional Diversity in the Circumpolar Arctic Tundra Using Seasonal Dynamics of MODIS NDVI

Epstein, Howard E. (1); Armstrong, Amanda Hildt (1); Alcaraz-Segura, Domingo (2); Tassone, Morgan (1); Montefiori, Elisa (2); Reynolds, Martha K. (3)

1: University of Virginia, United States of America; 2: University of Granada, Spain; 3: University of Fairbanks, Alaska, United States of America

The Arctic is a region with a high degree of spatial variability in ecosystem functioning, and one that is changing dramatically over time due to dynamics in climate and land use. To assess the spatial and temporal heterogeneity of ecosystem functioning, we identified Ecosystem Functional Types (EFTs), patches of the land surface that process energy and matter in similar ways and potentially show coordinated responses to environmental factors. We classified EFTs for the circumpolar Arctic tundra using three key functional attributes, derived from the seasonal dynamics of the MODIS Normalized Difference Vegetation Index (NDVI) from 2001- 2017: mean growing season NDVI, date of maximum green-up, date of maximum senescence. Using the new raster version of the Circumpolar Arctic Vegetation Map (CAVM), we assessed the correspondence between vegetation structure and ecosystem functioning for each of the 5 tundra bioclimatic subzones and the 15 defined physiognomic units. Finally, we determined ecosystem functional diversity as EFT richness within a 7x7 pixel moving window, and evaluated the environmental controls (climatic geological, anthropogenic) on the spatial patterns of EFTs and EFT richness, and the temporal dynamics of ecosystem functional diversity. This functionally based framework can assess landscape heterogeneity that is not solely determined by ecosystem structure (e.g. vegetation composition), and aids in the identification of “functional hotspots,” as possible targets for conservation priorities.

Bridging Earth science and biodiversity with the regional Earth System Data Lab for Northern South America

Estupinan-Suarez, Lina M. (1,2); Gans, Fabian (1); Londoño, Maria Cecilia (3); Sierra, Carlos A. (1); Burbano, Jaime (3); Mahecha, Miguel D. (4)

1: Max Planck Institute for Biogeochemistry, Germany; 2: Friedrich Schiller University of Jena, Germany; 3: Humboldt Institute, Colombia; 4: Leipzig University, Germany

Tropical ecosystems are experiencing massive land use transformation threatening multiple Earth spheres. In tropical South America, species experience habitat loss due to the expansion of the agricultural frontier in tropical dry forest and savannas. Deforestation is rapidly increasing not only in the Amazon forest but also in the Choco region. All these ecosystem changes have a large impact from regional-to-global scales for carbon and water cycling and methane emissions. To gain a better understanding of the process occurring and its implications across spheres, it is necessary to integrate data streams from different fields and work simultaneously with different research disciplines. This can now be achieved due to the plethora of spatio-temporal data streams that are constantly generated to characterize and monitor ecosystems. Nevertheless, the big data era brings challenges for storing, processing and more importantly our capacity of analyzing outcomes and communicating them timely and properly. In a Colombian-German collaboration, we developed a regional Earth System Data Lab (regESDL) for Northern South America at a moderate resolution (0.0083d). Our aim was to facilitate data access and efficient processing to data streams, but also to integrate regional maps of biodiversity and ecological regionalization to investigate ecosystem function. We showcase the regESDL application with a case study to analyze unimodal and bimodal regimes pixelwise. Further, we repeated the analysis for biotic units, that are defined based on their Beta-biodiversity values, as a level of aggregation. The evaluated variables were Gross Primary Productivity, and indices of standing vegetation or greenness (NDVI, EVI, LAI, FAPAR) acquired from remote sensing sensors and spinning from 2001 to 2009. Our findings show regional patterns highlighting forest with unimodal seasonality, and savannas where annual and semiannual oscillations are equally important or bimodality dominates. The regESDL is a variant of the Earth System Data Lab, this is an open software available at the GitHub repository.

Measuring the integrity of forests globally

Grantham, Hedley; Duncan, Adam; Evans, Tom; Jones, Kendall; Watson, James

Wildlife Conservation Society

Many global environmental agendas, including halting biodiversity loss, reversing land degradation, and limiting climate change, depend upon retaining forests with high ecological integrity, yet the scale and degree of forest modification remains poorly quantified and mapped. In this talk we will present a new global forest index that measures landscape-level forest integrity by integrating data on direct human pressures on forests, and forest pressures associated with proximity to these direct pressures, and an index on lost forest connectivity to generate the first globally-consistent, continuous index of forest condition as determined by degree of anthropogenic modification. We shows that globally, only 17.4 million km² of forest (40%) can be considered having high integrity and only 27% of this area is found in nationally-designated protected areas. The results of this study are fundamental to current discussions underway regarding the Convention on Biological Diversity, since the current draft of the post-2020 Global Biodiversity Framework proposes both a goal and an action target relating to ecosystem integrity and there is active discussion amongst Parties about how best this can be quantified and monitored. The results are also highly relevant to the delivery of the Paris Agreement under the UN Framework Convention on Climate Change since special consideration needs to be given to forest carbon reservoirs and sinks with high ecological integrity, both within Nationally Determined Contributions and in international finance mechanisms such as the Green Climate Fund.

The dynamics of the Amazon forests and the role of forest structure - linking vegetation modelling and remote sensing

Huth, Andreas (1,2); Huth, Fischer (1); Taubert, Franziska (1); Knapp, Nikolai (1); Bohn, Friedrich (1); Roedig, Edna (1)

1: Helmholtz Centre for Environmental Research - UFZ, Germany; 2: iDiv - German Centre for Integrative Biodiversity Research

Precise descriptions of forest productivity, biomass, and structure are essential for understanding ecosystem responses to climatic and anthropogenic changes. However, relations between these components are rarely investigated, in particular for tropical forests.

We developed an approach to simulate forest dynamics of around 410 billion individual trees within 7.8 Mio km² of Amazon rainforest (using the FORMIND forest model). We then integrated remote sensing observations from Lidar (forest height map) in order to detect different forest states and structures caused by small-scale to large-scale natural and anthropogenic disturbances.

Under current conditions, we identified the Amazon rainforest as a carbon sink, gaining 0.56 Gt C per year. We also estimated other ecosystem functions like gross primary production (GPP) and woody aboveground net primary production (wANPP), aboveground biomass, basal area and stem density.

We found that successional states play an important role for the relations between productivity and biomass. Forests in early to intermediate successional states are the most productive and carbon use efficiencies are non-linear. Simulated values can be compared to observed values at various spatial resolutions (local to Amazon-wide, multiscale approach). Notably, we found that our results match different observed patterns (e.g., MODIS GPP).

We conclude that forest structure has a substantial impact on productivity and biomass.

It is an essential factor that should be taken into account when estimating current carbon budgets or analyzing climate change scenarios for the Amazon rainforest.

Ecosystem Disturbance: progress towards an Essential Biodiversity Variable

Leitão, Pedro J. (1); Balke, Thorsten (2); Benedetti-Cecchi, Lisandro (3); Berger, Uta (4); Chuvieco, Emilio (5), Fernandez, Miguel (6); Fernández, Néstor (7); Hostert, Patrick (8); Huth, Andreas (9); Kissling, Daniel (10); Lausch, Angela (9); Neumann, Carsten (11); Normand, Signe (12); Schröder, Boris (1); Schrodt, Franziska (13); Senf, Cornelius (14); Skidmore, Andrew (15); Thorn, Simon (16); van de Koppel, Johan (17); Zambrana-Torrel, Carlos (18)

1: Technische Universität Braunschweig (Germany); 2: University of Glasgow (UK); 3: University of Pisa (Italy); 4: Technische Universität Dresden (Germany); 5: Universidad de Alcalá (Spain); 6: NatureServe (US); 7: iDiv -German Centre for Integrative Biodiversity Research (Germany); 8: Humboldt-Universität zu Berlin (Germany); 9: UFZ - Helmholtz Centre for Environmental Research (Germany); 10: Daniel Kissling, University of Amsterdam (Netherlands); 11: GFZ - German Research Centre for Geosciences (Germany); 12: Signe Normand, University of Aarhus (Denmark); 13: University of Nottingham (UK); 14: Technical University of Munich (Germany); 15: University of Twente (Netherlands); 16: Universität Würzburg (Germany); 17: NIOZ (Netherlands); 18: EcoHealth Alliance (US)

Contemporary global change is, among others, reflected in changing natural and anthropogenic disturbance regimes. It similarly relates to a potential loss in ecosystem resilience and an ecosystem's capacity to resist these disturbances. Disturbance regulation is therefore a key ecosystem function, and an Essential Biodiversity Variable (EBV) related to ecosystem disturbance has been proposed for the global monitoring of biodiversity change. Remote sensing offers great potential for the global monitoring and characterisation of disturbance and recovery dynamics. The understanding of these dynamics requires, however, the integration of different expertise by bringing together knowledge from disturbance ecology, ecosystem resilience, and remote sensing disciplines.

Cattle intensification as a global driver of diversity and ecosystem services loss in pastures around the world

Noriega, Jorge Ari

Department of Biogeography and Global Change, Museo de Ciencias Naturales (MNCN-CSIC), Madrid, Spain; Laboratory of Zoology and Aquatic Ecology - LAZOE, University of los Andes, Bogotá, Colombia

Biodiversity provides ecosystem services that sustain human life. However, the anthropic disturbance is affecting negatively the diversity, functioning, and provisioning of these ecosystem services. One of the main drivers of this effect is land-use intensification, which is an important factor in pastures used for livestock breeding. Dung beetles are important in removing waste on these ecosystems and contributing to the cycling of nutrients. However, their action could be hampered by land-use intensification, impacting negatively their diversity, functional structure, ecosystem services they provide, and causing potential local extinctions. In this study, we conducted a global multi-site experiment in 38 sites (24 countries in five continents) to understand the effect of cattle density on dung beetle diversity and dung removal. For each sampling site, we selected an area with extensive and another with intensive cattle use, and in each of them, we quantified dung removal through an experimental approach, sampled dung beetle's diversity, and quantified functional diversity (FD). Pairwise comparisons were used to evaluate differences in diversity and dung removal of intensive and extensive areas. Structural equation models (SEM) were performed for disentangling the relative importance of cattle intensification, climate, and diversity on dung removal rates. Cattle intensification has an overall negative effect on species richness but not on abundance, evenness, FD, and dung removal. A SEM model, using cow density as a proxy of cattle intensification, shows a direct negative effect of intensification on dung diversity and dung removal. However, in the SEM models built separately for extensive and intensive sites, the main drivers are different; for extensive sites, richness and climate affect dung removal, while for intensive sites abundance drives dung removal. These results highlight the negative impact of land-use intensification on biodiversity and ecosystem services, and the potential loss of biodiversity in a global perspective.

Monitoring deforestation and degradation of Southern African Miombo Woodlands using cloud computing and time series analysis

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The Miombo Woodland ecoregion in Southern Africa encompasses savannas with a gradient from dry-subhumid to semi-arid. Due to its floral and faunal diversity it is an area of outstanding conservation value, while at the same time demographic developments in all of the included countries drive strong land use transformation processes with different trajectories.

We used Google Earth Engine™ to address the extended Miombo ecoregion as represented in the WWF-Terrestrial Ecoregions of the World, which covers 11 countries and an area of ~3.8 Mio km². We computed monthly aggregated EVI values for the period 2000 – 2018 based on the version 6 16-day EVI product (MOD13Q1.006) and implemented a time series analysis method similar the Continuous Change Detection and Classification (CCDC) algorithm. We modelled the time series in a reference period using ordinary least squares regression of the first order harmonic that was derived from the discrete Fourier transform of the VI time series. Coefficients for intra- and inter-annual change were employed to predict VI for the next date and a breakpoint was stored if an RMSE threshold was exceeded a set number of times. The procedure was repeated for the time series following the breakpoint, or the window moved on if no breakpoint was detected. Then different phenology-related metrics (mean EVI, Trend, Amplitude, Phase, Magnitude of Change and RMSE) were calculated for each segment of the time series.

The time series analysis yielded various temporal metrics that describe the overall development, a variable number of breakpoints for each pixel, and a set of phenology metrics for each pixel depending on the number of temporal segments. Concomitant with the length of the observation period, most regions are dominated by a single breakpoint, while two or more breakpoints are rare. Hot spots of change are mainly found in the central Miombo regions in Angola and Zambia; in particular in the former this is largely owed to a significant expansion of subsistence agriculture following the end of the civil war in 2000 with subsequent repatriation of refugees and investments in infrastructure.

To assess validity of our results, we selected various reference areas that are representative of key processes and jointly evaluated phenological properties of the last segment, trend and breakpoint parameters with temporal profiles and corresponding Landsat images. We found these to confirm the credibility of our approach, which was further corroborated by local case studies assessing time series at higher resolution.

Ongoing work includes a geostatistical analysis of metrics to link them to driving social-ecological processes. In particular, fire regimes that are strongly human driven in this region may be key in explaining some of the visible patterns as suggested by many authors.

Using near-term ecological forecasting of satellite data to link traits, communities and ecosystem function

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We present a hierarchical Bayesian modelling framework that allows us to forecast remotely sensed vegetation indices in a fire-dependent and seasonally fluctuating ecosystem, the Fynbos of South Africa. This framework allows several applications including: 1) detecting near real-time changes in the state of the ecosystem by comparing observed vegetation signal with the model forecasts; 2) determining the influence of plant traits on vegetation productivity and seasonality; 3) forecasting changes in vegetation productivity and seasonality under altered climate or community composition; and 4) estimating ecosystem properties like leaf area index (LAI) or above ground biomass. As such, it provides the means to draw linkages across and/or monitor several EBV classes.

Copernicus new 10m Vegetation Phenology to monitor ecosystems

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Earth observation derived land surface phenology (LSP) provides important information on the status and dynamics of ecosystems. The Copernicus land service is preparing the release of a new 10m continental scale vegetation phenology (VP). With both Sentinel 2 satellites providing operationally greenness indicators at 10m spatial resolution in a 3-5 day revisit time, seasonality can be characterized at unprecedented spatial detail. The vegetation cover can be described by its physiognomy and dynamics, and hence are linked to phenology and its change in space and time. By accurately calibrating spaceborne greenness phenology with ground observed phenology (GP) from multiple sources, a pan European vegetation phenology and its derived vegetation productivity datasets (VPP) will be provided in the portfolio of the Copernicus land service by end 2020.

This new service can contribute as an intermediate between remote sensing data and biodiversity indicators used to inform policies. Within the GlobDiversity project (ESA), a Phenology product is considered a remote sensing enabled Essential Biodiversity Variable (EBV) used to i.e. monitor fauna damage, ecosystem and biome identification and mapping, species distribution modelling and abundance, invasive species monitoring, as well as animal and bird movement ecology. The Copernicus VP intends to provide also the seasonal trajectories which depict the seasonal dynamics of the plant growth in a flexible way, which could be tuned to monitor the different seasonal activities of organisms.

The talk will present an overview of the new upcoming 10m Vegetation Phenology Copernicus service as well as the results from the GlobDiversity project using Phenology variables as Essential Biodiversity Variable.

A new metric for evaluating ecosystem condition over time using remote sensing to build ideal distributions of the time since disturbance

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Developing a standardized approach to measuring the state of biodiversity in landscapes undergoing disturbance is crucial for evaluating and comparing change across different systems, assessing ecosystem vulnerability and the impacts of destructive activities, and helping direct species and community recovery actions. Existing ecosystem metrics of condition fail to acknowledge that a particular community could be in multiple states, and the distribution of states could worsen or improve when impacted by a disturbance process, depending on how far the current landscape distribution of states diverges from pre-anthropogenic impact baseline conditions. We developed a way of rapidly assessing ecosystem condition when the distribution of age classes representing increasing time since last disturbance is suspected to have diverged from an ideal benchmark reference distribution. Our metric quantifies the the summed shortfall of vegetation age-class frequencies relative to a reference age-class distribution of time since last disturbance. By accounting for and penalizing too-frequent and too-rare disturbances, the summed shortfall metric responds to fine-scale changes in age classes over both the short-term and long-term. It can be parameterised through remote-sensing of vegetation loss post-disturbance and either empirical or expert-elicited data on the reference state, i.e. the tolerable time since disturbance, can account for uncertainty in the reference state, and can be applied to any disturbance such as wildfire or logging that resets community age classes when it occurs. We demonstrate the use of the summed shortfall metric for evaluating the impacts of the 2019/2020 mega-fires in Australia on threatened ecological communities. Climate change is expected to worsen the frequency, intensity, and impacts of extreme events such as wildfire around the globe. Metrics that accurately evaluate ecosystem degradation resulting from disturbances are crucial to enable rapid post-disturbance assessments of ecosystem vulnerability under IUCN Red Listing of Ecosystems and ensure recovery actions are delivered in a timely manner. To fully describe ecosystem degradation, we recommend that our summed shortfall metric, focused on habitat quality and informed by biologically meaningful baselines, be added to existing condition measures focused on vegetation extent. This will improve evaluation of change in ecosystem states and enhance management of ecosystems in poor condition.

Session: Ecosystem Functions

Poster presentations

Gap analysis of the Arctic protected area network to represent Tundra's functional heterogeneity

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Geographic conservation priorities need to be based not only on species composition or ecosystem structure, but also on the functional dimensions of biodiversity, particularly in the Arctic Tundra, where global change is causing a rapid effect on the functional characteristics of an ecosystem. The Arctic is a region that has a relative high degree of spatial variability in ecosystem functioning, but it is dramatically changing mainly due to climate and land-use change. Our goal is to incorporate satellite-derived variables that describe ecosystem functioning in the establishment of geographic conservation priorities. In this work, we explored what ecosystem functional types are already protected and how the actual protected area network represents the regional heterogeneity of ecosystem functioning. To evaluate the representativeness of the network of protected areas we used two approaches based on a continuous and a discrete characterization of ecosystem functioning derived from key attributes obtained from the seasonal dynamic of the MODIS Normalized Difference Vegetation Index (NDVI) and related to the productivity, seasonality and phenology of carbon gains dynamics. In the continuous approach, the characterization of the ecosystem functioning is continuous variables named ecosystem functional attributes (annual mean of NDVI and seasonality and phenology of the start and end of the growing season). The discrete approach is based on the identification of Ecosystems Functional Types (EFTs), a classification based on the former attributes. Each EFT is assumed to represent a patch of the land surface that processes energy and matter in similar ways and potentially shows coordinated responses to environmental factors. With the first approach, we identified the singularity and representativeness of protected areas. With the second, we identified as conservation gaps those ecosystems with differentiated functional behaviour not yet protected by the protected area network.

Effects of windthrow disturbances in *Quercus mesic deciduous forests* (European part of Russia)

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Catastrophic mass windthrows and single windfalls in *Quercus mesic deciduous forests* located in plains and uplands are poorly studied, probably due to the relative rarity of these forests at the present time. However, under conditions of climate warming, the area of broadleaved forests can significantly increase, which determines the particular relevance of their study. Estimates of contributions of windthrows and dead woods to the overall carbon balance, to the cycle of chemical elements are very contradictory; additional detailed studies are necessary, especially in connection with forecast and assessment of the ways of implementation of ecosystem functions of forests which develop with or without spontaneous dynamics.

The aim of our project is to test the idea that fallen trees and pit-and-mound topography caused by treefalls with uprooting are important agents of ecosystem functioning in the temperate forest region: they increase the biodiversity, the intensity of element cycles in the ecosystems and nutrients supply in the soil.

The study is conducted in the Kaluzhskie Zaseki State Nature Reserve (coordinates 53.34°N and 35.46°E) where a catastrophic windthrow occurred in 2006 on a total area of 285 ha. Mature *Populus tremula*, *Betula pendula*, and *B. pubescens* stands and to a lesser extent mature mixed stands of *Quercus robur*, *Fraxinus excelsior*, *Ulmus glabra*, *Tilia cordata*, *Acer platanoides*, *A. campestre*, and *Picea abies* were damaged by the windthrow in 291 separate patches, the area of which ranged from 0.04 to 51 ha. In 2010, the volume of fallen trunks varied from 198 to 463 m³ ha⁻¹; a number of tree regrowth varied from 9000 to 17300 stems ha⁻¹. Besides the area of catastrophic windthrow, there is a 11 ha long-term tree monitoring plot in the Reserve. The plot is located in uneven-aged multispecies old-growth forest where the oldest trees (among those whose age could be determined by an age bore) were *Quercus robur* up to 310 years old. The plot was established in 1986 and it was not affected by the catastrophic windthrow in 2006 while local treefalls often occur in the plot. Two inventories of tree individuals with diameter at breast height from 5 cm were performed in 1986-1988 and 2016-2018. There were registered 5310 and 5139 living trees in the plot during these inventories, respectively; 60% of the living trees were preserved for 30 years. Dynamics of vegetation, rate of wood decomposition and changes in the chemical composition of fallen trunks, changes of soil characteristics under the fallen trunks of different species will be studied as in areas of catastrophic mass windthrow, as in patches of single windfalls of *Quercus robur* which fell in different time.

The project is fund by the Russian Foundation for Basic Research (project 20-04-00733).

Drivers of Spatial and Temporal Variability in Ecosystem Functional Diversity on the Yamal Peninsula, Siberia, Russia

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The seasonal dynamics of primary productivity can be used to define Ecosystem Functional Types (EFTs), patches of the landscape that function similarly and have potentially coordinated responses to environmental drivers. Changes in ecosystem functional diversity, defined here as the variation in the seasonal dynamics of primary productivity across a landscape, can be inferred from trends in EFT richness (the number of EFTs within a defined area) (Paruelo et al. 2001, Alcaraz-Segura et al. 2013). Arctic functional diversity likely varies spatially and temporally due to interactions with climatic, geologic, biological, and anthropogenic drivers; however, the effects of these drivers on EFT distribution and functional diversity in the Arctic have yet to be resolved. This research aims to disentangle the effects of environmental and anthropogenic drivers on EFT distribution and functional diversity of the Yamal Peninsula, a hotspot for change in the Arctic that is characterized by a steep climate gradient from north to south, ice-rich continuous permafrost, diverse Arctic vegetation, indigenous reindeer herding, and natural resource (gas) extraction (Walker et al. 2009, Walker and Reynolds 2018).

This analysis used multiannual time series of satellite-derived EFT richness and climatic, geologic, biological, and anthropogenic driver variables to determine the relative influence of each driver on the magnitude and direction of the Yamal Peninsula EFT richness trend between 2001 and 2018. Additionally, the drivers of EFT and EFT richness distribution across the Yamal Peninsula were analyzed. The spatial patterns of climatic drivers (Summer Warmth Index [SWI], mean growing season precipitation, and snow-free period onset date) were the primary drivers of EFT distribution. Climate variables likely influenced this distribution through shrubification and longer growing seasons in areas with high SWI, high mean growing season precipitation, and an early mean snow-free period onset date. Conversely, spatial and temporal variation in EFT richness across the Yamal Peninsula was primarily driven by fine-scale changes in the landscape caused by geologic, biological, and anthropogenic drivers that mediate vegetation response to climatic drivers.

Generation of Net Primary Productivity as Remote Sensing enabled biodiversity product in the myVARIABLE pilot of e-shape

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Primary productivity is recognized as an Essential Biodiversity Variables (EBVs) under EBVs 'Ecosystem Function' class by GEOBON. According to existing literature, primary productivity has been one of the most important applications attempted by satellite remote sensing. The wide array of canopy geometry and life-cycle dynamics at large scales makes the estimation of primary production from remote sensing data very challenging. Primary productivity is either directly or indirectly linked to a number of other remote sensing- enabled biodiversity products including canopy chlorophyll content, leaf fraction exposed to light, absorbed photosynthetic active radiation, leaf area index and land use/cover change which are critical to understanding plant functioning.

In the myVARIABLE pilot of the EuroGEOSS Showcases initiative (e-shape), we aim to develop primary productivity as an RS-EBV describing 'Ecosystem Physiology' and 'Species Physiology', being calibrated and validated by European observation networks including eLTER and other in situ data to support delivery at European level. Estimation of primary productivity involves using process-based models, semi-empirical light use efficiency (LUE) models or statistical models. The complexity and uncertainty of parameterization of process-based models, underlying assumptions in LUE models and dependency of statistical models to altering environmental conditions will be evaluated and assessed in order to propose and select the best approach for estimation of primary productivity at the European level using Sentinel-2 data.

Session: Ecosystem Services

Flash presentations

Use and supply of cultural ecosystem services in Bavarian Forest National Park

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Conflicts in the management of protected areas arise when its objectives are contradicting such as nature protection vs tourism. The integration of the concept of cultural ecosystem services to the context of nature conservation in protected areas offers a broad spectrum of applied areas. The Bavarian Forest National Park is framed as a protected area for the conservation of the site-specific biodiversity and ecosystem processes but also has to implement plans for education and recreation. Promotion of tourism and the significance of protected areas in their function as regional attractions can play a crucial role for the acceptance of a protected area by the local population. However, the ongoing increase of visitors entering the park arise questions on the adverse effects of people using the park in diverse ways. Therefore, it is important to investigate the demand, use and supply of cultural ecosystem services and whether they align to adapt management strategies. Differences in the demand and use of these services from local visitors vs tourists coming from further away have to be taken into consideration. We conducted a survey asking 500 visitors of the Bavarian Forest National Park, including local visitor and tourists, to grade several cultural ecosystem services and to map their location around the park including a 10 km buffer. Additionally, we mapped the potential supply of cultural ecosystem services based on biophysical indices that were derived from earth observation data. The results suggest that landscape enjoyment and recreational activities are the most commonly used services. Local visitors frequently use a more diverse range of cultural ecosystem services as well as perceive the restorativeness of the Bavarian Forest National Park higher than tourists. We identified several matching and mismatching hotspots of use and supply of cultural ecosystem services in the study area. The majority of hotspots of use are found at the main attractions suggested by the National Park. This finding reinforces the possibility to direct visitor flows and to reconcile biodiversity conservation and the enjoyment of cultural ecosystem service through an informed and sustainable management of the resources.

African Man and Biosphere Reserves: guidance to assess ecosystem services. A manual for African BR managers

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The idea of documenting ecosystem services for Man and Biosphere (MAB) Reserve managers came from a need expressed by the AfriMAB network back in 2013. During a general assembly about “Green Economy and ecosystem services”, the concept of ecosystem services (ES) appeared to be quite new for most participants. They needed to know more and be capacitated regarding ES issues for a better management of the Biosphere Reserves (BR). In 2017 the EVAMAB project (“Economic valuation of ecosystem services in Biosphere Reserves: testing effective rapid assessment methods in selected African Biosphere Reserves (BR)”) was launched to address this need. The project involved many MAB stakeholders, identified and assessed good practices related to ES in different countries. This led to the idea to summarize its main findings and lessons learned in an easy to use manual that would inspire MAB managers and other stakeholders to address ES in their reserves. The manual aims to outline the significance and value of ecosystem services for the management of African BRs; increase the awareness, knowledge and use of ecosystem services among stakeholders involved with African BRs; contribute to sustainably manage ecosystems and their services in African BRs and to support the management of BRs in favour of both Nature and People. It is structured into five chapters: 1. Ecosystem Services; 2. Biosphere Reserves; 3. Ecosystem Services Assessment Tools; 4. How to value ecosystem services?; 5. From ecosystem services assessment to actual change.

Despite the rich literature on protected areas and their management, this Manual fills a knowledge gap. The purpose of the present manual is to present a user friendly "package" or guidance to the MAB decision makers and managers, specifically and explicitly for them, and especially in the African context. The target groups of this manual are multiple, as the management of a Biosphere Reserve does not rely on just one or two actors. However, this manual intends to primarily reach the managers and administrators of African Biosphere Reserves, as they are in the field and need to take day-to-day decisions, defuse conflicts, and are in dialogue with many stakeholders. The manual should ideally be useful to different types of BRs : those managed by a national authority or NGO with communities living in the surrounding area, or community-led biosphere reserves. It can also give guidance to authorities and communities interested in establishing a new biosphere reserve. During this flash presentation, the main content and objectives of this manual, to be produced in 2020, will be outlined.

Session: Ecosystem Services

Oral presentations

Monitoring four decades of dynamic changes in Lake Chad Ecosystems with Google Earth Engine

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Lake Chad is a shallow endorheic basin located in the Sahel region of the Sahara Desert. It is the fourth largest lake in Africa and the sixth largest lake in the world. The Lake and its basin are known to provide ecosystem services to an estimated forty–five million people living in Nigeria, Cameroon, Niger and Republic of Chad. Mapping the spatial heterogeneity of ecosystem services of Lake Chad requires large volume of information. Satellite based remote sensing has the potential for cost effective monitoring of ecosystem services from global to local scale. We explore the remote sensing data within Google Earth Engine platform for time series decadal analysis of ecosystem changes in Lake Chad using dry season data sets of Landsat images from 1980 to 2020. Four major ecosystems were assessed based on the World Wild Life fund ecosystem classifications and needs assessments of 2018 (namely: Water, Reeds islands, Inundated/ irrigated land, Archipelagos). Also 1001 points were randomly distributed across the classified ecosystem to assess and determine the climatic changes within Lake Chad using precipitation and humidity data from Worldclime database in GEE. Results the analysis shows that the lake water size reduced from 10703.03 to 2779.41km² (46.06–11.96%) from 1980– 2020, Archipelagos increased by 43%. The Reeds ecosystem of the lake reduced by 11.05% while inundated/ irrigation ecosystem increased from 25.45% to 43. 14% within the study period. A trend of the deseasonalized precipitation dataset showed that there was steady decline in the mean precipitation value in Lake Chad from through 1979 to early 1980s. This, however, was followed by successive little steady increase in mean precipitation from 1990 to 2013. Mean precipitation for Lake Chad was at its lowest for January to April and November to December. In the month of May, mean precipitation was observed to start increasing until it reaches its peak value in the month of August which is then followed by sharp declines in the succeeding two months, September and October. For the temperature plot, no significant change was detected in the temperature values of the study region.

Evaluating predictions of the InVEST seasonal water yield model

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Water related ecosystem services (ES hereafter) are highly valued by the general public and information regarding water ES is increasingly being demanded by decision makers. The ability to reliably represent watershed processes through models is a pivotal element for decision-makers and managers to preserve and increase water ES. This is particularly relevant in the context of current both land cover and climate changes, that threaten many South American countries like Chile. In the present study, we implement the InVEST Seasonal Water Yield model (SWYM) in 224 catchments encompassing varying climatic, geographical and anthropogenic conditions in southern Chile. We assess model accuracy using real monthly catchment streamflow (combination of quickflow+baseflow) records for 33 basins. We test this model for three years that count with land use information (1998, 2007 and 2013). We hypothesize that climatic and geographical variables are of high importance for model estimations, and that predictions are more accurate in less intervened and larger basins. To test our hypothesis, we compare SWYM performances, through the Pearson correlation coefficient, for monthly quickflow values against total streamflow values, and for annual streamflow values against the estimated streamflow. We describe study area regions watersheds characteristics via a PCA analysis and calculate the squared Pearson correlation coefficient (r^2) for describing environmental variables relationships. Results show that r^2 were low to medium for monthly outcomes and higher in central regions (more rainy) of the study area. Values of r^2 improved when analyzing annual values and was higher in northern (more arid) regions. PCA shows a clear divergence of the variables impacting modelling results in different study area regions, highlighting the importance of evapotranspiration, presence of glaciers and wetlands, among others. Results suggest that the SWYM would profit from the monthly differentiation of baseflow, which would make validation more accurate. Due to climatic and geographical conditions, the SWYM could also take advantage of a more flexible input data system allowing inclusion of more variables in the model, particularly regarding use by local stakeholders who may have access to specific data. This study provides the basis for future modelling and predictive analyses of water supply, land cover change and climate scenarios, an aspect that is crucial for decision makers to allocate limited available resources in a context of changing environmental conditions.

Landscape aesthetics spatial modelling and mapping

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Cultural ecosystem services such as aesthetic value are highly context-specific and often present difficulties in their assessment. Landscape aesthetics has been studied across different disciplines, including psychology, anthropology, evolutionary biology and landscape planning. Whilst this field has grown in socio-ecological research and public interest, it is still missing quantitative and standardised techniques for assessment. Here we present the results from a case study in the northern English Protected Area (PA) of the Yorkshire Dales National Park using social media images, probability modelling and machine learning. Here we show that probability models can be used to rank-order images for aesthetic value and upscale the results for over 22k images to create a map of landscape aesthetic value for the PA.

Ecosystem Functional Diversity – A promising EBV in Ecosystem Service Models

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Satellite-derived Ecosystem Functional Types are a promising way to characterize the regional patterns of ecosystem functional diversity. EFT diversity could improve our modeling and understanding of diversity-driven ecosystem services such as pollination. However, before such products can be integrated in ecosystem service modeling, we need to better understand the spatial patterns in satellite-derived EFTs and EFT diversity across different spatial scales, and whether they represent real patterns on the ground. In this study, we first extracted EFT using 250-m MODIS and 30-m Landsat data from 2001 to 2019 based on three attributes of EVI in Costa Rica. We compared MODIS-based EFT and EFT diversity with Landsat-Based EFT and EFT diversity, and for both products we examine EFT assemblages in different ecoregions, life zones and floristic provinces. These comparisons provide a first step toward replacing land cover as the primary input for ecosystem service modeling, better capturing the true heterogeneity in ecosystem functioning that exists across landscapes.

Rethinking the future of the socioecological systems underlying high nature value farmlands

Lomba, Angela

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Farmlands represent the largest terrestrial ecosystems in the Anthropocene. When managed under low-input farming systems, farmlands are associated with diverse cultural and natural heritage around the world. Known as high nature value farmlands (HNV farmlands) in Europe, these farmlands and their underlying farming systems evolved as tightly coupled socioecological systems, and are essential to biodiversity conservation and the delivery of ecosystem services to society. However, HNV farmlands are vulnerable to socioeconomic changes, leading to either agricultural intensification or land abandonment. Here, we use scenarios to envision alternative plausible futures for HNV farmlands and discuss the related management options and expected socioecological outcomes.

Departing from an overview of the socioecological pillars underlying the value of HNV farmlands and their delivery of multiple ecosystem services to wider society, examples of high nature value farmlands worldwide are presented. Then scenarios are used to envision alternative plausible futures for HNV farmlands and discuss their implications for land management and expected socioecological outcomes.

Finally, focusing on a future where HNV farmlands are embraced as promising 'Seeds of a Good Anthropocene', requirements to guide a paradigm shift towards socially, economically and ecologically viable HNV farmlands are presented and discussed. This research was funded by FEDER Funds through the Operational Competitiveness Factors Program - COMPETE and by National Funds through FCT - Foundation for Science and Technology within the scope of FARSYD project - 'FARming SYstems as tool to support policies for effective conservation and management of high nature value farmlands' (PTDC/AGR-REC/5007/2014 - POCI-01-0145-FEDER-016664).

Characterizing habitats and species types at fine spatial scales in the Southern Highland landscapes of Tanzania: implications on ecosystem services.

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Tanzania is endowed with a number of wildlife species inhabiting different landscapes and ecosystems. The wildlife species constitute part of the biodiversity assemblage in Tanzania and offer various ecosystem services. Some of the recorded habitat types include wetlands, planted trees (pines, eucalyptus), wooded grassland with scattered trees, bamboo forests, montane forests, montane grasslands, agricultural fields and mixed habitats with forest-agricultural land-montane grasslands. All these different habitats are managed differently and in different land categories (village lands, reserved lands, and general/public land), regions and communities. There are various value chains benefits from ecosystem services offered by different wildlife species (e.g. pollinators, decomposers and seed dispersers). At least large mammals (large taxa) are known in the southern highlands. However, little is known about the lower taxa and the valuable ecosystem services they offer. The existing land use and management have implications on habitats as well as species in the southern highlands of Tanzania. Therefore, major gaps for further study will be to: assess how different land management practices affect occurrence and distribution of pollinator species; assess occurrence and distribution of different pollinators (for different crops) in different localities (e.g. butterflies, bats, birds, bees, etc.); and assess occurrence and distribution of decomposers in different sites (e.g. ground beetles). Different methods will be used to study species and their ecosystem services in the study area. The ultimate goal is characterize habitats at fine spatial scales, their potentials on ecosystem services as well as identifying policy options and effectiveness to improve biodiversity conservation.

Mapping Global Protected Areas' Ecosystem Service Values by Benefit Transfer: A Review and Application of Available Methods

Schägnner, Jan Philipp; Weynants, Melanie; Capitani, Caludia; Schmidt, Stefan

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Due to scarcity of land on our planet nature conservation agencies have to defend their protected areas against competing uses. Communicating the ecosystem service value of protected areas is one option to increase their acceptance and to stimulate funding. Representing ecosystem service values of protected areas can also contribute to spatial prioritisation for protected area network extension in light post2020 Global Biodiversity Framework, specifically on value-based opposed to area-based PAs target designation.

However, deriving valid ES value estimates for individual PA is a costly and time-consuming exercise. A quicker and cheaper alternative to primary valuation may be benefit transfer or ecosystem service value mapping, which transfer values derived at some study site to one or several policy sites. Benefit transfer and value mapping has been applied from local to global scale, but its validity and usefulness remains controversial. Transfer errors add to the imprecision in primary ecosystem service valuation, which may lead immense uncertainties in the value estimates. Monetary value estimates may not capture the multiple values and bio-physical conditions of the considered ecosystems.

In this study we review all benefit transfer and ecosystem service value mapping approaches that have been conducted at the global scale and reproduce them to estimate ecosystem service values for each individual protected area worldwide. We compare the results and discuss their divergences, weaknesses, strengths, and policy relevance. Based on our findings, we present a 10-step plan to improve future benefit transfer and ecosystem service value mapping approaches.

An expert-based reference list of variables for characterizing and monitoring social-ecological systems

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The social-ecological system (SES) approach is fundamental for addressing global change challenges and to developing sustainability science. Over the last two decades, much progress has been made in translating this approach from theory to practice, although the knowledge generated is still sparse and difficult to compare. To better understand how SESs function across time, space and scales, coordinated, long-term SES research and monitoring strategies under a common analytical framework are needed. For this purpose, the collection of standard datasets is a cornerstone, but we are still far from identifying and agreeing on the common core set of variables that should be used. In this study, based on literature reviews, expert workshops, and researcher perceptions collected through online surveys, we developed a reference list of 60 variables for the characterization and monitoring of SESs. The variables were embedded in a conceptual framework structured in 13 dimensions that were distributed throughout the three main components of the SES: the social system, the ecological system and the interactions between them. In addition, the variables were prioritized according to relevance and consensus criteria identified in the survey responses. Variable relevance was positively correlated with consensus across respondents. This study brings new perspectives to address existing barriers in operationalizing lists of variables in the study of SESs, such as the applicability for place-based research, the capacity to deal with SES complexity, and the feasibility for long-term monitoring of social-ecological dynamics. This study may constitute a preliminary step to identifying essential variables for SESs. It will contribute towards promoting the systematic collection of data around most meaningful aspects of the SESs and to enhancing comparability across place-based research and long-term monitoring of complex SESs, and therefore, the production of generalizable knowledge.

Session: Ecosystem Services

Poster presentations

Two step approach ecological niche model of invasive algae: *Asparagopsis armata* case of study in Azores archipelago

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We are facing global loss of biodiversity due to climate change. This will lead to unpredictable changes in ecosystems, affecting the goods and services they provide as well as facilitating introduction of non-indigenous marine species (NIMS). NIMS are one of the major threats to marine biodiversity and therefore, there is a strong need to assess, map and monitor these alien species. The apparition of NIMS is especially dangerous in fragile ecosystems and it is of great importance to better understand the invasion mechanisms of these invasive species. This is the case of invasive algae *Asparagopsis armata*, present in Azores archipelago. In this study we propose a methodology to characterize the ecological niche of this invasive algae, alongside the native *Asparagopsis taxiformis*, to better understand its distribution and potential impact on native communities and ecosystem services (ES). These objectives move along EU Biodiversity strategy for 2020 goals and the need of Mapping and Assessment of Ecosystems and their Services (MAES). The lack of reliable high-resolution data makes this task a challenge. Within this scope, we propose a combination of Remote Sensing (RS), Unmanned Aerial Vehicle (UAV) based imagery together with in-situ field data to build ecological niche modelling approaches as a cost-effective methodology to identify and characterize vulnerable marine ecosystems. Our results show that this combination of resources and methodologies can help achieve a cost-effective methodology to monitor and better understand marine species ecological niche and the consequences of NIMS invasion in fragile ecosystems like small islands when facing scarce data scenarios as a first step to achieve MAES in Outermost Regions (ORs) of Europe.

Assessing ecosystem services in African Biosphere Reserves: A review and user-informed classification of existing tools

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African Biosphere Reserves (BR), which are to be living labs for sustainable development, embody the idea of synergies between people and nature. This idea, at the core of the Unesco Man and the Biosphere (MAB) programme, is supported by the concept of 'ecosystem services' (ES), which highlights the linkages between biodiversity conservation and human development.

While the concept of ecosystem services is by now well-known, its translation into actual management decisions is still uneven. Gaining knowledge about ES provision, use and trends in BRs, and the risks that they are facing, are key for sustainable management. An assessment of their social and economic value can provide important leverage to safeguard and manage BRs and their ES, acknowledging the interests of a wide range of stakeholders. This is especially the case in African BRs that are facing high anthropogenic pressures such as rapid population growth, their strong dependence on natural resources for livelihoods, and competing stakeholder interests in challenging governance conditions.

To ensure that ecosystem services contribute to improved decision-making, the assessment of these services -and their contributions to human wellbeing- needs to become systematic, quantifiable, robust and credible. Solid methods to assess and map ecosystem services exist and many decision-support tools have been developed in recent years, but they remain insufficiently known, used and communicated. Their applicability and user-friendliness are often context-, site- and user-specific. Moreover, their application is often limited due to high demands of data, skills, time and resources.

The diversity of rapidly evolving ecosystem services assessment tools requires a systematic and informed selection, in order to ensure that prospective tool users select the most adequate tool, aligned to their needs and context. Some reviews were already performed to classify these methods and analyse their trade-offs. However a review of widely applicable, rapid and affordable tools to assess multiple ecosystem services in the specific context of African BRs, building on the expectations of the prospective users of such tools, was still lacking.

Through a Delphi survey we identified the perspective of prospective users of ES assessment tools (e.g. African BR managers) on management challenges and preferences regarding tool format and objectives. A review of existing ES assessment tools was conducted and ended in a selection of seventeen tools considered the most suitable for the context of African BRs. We propose a user-friendly tool selection process and guidance to users to select the most suited tool for their needs. The selection is based on user-generated criteria such as requirements regarding data input, necessary skills, outputs and types of ecosystem services addressed. The use of the Delphi survey and the focus on African BRs are new elements that contribute to the theory and practice of ecosystem services assessment.

Modelling the impact of agricultural policies on biodiversity and ecosystem services

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Session University Olomouc

Although the goal of protecting biodiversity is strongly anchored at various political levels, the loss of biodiversity is progressing at a rapid pace - a loss that is often associated with irreversible consequences and entails high consequential social costs. Biological diversity is the basis for various ecosystem services in agro-ecosystems and their related natural resources – including food, bioenergy, water and carbon storage and thus essential for human well-being and economic activity. To maintain economic growth, as well as nature’s benefits to people and the livelihoods of 10 million EU farmers, policy instruments and subsidies must be revised and assisted by new indicators that incorporate well-being, environmental quality, employment and equity, biodiversity conservation and nature’s ability to contribute to people. However, existing impact assessment models for agricultural policies, focus on narrow aspects of agricultural economics (e.g. income), do not appropriately address the complexity of decisions made by farmers and ignore the wider impacts of policy on natural, social and cultural assets in rural areas. The four-year RIA BESTMAP – Behavioural, Ecological and Socio-Economic Tools for Modelling Agricultural Policy, funded under RUR-04-2018, will develop a novel modelling framework, using a suite of interoperable and customisable agent-based, biophysical and geostatistical models linked to existing data and remote sensing, to take into account the complexity of farmers’ decision-making. The framework will be operationalized by using co-design workshops, existing georeferenced datasets and the experience of EU institutions, national, regional and local decision-makers, expert personnel and other researchers. The approach will be first developed and demonstrated in five regional case studies across Europe covering heterogeneous agricultural, socio-economic and political backgrounds. Case study results will be synthesised and scaled up to EU level. The poster presents the BESTMAP modelling framework and first results on farmers decision-making.

Session: Ecosystem Structure

Oral presentations

GEO BON's Ecosystem Structure Essential Biodiversity Variables Are Complete: Here's what they look like and why

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The Ecosystem Structure EBV Class is intended to capture the key variables that describe an ecosystem's physical, three-dimensional structure. After much discussion the Ecosystem Structure Working Group converged on three variables, each of which will be discussed in this presentation.

Ecosystem Distribution. This EBV characterizes the horizontal coverage of an ecosystem. In this context "Ecosystem" is broadly defined to include habitats, land cover classes, aquatic biogeographic regions, functional types or any other useful biological category. Understanding where ecosystems (broadly defined) are and how their distribution is changing is a core piece of information for conservation management and a basic input for many derived products. It is a unitless fraction from 0.0 to 1.0 for locations on a grid, though for mixed grid cells coverage fractions for each ecosystem type in the cell can be used if available. Key derived products include ecosystem location, ecosystem size, ecosystem fragmentation, and landscape structure/heterogeneity.

Ecosystem Vertical Profile. This EBV characterizes the vertical distribution of a biological entity in an ecosystem. The specific biological entity can vary—examples include living biomass, dead biomass, Leaf Area Index, or a useful measure of a particular group of plant or animal. It is important because it affects the number, variety, and location of the potential niches that an ecosystem harbors. It also reflects certain aspects of the state of an ecosystem, such as whether it is reproducing or being invaded by a non-native species. It is captured as the value of the biological entity of interest (e.g., biomass in kg/m²) at a variety of different heights from the ground surface or (for aquatic systems) depths from the water surface. Important derived products include ecosystem height or depth, ecosystem vertical complexity, gap size and frequency, and ecosystem layering.

Ecosystem Live Cover. This is the fraction of live cover projected onto a gridded horizontal surface, where live cover is broadly defined as sessile living biomass. This includes, for example, plants, molluscs, coral, and biocrusts, but excludes subsurface organisms such as soil bacteria. It is important because it can be an indicator of recovery after disturbance; it affects erosion, carbon and nitrogen cycles, and an ecosystem's microclimate; and its seasonal variation is an important property for many ecosystems. Ecosystem Live Cover is a unitless fraction from 0.0 to 1.0. Live cover maps are an important derived product, and live cover is an important input to many models.

Mapping Vegetation Structure Gradients in Colombia

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Climate, soils, and land use are among the main drivers of vegetation structure in the tropics. Until recently, our primary source of information on vegetation structure at broad geographic scales has been multispectral satellite imagery. Though invaluable for providing estimates of vegetation cover, such imagery cannot provide measurements of vegetation height or vertical distribution of vegetation in canopies. Here we use dissimilarity modeling with spaceborne lidar data from the Global Ecosystem Dynamics Investigation to map how different elements of vegetation structure respond to environmental and land use gradients in Colombia. We find that different vegetation structure elements respond in different ways across gradients, leading to distinct combinations of climate, land use, and vegetation structure in different parts of the country.

Dynamic Seascape Metrics as Essential Biodiversity Variables: quantifying habitat extent and diversity for the global ocean

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Until recently, understanding the responses of marine ecosystems to environmental change was hampered by the lack of an observational framework to assess the diverse lifeforms, microbes to megafauna, simultaneously with measures of the dynamic fluid matrix within which they live, feed, reproduce, interact, and move. While landscape definitions provide practical boundaries and an observational context of habitat quality, heterogeneity, and extent, pelagic seascape ecology requires a dynamic geographic framework to track changes in an ecosystem that continually changes in extent and location. This framework would help quantify mechanistic relationships between habitat community structure and ecosystem functioning. It would ultimately determine the vulnerability or resilience of pelagic organisms or systems to global change.

We developed such a biogeographic framework of dynamic and synoptic seascapes from satellite- and model-based fields that characterize phytoplankton responses to multi-scale physicochemical changes in surface water masses, complementing static and/or three dimensional classifications such as Ecological Marine Units generated by Esri and the US Geological Survey in the context of GEO BON. As part of the US and global efforts to create a marine biodiversity observation network (MBON), seascapes are validated and extended in time and depth through the integration of in situ bio-optics, long term ecological studies, and marine ecosystem models.

We focus on dynamic seascape metrics as a prototype for marine Essential Biodiversity Variables, particularly for marine ecosystem structure. We document trends and interannual variability of seascape identity, extent, and habitat diversity. We also discuss potential effects of habitat extent and diversity on seascape habitat-species relationships for benthic, planktonic, and forage fish assemblages in subtropical, temperate, subpolar, and polar ecosystems.

Seascape maps are produced in near real-time and served to the community via NOAA CoastWATCH, providing : 1) a biogeographical framework for biodiversity assessments, 2) an objective means to conduct ecosystem comparisons, 3) a means to track movement and habitat usages of marine fisheries, 4) a means to quantify interannual variability in the quality and availability of critical habitats, and 5) a means to identify surface habitat diversity hotspots in the global ocean and examine how these change over time and space.

Using airborne laser scanning to derive Essential Biodiversity Variables (EBVs) of 3D habitat structure at a national scale

Kissling, W. Daniel (1); Koma, Zsófia (1); Meijer, Christiaan (2); Ku, Ou (2); Nattino, Francesco (2); Seijmonsbergen, Arie C. (1); Grootes, Meiert W. (2)

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Monitoring changes in 3D habitat structure is of key importance for conservation, restoration, biodiversity science and policy because the diversity, distribution and abundance of animals, plants and other taxa is tightly linked to the horizontal and vertical structure of their habitats. While Essential Biodiversity Variables (EBVs) of ecosystem structure are advancing, the limited availability of spatially contiguous and temporally repeated measurements of 3D habitat structure still impedes major assessments of habitat modification beyond changes in land cover or ecosystem distribution and extent. Using country-wide, multi-temporal Airborne Laser Scanning (ALS) surveys from the Netherlands from three time slices extending over a >20 years period, we show that massive amounts of data derived from Light Detection And Ranging (LiDAR) technology (an active remote sensing technique) can be used to quantify cover, height, horizontal and vertical variability of vegetation over broad spatial extents and at high resolution in a spatially contiguous manner. We illustrate the application of a novel, free and open-source software tool ('Laserchicken') embedded in a High Performance Computing (HPC) workflow ('lcMacroPipeline') which enables the efficient, scalable and distributed processing of multi-terabyte LiDAR point clouds encompassed of hundreds of billions of individual points. The resulting national, open-access EBV data product is available for biodiversity applications, and the workflow and software is extendable to other computational platforms and ALS datasets. We discuss the limitations and prospects of ALS-based LiDAR EBVs and highlight important steps for the future development of national and regional LiDAR EBV data products.

Structure metrics to generalize biomass estimation from lidar across forest types from different continents

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Forest aboveground biomass is a key variable in remote sensing based forest monitoring. Active sensor systems, such as lidar, can generate detailed canopy height products. Relationships between canopy height and biomass are commonly established via regression analysis using information from ground-truth plots. In this way, many site-specific height-biomass relationships have been proposed in the literature and applied for mapping in regional contexts. However, such relationships are only valid within the specific forest type for which they were calibrated. A generalized relationship would facilitate biomass estimation across forest types and regions. In this study, a combination of lidar-derived and ancillary structural descriptors is proposed as an approach for generalization between forest types. Each descriptor is supposed to quantify a different aspect of forest structure, i.e., mean canopy height, maximum canopy height, maximum stand density, vertical heterogeneity and wood density. Airborne discrete return lidar data covering 194 ha of forest inventory plots from five different sites including temperate and tropical forests from Africa, Europe, North, Central and South America was used. Biomass predictions using the best general model (nRMSE = 12.4%, $R^2 = 0.74$) were found to be almost as accurate as predictions using five site-specific models (nRMSE = 11.6%, $R^2 = 0.78$). The results further allow interpretation about the importance of the employed structure descriptors in the biomass estimation and the mechanisms behind the relationships. Understanding the relationship between canopy structure and aboveground biomass and being able to generalize it across forest types are important steps towards consistent large scale biomass mapping and monitoring using airborne and potentially also spaceborne platforms.

Reconstructing the fine-scale habitat structure of wetlands for biodiversity science and ecosystem mapping

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One of the main challenges in ecology is to derive spatially contiguous information on habitat structure at a fine resolution over broad spatial extent. Although the importance of habitat structure for biodiversity science and ecosystem management has been recognized in the conceptual framework of Essential Biodiversity Variables (EBVs), an operationalization with such information in a standardized way is still lacking. Here, we take advantage of Airborne Laser Scanning (ALS) data which uses Light Detection and Ranging (LiDAR) technology and analyze three different aspects of how the fine-scale habitat structure within wetlands can benefit ecology and national biodiversity and ecosystem mapping. First, we demonstrate for reedbeds along lakeshores how ecological in-situ field measurements of vegetation height, biomass and foliage height diversity, as well as digital photographs of canopy openness, allow us to calibrate ALS-derived data products of 3D vegetation structure within wetlands. Second, we developed a workflow based on country-wide ALS data to classify and map the fine-scale (5 m resolution) variability of land cover and habitat types, using vegetation maps from field surveys as annotation data and tested on a selected Dutch wetland area. Third, we perform a country-wide ecological niche analysis for three closely-related reed warbler species to demonstrate how high resolution (10 m) LiDAR data can gain unprecedented insights into the fine-scale habitat use and niche separation of wetland birds. Our results show that ALS data have great potential for biodiversity science and ecosystem mapping beyond typical forestry applications, e.g. for quantifying, mapping, and analyzing the fine-scale structure of reedbeds and other wetland habitats. Hence, country-wide LiDAR data provide crucial information for mapping and monitoring ecosystem structure and for national reporting of biodiversity status and trends. Our exemplary analyses within wetlands provide suggestions for prioritizing habitat EBVs and for promoting the remote sensing of habitat structure within terrestrial Biodiversity Observation Networks (BONs), even in non-forest habitats.

NextGEOSS's web -based community portal for European habitat suitability modelling for monitoring biodiversity using in situ vegetation plot data and RS-enabled EBVs

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EBVs have been proposed as a layer between biodiversity observation and biodiversity indicators, used in policy. More specifically, EBV classes – such as species traits, species populations, ecosystem functions as well as ecosystem structure – are being implemented by ecologists to identify global monitoring priorities.

To support this there is an urgent need for remote sensing enabled EBVs to fill the spatial and temporal gaps between in situ observation data of biodiversity. In other words, without remotely sensed synoptic, systematic and continuous observations, a global framework for monitoring biodiversity cannot exist. Several RS-EBVs are anticipated to be derived from satellite remote sensing, because satellite remote sensing is the only methodology able to provide a global coverage and continuous measures across space at relatively high spatial and temporal resolutions.

Habitats are very significant as an indicator for biodiversity and habitats have a strong links to species of which many are not being monitored at all. The NextGEOSS habitat mapping suitability interactive web facility (<https://www.synbiosys.alterra.nl>) uses more than 1 million European in-situ vegetation plot data in combination with climate, topographic, soil data, next to RS-enabled EBVs to produce European habitat suitability maps for each EUNIS habitat type (at level 3) using the MAXENT habitat distribution model (HDM). In situ plot observation data (derived from the EVA database; <http://euroveg.org/eva-database>) are available for 160 EUNIS terrestrial habitats . The model can be executed by end-users by making a selection of currently 30 predictors, comprising 7 climate parameters, 7 soil parameters, and 13 RS-EBVs (LULC, vegetation height, Inundation, Phenology, LAI).

For the modelling Maxent version 3.4.1 is used. The habitat suitability model is running in the cloud on Terradue servers. Model raster output can be downloaded by the client for further processing. End-users are invited not only to use the NextGeoss community portal for finetuning European habitat suitability maps but also to give their feedback.

Monitoring the relative magnitude of fragmentation (RMF) at a global scale

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Ecosystem degradation typically leads to habitat fragmentation which alters the quality and connectivity of habitats, creates detrimental edge effects and poses threats to the world's biodiversity and ecosystem functions. Monitoring ecosystem fragmentation is thus of key relevance for biodiversity science and policy. However, quantification of global ecosystem fragmentation is challenging. We use an existing spatially contiguous, global remote-sensing data product (i.e. the 27-year annual ESA CCI land cover maps which can be categorized as an EBV 'Ecosystem Distribution') to derive an annual (27 year) time-series of the Relative Magnitude of Fragmentation (RMF) at a global scale and with a spatial resolution of 300 m. From this derived EBV data product, we then calculate an RMF indicator of ecosystem degradation, i.e. the changes and rate of changes in fragmentation of ecosystems (e.g. forests) over the last 27 years. This can provide important information for measuring biodiversity changes as it directly links to the post-2020 global biodiversity framework of the Convention on Biological Diversity (CBD), especially Goal 1 (no net loss in ecosystem integrity) and the related Target 1 (retain and restore ecosystems). To assess the change in ecosystem fragmentation, we calculate, for every 300 m pixel and its neighbourhood (e.g. all eight adjacent grid cells or all grid cells in a given radius, such as 1 km around a focal cell), a metric that is called the entropy-based local indicator of spatial association (ELSA). This ELSA metric quantifies the relative magnitude of fragmentation of a specific land cover type for each landscape around a pixel. To illustrate the method, we focus on the forest by aggregating the 14 tree cover related land cover types from the ESA CCI product into 'forest' and by measuring its fragmentation relative to the other (non-forest) land cover types. The ELSA metric can be used for both binary and multinomial categorical spatial data and quantifies the degree of fragmentation at each location relative to neighbouring locations, simultaneously incorporating both the spatial composition and the configuration of land cover types. The values of ELSA vary between 0 and 1, denoting lowest and highest fragmentation, respectively. The calculated RMF values of each 300 m pixel can be aggregated (e.g. averaged) at any coarser spatial resolution (e.g. country, national park, region) to summarize trends and the magnitude of ecosystem fragmentation for a specific area across time. The values are also comparable across regions and national boundaries, and thus scalable because they are relative on a scale from 0 to 1. The RMF thereby provides unprecedented insights into the spatial patterns and temporal dynamics of ecosystem fragmentation over the last three decades and offers a promising tool for monitoring biodiversity change at a global scale.

Identifying prioritized forest patches for wildlife connectivity in two urban wetlands of Peninsular Malaysia using dual-stage landscape patches' prioritization approach

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The insufficient baseline data of most fragmented tropical wetlands that support high biodiversity and ecological services within urban settings remains one of the major issues in their management effectiveness. Therefore, it becomes imperative to know the level of habitat fragmentation and develop a novel approach to identify prioritized forest patches and establish corridors to sustain wildlife within this patched and fragile ecosystem. This study aimed to determine the extent of land use/land cover (LULC) classes, compute the landscape metrics at the class and landscape levels and identifying potential wildlife connectivity areas (PWCA) of Paya Indah (PIW) and Putrajaya (PW) wetlands, Peninsular Malaysia. A pixel-based image classification method, LecoS plugin and Conefor package in QGIS and ArcGIS software were employed for image classification, landscape metrics' computation and nodes/distance files' creation respectively. The nodes prioritization involved a dual-stage prioritization approach (Arithmetic Mean and Corridor Analysis) to determine the PWCA. A total number of 5 and 4 LULC classes were identified in PIW and PW respectively. It was observed that the semi-closed secondary forest occupied the highest LULC mass in PIW (391.77ha, 24.80%) and PW (395.79ha, 27.87%). A total number of 24 landscape metrics were computed at both class (18) and landscape (6) levels. At the class level, marsh swamp/lotus swamp vegetation (1,958) and lake (2,100) had the highest number of patches in PIW and PW respectively. Overall, PW recorded a higher number of highly prioritized nodes (207) and a total number of nodes (1,921), than PIW. In contrast, PIW recorded higher overall connectivity indices than PW. Thus, the landscape of PW is highly fragmented than PIW with the PWCA of both sites situated at their northern edges. It is recommended that these areas should be adopted as priority conservation areas for forest restoration programmes to create wildlife corridors within the two fragmented wetland ecosystems.

Global Data On The Annual Extents Of 69 Terrestrial, Marine, And Freshwater Ecosystem Types Over Three Decades

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Widespread changes in the area, fragmentation, and integrity of ecosystems are a major driver of biodiversity change and loss of ecosystem services worldwide. These changes are expected to further accelerate under future land-use and climate changes, potentially leading to widespread environmental degradation and socioeconomic hardship. Detailed information on global, spatiotemporal dynamics in the extents of major ecosystem types is thus essential to understand, anticipate, and address a broad range of environmental problems. Accordingly, the Group of Earth Observations Biodiversity Observation Network (GEO BON) identified the development of global data products on ecosystem extents as an Essential Biodiversity Variable, and a priority for global biodiversity monitoring. We will present a series of global, high-resolution gridded data cubes that capture the annual areas of occupancy for each of 69 standardized terrestrial, marine, and freshwater ecosystem types over a 27-year period. To achieve this high thematic detail, we built on decades of global environmental mapping efforts by integrating 24 global products and 59 derived variables (>100 TB in total, mostly remote-sensing derived) covering land-cover, hydrology, climate, elevation, coastal and stream topography, soil, and other environmental dimensions. The depicted ecosystem types conform to the habitat classification scheme of the International Union for Conservation of Nature's Red List of Threatened Species, assuring interoperability with ongoing assessments of the species habitat preferences. Exemplary application fields include monitoring of species habitats to support conservation interventions, testing hypotheses on biodiversity-change drivers and mapping of global ecosystem services. We will characterize recent dynamics in selected ecosystems to showcase the potential of the presented datasets, which will be published soon as open-access products following FAIR principles.

A New Map of World Terrestrial Ecosystems at 250 m - Ecosystem Extent Data for the Planet

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Under commission to GEO, and within the framing of GEO ECO (GEO's Ecosystems Initiative), the U.S. Geological Survey, Esri, and The Nature Conservancy have collaborated to produce a new 250 m World Terrestrial Ecosystems (WTEs) map and associated tools for leveraging the data. The ecosystems were mapped using a structure-based approach that identifies unique expressions on the landscape of climate regime, terrain diversity, and macroscale vegetation assemblages. There are 431 WTEs at the globally aggregated level, or 1778 WTEs when disaggregated by biogeographic realm (e.g. Neotropical, Australasian, etc.). Each ecosystem is composed of multiple spatially explicit occurrences on the landscape, enabling the calculation of Ecosystem Extent (an Essential Biodiversity Variable in the Ecosystem Structure EBV group) for any area of interest ranging from a local protected area to the entire planet. The new WTEs differ from the global ecological units (ELUs) that were produced by USGS and Esri in 2014 in both number/level of aggregation (the WTEs are fewer and more generalized than the ~4000 ELUs) and derivation (IPCC and FAO criteria were used to develop the WTE classes). The data are freely available in the public domain and as an Esri Living Atlas resource. The Nature Conservancy are using the WTEs as the basis of their organization-wide geographic priority setting.

Global patterns of tropical forest fragmentation

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Remote sensing allows for the quantification of global deforestation with high spatial resolution and enabled us to achieve substantial advances in the analysis of the continental-wide fragmentation of tropical forests. We identified roughly 130 million forest fragments in three continents that show surprisingly similar power law size and perimeter distributions as well as fractal dimensions. Power law distributions have been observed in many natural phenomena like wild fires and earth quakes. Here, the principles of percolation theory provide one explanation for the observed patterns and suggest that forest fragmentation is close to the critical point of percolation. Simulation modelling supports this hypothesis and reveals that the observed patterns do not only emerge from random deforestation (as described by percolation theory) but also from a wide range of deforestation and forest recovery regimes. Predictions of our models outline that additional forest loss will strongly increase the total number of forest fragments (maximum by factor 33 over 50 years while fragment sizes decrease) – a consequence that can be only partly mitigated by reforestation and forest protection.

Empowering Local Biodiversity Action from a Global Perspective: a Roadmap to Derive Ecosystem Morphological Traits from LIDAR data

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LIDAR technologies are regarded as essential for monitoring biodiversity assets, thanks to their capacity to deliver information on ecosystem structure, which is key to determining species distributions and ecological niches. However, handling and processing LIDAR requires a high level of specialization, and often high computing performance capabilities too. In Valbuena et al. (2020) we suggested a sensor- and platform-independent framework for standardizing morphological traits of ecosystems that can be extracted from LIDAR datasets. Our proposal was to effectively digest LIDAR datasets, as well as other sources of 3D remote sensing data, into a set of simple and concise indicators of ecosystem structure – height, cover and structural complexity – that may be easily understood and employed by non-specialized conservationists and other interested stakeholders. Available satellite LIDAR include the Global Ecosystem Dynamics Investigation (GEDI) and IceSAT-2 missions, currently completing the first comprehensive global collection of LIDAR data. However, the use of available satellite LIDAR data faces critical limitations to effectively provide information useful for Essential Biodiversity Variables (EBVs): (1) satellite LIDAR is based on the acquisition of discretely sampled pulses; (2) satellite LIDAR missions are not designed to revisit any given location twice; (3) there is no planned further deployment of satellite LIDAR sensors before 2030. For these reasons, we advocate to generate a system flexible enough to incorporate publicly-available airborne LIDAR data from national surveying programmes. The combination of satellite and airborne LIDAR for global assessments over long periods of time would imply a vast amount of information difficult to handle in practice. The way forward is to develop tools that can facilitate national BONs to independently derive globally-consistent standardized EBV products from LIDAR datasets. This would enable a crowdsourced computation of ecosystem structure EBV products, which can then be used to feed the GEO BON portal for global assessments. In our roadmap we propose that the derivation of ecosystem traits from satellite LIDAR would set a precedent for the airborne LIDAR to follow, and merging workflows with open-source software tools like rGEDI (Silva et al. 2020) or Laserchicken (Meijer et al. 2020) to enable processing of LIDAR data at global scales and sustained over time. In the context of the new global biodiversity framework 2021-2030, such an approach will not only help monitoring against global biodiversity targets but also inform local conservation and restoration priorities and decision making based on up-to-date ecosystem structural information.

Meijer et al. (2020) Laserchicken - A tool for distributed feature calculation from massive LiDAR point cloud datasets. *SoftwareX* [under review].

Silva et al. (2020) rGEDI: NASA's Global Ecosystem Dynamics Investigation (GEDI) data visualization and processing. <https://CRAN.Rproject.org/package=rGEDI>

Valbuena et al. (2020) Standardising Ecosystem Morphological Traits from 3D Information Sources. *Trends in Ecology and Evolution* [in press]. <https://doi.org/10.1016/j.tree.2020.03.006>

Essential Biodiversity Variable Fragmentation

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GlobDiversity is the first project designed to develop and engineer RS-enabled EBVs. Reducing the rate of habitat loss and fragmentation is essential to protect biodiversity and to maintain the ecosystem services vital to human wellbeing (Aichi-Targets 5,14). Fragmentation is related to the EBV 'Ecosystem structure'. Monitoring EBV-Ecosystem-structure can be supported by remote sensing through the collection of information on the spatial distribution of habitats, how fragmented they are, and the impact on the distribution of species in those habitats. EBV-Fragmentation is defined as: "The EBV-Fragmentation should measure structural ecosystem discontinuity in a defined time-space. This can include connectivity, core, and edge characterizations, calculated across a range of scales as long as the EBV is globally applicable, scale-free, and ecologically meaningful". There is broad recognition that fragmentation affects both biodiversity and ecosystem functioning. The fundamental role of habitat in limiting species richness is emphasized by the fact that habitat loss is causing habitat fragmentation, and is the main cause of declining biodiversity worldwide.

Our implementation of the EBV-Fragmentation uses the LARCH-SCAN-Hanski-metric and focuses on the effects of dispersal on persistence of organisms across habitat types. This can be calculated as a stack of spatial-temporal metrics based on multiple dispersal distances and (remotely derived) habitat types. The metric uses a formula that describes dispersal curves of birds which is applied for measuring connectivity in metapopulation models (Hanski, 1994). Habitat further away is accounted for less than habitat nearby, using Hanski's negative exponential function for cohesion ($e^{-\alpha d}$); using a species specific dispersal capacity and distances between cells. The spatial cohesion of a habitat cell is determined by weighting the carrying capacity of all cells within the potential dispersal distance. The spatial resolution will vary by the used product.

Calculation is based on a sequence of steps: First a habitat input map is generated. Habitat can be selected from remoted sense based land cover products, directly or by combining them though pre-processing. In the next step, to serve a variety of species ranges, the LARCH SCAN-Hanski-metric is calculated for each habitat-class from a chosen product. This is creating Individual output cohesion maps, which can then be combined to represent the habitat/species of choice. To suit the specific dispersal capacity of species, fragmentation was calculated using four different distances: 500m, 1000m, 5000m and 10000m. Last step derives clusters of connected habitats cells, to construct ecological networks. Based on the thresholds given by Rybicki & Hanski (2013) metapopulation processes start when the ecosystem is less than 20% present in the landscape. This corresponds with values of 0.2 in the LARCH-SCAN-output-maps, but species- and scale specific thresholds can be used. Cohesion maps can be used for planning corridors between local patches or to improve weaker spots in networks

Session: Ecosystem Structure

Poster presentations

Potential areas with attributes of high conservation value in the Guachochi region, Chihuahua, Mexico

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Currently, the study of Areas with Attributes of High Conservation Value (AcAVC) is linked to the management and conservation of biodiversity in the National Strategy for Sustainable Forest Management for the Increase of Production and Productivity. The objective of the study was to identify the potential areas with high conservation value attributes in the Guachochi region. The results estimate that the AcAVC1 links a RAMSAR site "Humedales de Guachochi" in 57,515 ha, the sites Sehuerachi, Yoquivo, Tatahuichi, Tuceros, Tonachi, Papajichi, El Retiro and La Gloria contain remaining forest of *Pseudotsuga menziesii* on 78.85 ha in addition to *Abies durangensis* having 10.1 ha. AcAVC2, ecosystems and mosaics at landscape scale, there are proportions of three Priority Land Regions (RTP), where the last remnants of the mature pine-oak forest are documented. For the AcAVC3, ecosystems and habitats, the network of riparian areas estimated 31,510 ha, 209.3 ha have a germplasm producing unit; the AcAVC4, ecosystem services estimated 105,246 ha; the AcAVC5, needs for the local communities, has 39,090 ha, and as AcAVC6, cultural values for the development of meetings and rituals in the worldview of the Rarámuri ethnic group, there are 115 ha in the localities of Norogachi and Sehuerachi.

Session: Community Composition

Flash presentations

Climate change and long-term modifications of fine-scale butterfly assemblages in the Western Italian Alps

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Climate change takes place at a faster pace at higher elevations, such as in the Alps where some sites experienced temperatures increasing of over 2°C in the last decades. These modifications can lead to corresponding changes in ecosystems and in the way species distribute in space and therefore interact with each other in communities.

This study focused on a fine-scale area community of butterflies, located in the Valasco valley in the Maritime Alps (NW Italy). This community was monitored for more than 40 years, aiming to understand whether species composition was modified as an effect of climate change. In 2019, seven plots located at different elevations, ranging from 1200 to 2200 m asl and representing different habitats, have been surveyed with semi-quantitative transects every two weeks, for the whole flight period. More limited monitoring activities were also performed in 2009 and 1978. Changes in climate conditions and trends of representative climatic variables in the last 60 years have been analyzed on a fine-scale resolution of 25 meters, coherent with the butterfly use of landscape. These data have been derived by statistical downscaling of the gridded Optimal Interpolation dataset developed by ARPA Piemonte, based on a large set of nearby meteorological stations and the ERA-40 re-analysis.

Results indicate that the Valasco valley experienced considerable climate modification in the last 60 years, such as a prominent positive trend in maximum daily temperature, with an increase of almost 3°C. Butterfly data, alongside, showed a significant increase of generalists and, partially, thermophilous species, supporting the hypothesis that local warming has affected the butterfly assemblages.

Temporal changes in benthic community composition and functional space in South Atlantic rocky reefs

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Throughout the world, coastal systems are under human occupation pressure. The monitoring of these ecosystems is crucial, and the establishment of standardized monitoring methods allows building solid baselines to understand the natural variability and differential susceptibility reef communities to local and global drivers. We evaluated the changes in relative benthic cover in subtropical rocky reefs in Brazil using widely applied ecological indexes (richness, Shannon index, Pielou evenness and Simpson index), taxonomic distinctness and functional measurements (functional richness, divergence, evenness, and Rao's entropy). The benthic community was sampled using digital images (30 x 30 cm) taken from three sites at two depth (3 and 6 m) quarterly from 2017 to 2019. Across two annual cycles of upwelling and downwelling, we evaluated which indicators captured the variation in the composition of benthic communities. Our aim was to test if broader and simple indexes would be able to capture the main temporal changes in dominant taxa as well as more complex approaches (functional indicators). The richness of species, species composition and taxonomic distinctness changed along the two years of monitoring with greater variation associated with periods of stronger upwelling. However, among the classical and functional descriptors, the same temporal changes were only reflected in the variation of species evenness (Pielou) and functional divergence (FDiv). The observed changes were mainly associated with the substitution in the dominance of macroalgae taxa, especially brown algae (*Sargassum* sp.). The massive contribution of macroalgae to the benthic community reinforces the importance of this Essential Biodiversity Variable, but the temporal substitution of species with similar functional attributes may pass undetected by some ecological indicators. Despite accounting for short-time changes, the effects of the upwelling bring substantial changes to environmental conditions which were evident in macroalgae assemblages, but such temporal shift in dominant species did not affect the community total functional space.

MBON activities in the Gulf of Maine support prediction of North Atlantic right whale foraging patterns

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The Gulf of Maine (GoM) is located at the southern margin of the North Atlantic Subarctic Biome. In the past decade the GoM has experienced rapid warming and other oceanographic changes that can be linked to climate change at larger basin scales. The North Atlantic Subarctic Biome is characterized by dominance of large lipid rich calanoid copepods that provide the foundation for higher trophic levels pelagic ecosystem. These copepods are remarkably successful in the seasonal subarctic conditions, storing lipids from phytoplankton in oil sacs that make up >50% body mass allowing to overwinter. Lipid-rich calanoid copepods are the primary food for North Atlantic right whales (NARW) and for forage fish such as herring and sand lance eaten by cod and other groundfish, tuna, seabirds and marine mammals.

The MBON Gulf of Maine project supports time series observations of plankton biodiversity at subannual scales, identified as a crucial gap for understanding phenological and long-term change in the Gulf of Maine pelagic marine ecosystem. The project also contributes to the development of statistical and dynamic models using MBON project and other data sources to understand and predict the Gulf of Maine lipidscape, which is primarily determined by the large lipid rich copepods. These lipidscape predictions have direct application as a data layer in models predicting NARW foraging habitat, contributing to inform management decisions about right whale foraging distribution related to regulation of shipping lanes and entanglement in fishing gear.

Session: Community Composition

Oral presentations

Assessment of eDNA as a biomonitoring tool for vulnerable deep-sea habitats

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High-throughput sequencing of targeted “barcode” loci in DNA extracted from marine environmental samples such as water and sediments (metabarcoding of environmental DNA, or eDNA) has exploded in popularity over the last few years due to the ability to generate a taxonomic community profile that usually surpasses what is obtainable from using traditional monitoring methods in terms of biodiversity and detection of rare taxa. Indeed, given the existing poor biodiversity inventory of many marine habitats coupled with their high cost and difficulty of access, eDNA biomonitoring of these remote ecosystems is attractive if reliable taxonomic inventories are obtained for a modest cost and with little required sample material. As part of the DEEP SEARCH (DEEP Sea Exploration to Advance Research on Coral/Canyon/Cold seep Habitats) project, we collected water samples from eight JASON2 Remotely Operated Vehicle dives using two identical 12L Niskin bottles at sites within canyon, cold-seep, and cold-water coral reef habitats along the U.S. Atlantic coast in April 2019. Use of an ROV allowed controlled water sample collection near features of interest. Duplicate samples of one liter of seawater filtered through a 0.2 μm Sterivex and ten liters of seawater filtered through a 0.8 μm cellulose nitrate filter were collected from each Niskin. Metabarcoding of microbial 16S rRNA and metazoan 18S rRNA sequences from eDNA extracted from water samples were performed on an Illumina MiSeq. The 1L and 10L samples recovered largely the same communities on each dive, and did not differ significantly in patterns of alpha richness. Differentiation among habitats in both microbial and metazoan community structure evidenced through multiple ordination and comparative analyses was clear, with the strongest differentiation between the shallow (~200m) and deep (~2000m) cold seep habitats. The implications of our findings for biomonitoring in the deep sea, as well as plans for expanding our analyses to include other barcode loci and water column samples collected via CTD, will be discussed.

Mapping tree diversity in the tropical forest region of Chocó-Colombia

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Developing methods to map diversity in tropical forests is indispensable for the sustainable exploration, use, and conservation of these habitats. However, the lack of maps showing forest structure for large areas is a main restriction to building maps of diversity in tropical forest regions. We developed a methodology to map α -diversity of trees in tropical forest regions at high spatial resolution (50m) using α -diversity estimations of inventories as response variables and forest structural metrics and environmental variables as predictors. To include the forest structural metrics in our models, we developed a method to map four of these metrics integrating LiDAR, multispectral, and SAR imagery. We evaluated these methods to map α diversity of trees in the Chocó region of Colombia (South America), a lowland tropical moist forest with high tree diversity and complex forest structure. We found that the relative errors (RE) of the Random Forest models used to map the four forest structural variables ranged from low to moderate; 11.7% for Vertical Canopy Heterogeneity, 14.3% for Canopy Height, 15% for standard deviation of normalized heights, and 17.4% for coefficient of variation of normalized heights. The maps of α -diversity also presented REs from low to moderate; the maps of Simpson and Shannon diversity indices obtained the lowest REs (6% and 13%), the map of richness had moderate RE (23%), and the maps of the effective number of species Shannon and Simpson presented the highest REs (47% and 64%). We also found that the northeast and the southern side of the Chocó Region tended to have lower tree α -diversity than the central areas. The highest concentration of tree α -diversity is located along the pacific coast from the center to the northwest of the Chocó Region. We used open resources (software and imagery), except for the LiDAR data, in our analysis. In 2020 data from LiDAR GEDI (Global Ecosystem Dynamics Investigation lidar) will become available to any user. Thus, our methods can be applied to monitor the tree α diversity of any tropical forest using GEDI data.

DNA collected from environmental samples reveals the diversity of extant mammals in a suburban reserve in California

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In conservation, faunal diversity surveys are essential to document eventual changes in diversity and abundance over time. They are, however, time-consuming, expensive, and usually detect a limited number of species. As an alternative to existing survey methods, conservation biologists are exploring Environmental DNA (eDNA), the collection of DNA from samples such as dirt or water, as one of the most promising tools for biodiversity surveys. Once DNA is extracted from the sample, it is sequenced and compared to databases in order to find out which species these DNA fragments belong to. While this may sound rather straightforward, many unknowns and issues are preventing eDNA from going mainstream. For example, we do not know how long the DNA stays detectable in the environment or how frequent a species must be to be detected. Most importantly, comparison with existing approaches are necessary, yet is lacking for terrestrial mammals.

In our study, we compared the detection of terrestrial mammals using eDNA analysis of soil samples against confirmed species observations from camera-traps. We took advantage of the ongoing long-term (~9-yr) camera-trapping study conducted at Jasper Ridge Biological Preserve, California, and found that all mammals regularly recorded with cameras were detected in eDNA. In addition, eDNA reported many unrecorded small mammals whose presence in the study area is otherwise documented. We also found that a longer DNA metabarcode achieved a similar efficiency as a shorter one, enabling a higher taxonomic resolution and meaning species were identified from these DNA fragments, as opposed to genus or family only.

These encouraging results support that eDNA-based monitoring should become a valuable part of ecosystem surveys. Unfortunately, we also report that the majority of known mammals are missing from reference databases, therefore hindering the applicability of this novel technology worldwide.

Exploring the Diversity of Zooxanthellae associated with Corals of Perhentian Island Marine Park by Deep Sequencing Approach

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Reef corals are hosts to a group of exceptionally diverse dinoflagellate symbionts in the family Symbiodiniaceae, consisted of numerous genetic “clades” that are now partitioned into a total of seven genera. These symbionts are critical components of the coral reef ecosystem. Loss of these symbionts in their coral hosts during the stress-related “bleaching” events can lead to mass mortality of the coral hosts and collapse of the associated reef ecosystem. Therefore, it is essential to characterize the partnership between the coral hosts and the zooxanthellae genetic clades. In this study, a total of 24 samples from 14 genera of reefal corals were collected from Perhentian Islands Marine Park, Terrengganu, Malaysia. The scleractinian corals collected consisted of *Acropora*, *Galaxea*, *Symphyllia*, *Platygyra*, *Diploastrea*, *Turbinaria*, *Favites*, *Favia*, *Porites*, *Leptoseris*, *Pachyseris*, *Fungia*, *Hydnophora*, *Echinopora*, *Pocillopora*, *Tubastrea*, and *Pectinia*. Here, we applied next-generation sequencing of the nuclear-encoded ribosomal RNA gene in the second internal transcribed spacer (ITS2) region to elucidate the genetic diversity of this dinoflagellate endosymbionts. Our findings showed the expected dominance of Clade C (genus *Cladocopium*) which constituted a great proportion of the coral species examined. Interestingly, Clade D, the genus *Durusdinium*, which is the stress-tolerant phylotype was also found to be dominant in several coral species (*Diploastrea*, *Pocillopora*) from Perhentian Islands. The outcomes of this study provide insights and baseline of the degree of biodiversity these algal endosymbionts possessed and their potential adaptive capabilities in our waters.

Slope exposure shapes fungal deadwood communities and their interaction with nitrogen-fixing bacteria

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Deadwood represents an important temporary carbon pool in montane ecosystems. Fungi and bacteria are cornerstone members of communities driving biochemical cycles and the occurrence of bacterial-fungal interactions can translate to major consequences for deadwood decomposition dynamics, soil carbon balance and, in turn forest productivity. However, climate influence on wood inhabiting fungi (WIF) community and their interactions with bacteria are still poorly understood. Therefore, we set up an in-field mesocosm experiment in the Italian Alps and monitored the effect of slope exposure (north- vs. south-facing slope) on the decomposition of *Picea abies* wood blocks and their microbiome over two years. Unlike fungal richness and diversity, there were significant compositional and functional differences in the WIF communities as a function of exposure during the two-year observational period. We observed that the enhanced decomposition of *P. abies* deadwood at the south-facing slope was accompanied by a higher abundance of wood-degrading operational taxonomic units (OTUs) such as *Mycena*, and a higher prevalence of mycorrhizal and endophytic OTUs. In contrast, Mucoromycota, primarily *Mucor*, and mixotrophic basidiomycetes with limited lignin-degrading capacities were more abundant at the northern slope. The colder, more humid conditions and prolonged snow-coverage at north exposure likely influenced the development of the wood-degrading microbial communities. Moreover, networks between WIF and N₂-fixing bacteria were composed of higher numbers of interacting microbial units and showed denser connections at the south-than at the north-facing slope. Nitrogen availability in deadwood is highly restricted, suggesting that WIF may take advantage from associations with N₂-fixing bacteria to meet their N requirements for vegetative growth and propagation. As such, the association of WIF to N₂-fixing Burkholderiales and Rhizobiales could have provided additional competitive advantages, especially for early wood colonization at south exposure.

Optimizing large-scale biodiversity sampling effort: towards an asymmetric and unbalanced data collection approach

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Understanding the distribution and abundance of life in the ocean is challenging because acquiring marine biodiversity data is difficult, costly, and time consuming. This typically limits sampling to relatively small areas or point sites. Historically, approaches to biodiversity sampling have advocated for equivalent effort across multiple sites to minimize comparative bias. When effort cannot be equalized, techniques such as rarefaction have been applied to minimize biases by reverting diversity estimates to equivalent numbers of samples or individuals. This may result in oversampling and wasted resources, or poorly characterized communities due to under-sampling.

What is the optimal sampling effort to characterize species composition and biodiversity?

Researchers from seven countries of the Americas have teamed up as part of the Marine Biodiversity Observation Network Pole to Pole of the Americas (MBON Pole to Pole) to survey rocky shore macro invertebrates and algal communities from 16 localities. They apply fixed-coverage subsampling techniques to evaluate biodiversity based on effort. The goal is to determine whether more or fewer samples are required to capture the level of biodiversity at a particular location. The network also used multivariate dissimilarity metrics based on randomized resampling methods to determine the minimum number of samples needed to characterize community composition at < 10 % multi-variate standard error (multi-se). Results show that oversampling varied between 25 % and several fold the minimum required value to estimate species richness at the high and mid-tide level of ~ 47 % of the localities. Multi-se analysis also showed that the majority of the localities were significantly oversampled for community composition.

Our toolkit advocates for an asymmetric and unbalanced sampling approach to support field programs in the collection of high-quality data with minimum effort. This approach can guide resource optimization strategies to effectively expand the geographic footprint or sampling frequency of biodiversity survey programs.

Assessment of coastal fish communities and benthic habitats using unbaited underwater video: from data collection to EBV data products

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Tracking progress toward the conservation of marine biodiversity and sustainable development goals requires assessments at spatial scales that are relevant for management actions. Scales are multiple and embedded, ranging from locally managed areas (e.g. Locally Managed Marine Areas), to national networks of Marine Protected Areas (MPAs), up to global reporting scales for international conventions and treaties.

Essential variables related to habitats and high trophic levels such as fish communities include fish abundance and distribution, biotic cover and composition according to the Essential Ocean Variables (EOV) view, and species distribution, taxonomic diversity, population abundance and structure, habitat structure and ecosystem composition and function under the Essential Biodiversity Variables (EBV) view. In both cases, assessing changes in these variables involves in situ measurements able to identify, count and measure of both fish species and habitat covers.

In coastal areas, anthropogenic pressures are intense and spatially organized, and benthic habitats are heterogeneous, both locally and at larger scales. Monitoring-based assessment of fish communities and benthic habitats in such areas generally suffers from a poor spatial replication, which makes the area-wide assessment of key biological components quite challenging. Issues for appropriate monitoring comprise cost-efficient and standardized observation protocols and data formats, spatially-scalable data workflows, compliance of data with the FAIR (Findable, Accessible, Interoperable and Reusable) principles, and minimizing the environmental impact of measurements, particularly in MPAs.

Underwater optical imagery has been more and more used over the last years as a non-obtrusive observation means for conspicuous biodiversity components. This paper presents the data obtained from a remote panoramic unbaited video technique developed from 2007 to survey both fish and habitat in a cost-efficient manner, and with no effect on the observations nor on the environment. The technique was consolidated, standardized and implemented in various ecosystems, both coral reef and temperate, and is now fully operational. We describe the protocol developed and the observations collected in the Pacific, the Indian Ocean and the Mediterranean, amounting to ca. 5000 concurrent observations of both fish (and marine turtles) and, biotic and abiotic benthic cover. Many observations could be collected in diverse habitats because field implementation is easy and fast, and because no diving nor scientific expertise was required on the field, meaning also that rangers and local communities may be involved.

We present the standardized procedure and workflow developed for field work, data curation and data management, image analysis, quantitative assessment and knowledge dissemination. The relevance of the workflow and data to the assessment of EBVs and EOVs related to fish and habitat is illustrated from data collected in New Caledonia.

Evaluating the use of underwater passive acoustics for assessing soundscape diversity

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Marine soundscapes have been recently used as a tool to passively monitor marine biodiversity in a wide variety of habitats. However, there is still a gap in knowledge in terms of how soundscape measurements relate to other biodiversity monitoring tools. Here, we evaluate the use of passive acoustic hydrophone data of ambient biological noise as a metric of soundscape biodiversity by comparing these data with paired measurements of fish biodiversity from remote video surveys, acoustically tracked animals, remotely sensed Essential Ocean Variables (EOVs), and thematically classified seascapes. Soundscape data will be collected from hydrophones strategically paired with acoustic telemetry receivers that are part of an array located in Biscayne Bay, Florida. The location of these hydrophones will allow for sampling along an urban gradient from downtown Miami to Biscayne National Park. The pairing of soundscape data with fish surveys, animal telemetry, EOVs, and seascapes will not only provide an operational framework for how these data can be coupled in future applications, but also allow for soundscape analyses along an urbanized gradient.

Seasonal climate and game density drive life-form composition in the southern Kalahari – results of 15 years of vegetation monitoring

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Climate change projections forecast strong temperature increase and a shift in seasonal precipitation for the southern African Kalahari. Population growth might lead to an increasing demand for land to farm with domestic livestock or game for income generation. In order to assess the potential impact of increasing land-use pressure and climate change on the biodiversity, the regional observation network SASSCAL ObservationNet established one of the biodiversity observatories (1 km²) of the network in the South African Kalahari to monitor the vegetation response to the environmental drivers.

Vegetation monitoring was conducted on 20 randomly selected permanent plots (100 m²) within the biodiversity observatory. For each plot individuals per species (abundance) were counted annually and grouped into eight life-form types (annual and perennial graminoid and forb, geophyte, dwarf and large shrub, tree). We calculated GLMM models (glmmTMB) with abundance per life-form type as response variable and seasonal SPEI, total annual rainfall, year, density of large game and springbok as fixed effects, plot as random effect and year as random slope.

Seasonal SPEI and density of game had the strongest effect on abundance per life-form type. Annual rainfall did not show any effect. The grazing large game had positive effects on the abundance of herbaceous life forms and dwarf shrubs. The predominantly browsing springbok had negative effects on perennial forbs, dwarf shrubs and trees. Directional trends in abundance per life form over time (increase of annual and decrease of perennial graminoids and forbs, as well as increase of large shrubs) suggest early stages of vegetation degradation and shrub encroachment, in response to both, herbivory and climate.

Our study showed that studies which aim to understand the dynamic of arid systems should include both, variance of intra-annual climatic conditions and herbivore density as environmental drivers, related to abundance per life-form / strategy type to reveal their specific responses to the environment.

Discriminating diatom and non-diatom phytoplankton from space

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Phytoplankton community composition is an essential biodiversity variable for aquatic ecosystems. This variable can be detected optically and remotely through the spectral shape of the light absorption coefficient of phytoplankton assemblages, $aph(\lambda)$, which varies with the community composition owing to interspecific differences in size and pigments. In coastal waters, however, remote sensing of $aph(\lambda)$ is subject to significant interference from other pigmented matter including iron-rich minerals and suspended humic particles. To improve the accuracy of satellite-derived $aph(\lambda)$, here we use the generalized stacked-constraints model (GSCM) [Zheng et al., *J. Geophys. Res.*, 2015] which allows the partitioning of satellite-derived total light absorption coefficient of seawater using more realistic spectral shapes for various absorption components. Matchups between $aph(\lambda)$ data derived using this approach and field-measured chlorophyll concentrations in the Chesapeake Bay suggest that in this region variability in the red-to-blue $aph(\lambda)$ band ratio, $aph(670):aph(440)$, is driven mainly by accessory pigments as opposed to cell size. Further, we show that this ratio can be used as a surrogate of diatom fraction of phytoplankton for Chesapeake Bay waters where diatom predominates almost year round. This conclusion is supported by a good correlation between satellite-derived $aph(670):aph(440)$ and field-measured phytoplankton cell counts data. In addition, seasonal cycle of diatom fraction as indicated by satellite-derived $aph(670):aph(440)$ is also consistent with literature reports for this region with stronger diatom predominance in spring and weaker in summer. These results highlight the effectiveness of using the GSCM-based approach to extract phytoplankton type information from satellite data for optically complex coastal waters.

Session: Community Composition

Poster presentations

Ryazan Region is a model territory for monitoring changes in the entomocomplexes of Central Russia.

Nikolaeva, Anna

Oka State Reserve, Russian Federation

Ryazan region is unique. It is located in three natural zones. Feather grass steppes and elements of the southern taiga are located here, because the entomofauna of the region is very diverse. Only in the list of invertebrates of the Oka Reserve includes about 4000 species. To inspect the territory and identify new and rare species, employees go on expeditions in the Ryazan region. Now we have accumulated material on invertebrates that are rapidly changing the northern boundary of the area. For example: *Argiope bruennichi* (Arachnida, Araneidae), *Mantis religiosa* (Dictyoptera), etc. Such species as *Scolia hirta*, *S. maculata* (Hymenoptera), *Melanargia russiae* (Lepidoptera) and others have become common now. Among the new species, there are potential pests, for example: *Cameraria ohridella* (Lepidoptera). We propose to identify key territories in various natural zones of the region and annually systematically monitor changes in the composition of the entomofauna (mark new species, make insect counts and determine change in habitats).

Beyond common biodiversity indices: a comparison of photo quadrat and insitu methods in rocky intertidal habitats in the Gulf of Maine

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Intertidal surveys have always been strategically challenging because they are bounded by wave conditions and the duration of the receding tide. But with rapid changes in the environment from climate change, there is an increasing need for intertidal surveys and biodiversity assessments that can be conducted quickly to monitor the impacts of climate change on biodiversity, particularly before and after extreme events. While tools such as photography can enable rapid assessments, the effectiveness of using photographs to identify biodiversity patterns is uncertain, especially so in habitats with complex topography. Our study compared biodiversity assessments of the rocky intertidal invertebrates and algae in the Gulf of Maine, using both in situ and photoquadrat methods. We found significant differences between survey methods in their prediction of standard biodiversity indices (species richness and Shannon Diversity index) where in situ methods identified higher biodiversity. However, when species composition was examined using multivariate analysis, we found no significant differences between the methods. Rather, we found that insitu quadrats are more adept at picking up on highly mobile species. Regardless, there still exist tradeoffs between both the different methods available as well as the analyses. Photo quadrats allot more time to identify species while insitu quadrats are superior in finding highly mobile species. And although our biodiversity results picked up on more species, our multivariate analyses produced highly overlapping plots which made it difficult to discern which method, if any, was more capable of picking up on less commonly observed species. This study suggests that common measures of biodiversity used by many ecologists use today do not always tell the full story, and argue that tradeoffs need to be considered carefully with regards to which method may be best.

Session: Species Populations

Flash Presentations

Integrating different survey data to estimate the national population size of willow ptarmigan in Norway

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A major challenge for ecologists is large-scale predictions of species' abundances and distributions based on scattered datasets. However, hierarchical modelling provides many opportunities to statistically connect different types of data in the same analytical framework. Here, we use the example of willow ptarmigan in Norway to show how different survey datasets can be integrated to predict the nation-wide distribution and total population size. We use a hierarchical model to combine standardized distance-sampling line transect survey data with opportunistic citizen science data. We compare different possible options for how the information in each dataset is shared in the model and assess the sensitivity of the model predictions to data from different regions.

Modeling Habitat Suitability for a Rare North American Shrub: The Case for Open Access Citizen Science and Herbarium

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Department of Forestry, Mississippi State University

Modeling a species habitat suitability has become a critical first step in conserving rare and imperiled plant species. These models allow conservationists to locate previously undocumented populations and prioritize populations and habitats for conservation. Mountain stewartia (*Stewartia ovata*) is a rare shrub or small tree endemic to the Piedmont and mountains of Georgia, Tennessee, and Alabama with isolated populations occurring in Kentucky, North Carolina, South Carolina, Virginia, and Mississippi, USA. The species is often misidentified or overlooked by land managers and conservationists. As a result, stewartia's habitat and distribution descriptions are insufficient for restoration and conservation use. Presented is the habitat suitability of the species across its natural range. Herbarium records (n = 25), research-grade iNaturalist observations (n = 25), and other author identified locations (n = 15) were used with 10 environmental layers to develop a maximum entropy model (Maxent). The resulting habitat suitability map was classified into bins for spatial analysis. A total of 264,210ha was designated within the top tier of which 78,896ha was found on publicly owned lands, indicating approximately 30% of the highest habitat suitability occurs within public, protected land. The presented model will allow plant conservationists to prioritize areas for conservation while also more fully describing the fundamental niche of the species. This study provides a framework for using natural history records and citizen science in tandem to meet conservation objectives. Further, this study would not be possible without both natural history records and citizen science, supporting the mounting evidence for the need to support institutions that provide these services.

Recovering the critically endangered black abalone using environmental genomics

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The once abundant black abalone, *Haliotis cracherodii*, has experienced dramatic declines throughout most of its range along the rocky intertidal shores of California since the mid-1980s, due to the fatal bacterial disease called withering syndrome. This marine invertebrate used to support an economically important fishery, however, the disease has caused black abalone populations to decline by more than 80% throughout southern California and as far north as Monterey, leaving only a few scattered individuals. Efforts to recover black abalone populations are underway, including plans to restore disease-impacted populations in the south with unaffected individuals from the north. However, two major challenges remain: 1) monitoring the species' range is complicated by its elusiveness, and 2) little is known about this species' population structure, making it difficult to establish effective restoration plans. In this talk, I will discuss my research which aims to tackle these issues using environmental genomics. Broadly, we aim to develop an environmental DNA approach which would make it possible to detect black abalones using collections of seawater. If successful, this approach could offer a rapid and inexpensive way of detecting the presence of black abalones in areas that are hard to access and survey. We also assembled the first black abalone draft genome and developed a non-invasive swabbing method to collect their DNA in the field. Using this method, a large population genetics survey is currently being undertaken at 35 sites along the coast of California, with the aim of estimating genetic diversity among different black abalone populations.

Estimating large herbivores in the Kafue Ecosystem and the Management Implications

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Department of National Parks and Wildlife, Zambia

Historically, large terrestrial herbivores were evenly distributed across large most parts of Zambia and not restricted to just the protected areas. Because of the declining numbers of large terrestrial herbivores that have been impacted on by a combination of factors including illegal harvest, habitat modifications, human encroachment into wildlife areas and climate change, monitoring of these animal populations is now a critical aspect of wildlife conservation. Assessing the status and trends of the large terrestrial herbivores is important for sustainable development strategies at all levels of conservation. A total of 58, 331 km² of the Kafue Ecosystem was surveyed during the long dry season when leaf cover was at a minimum and visibility at a maximum. The survey procedure was based on a standardized wildlife aerial survey approach using aerial stratified random sampling methods. The population estimates of elephants were $4,606 \pm 3,390$ showing a slight increase of 3% from the 2011 survey while the carcass ratio was estimated at 9%. Buffalo was estimated at $6,352 \pm 2859$ compared to the 2011 survey which recorded 1,446 buffalo. Puku population showed a reduction by about 35%. Red lechwe showed a significant increase from an estimated 8,465 in 2011 to $17,388 \pm 5878$. For other species of importance as prey species and in consumptive tourism impala ($21,065 \pm 6,908$); sable antelope ($16,179 \pm 3,549$); eland ($3,127 \pm 2,194$); and zebra ($1,300 \pm 374$) were estimated. These population estimates are considered to be meaningful to wildlife management decision-making processes. While poaching remains the most significant force acting against the maintenance of wildlife populations, vigorous efforts in law enforcement are producing results and having the desired effect of reducing illegal activity as seen in the western boundaries of the Kafue Ecosystem.

Session: Species Populations

Oral Presentations

bRacatus: an R package to estimate the accuracy and the biogeographical status of georeferenced biological data

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Understanding species distributions and abundances is critical for ecological research, but available data are typically incomplete, biased and imprecise. Crucially, the accuracy (valid vs. erroneous record) and biogeographical status (native vs. alien) of individual georeferenced data points is often unclear, challenging their confident use in distribution modelling, analyses of biodiversity patterns or other analyses. We introduce bRacatus, an R package developed to address two questions: i) is a given georeferenced datum a true or a false record? ii) Does it represent a native or an alien occurrence? We developed a new method based on the spatial context provided by coarse-grain reference regions of native and/or alien distribution. By estimating records' likelihoods along two axes, i) "certainly false to certainly true", and ii) "certainly native to certainly alien", the framework avoids artificial thresholds of data filtering and instead allows propagating uncertainties in subsequent analyses. We trained and tested our method on 400 terrestrial species of amphibians, birds, terrestrial mammals, and vascular plants from all continents. bRacatus showed good predictive power (mean AUC > 0.9; mean RMSE < 0.3) for both the accuracy and biogeographical status. The models' high performance also holds true when applied to regions, range sizes, and data types not used in the training. Additionally, tests using checklists instead of range maps as reference regions have shown overall good performance across different levels of data completeness. bRacatus is a flexible and user-friendly tool that enables researchers to assess data's accuracy and biogeographical status of species occurrence records, population abundances, community composition or any other type of georeferenced biodiversity records. Currently, we are discussing the possibility of incorporating our method into GBIF's data evaluation workflow. We propose bRacatus as the necessary first step in addressing the inherent uncertainty of point observations, ultimately leading to more accurate ecological inference and predictions.

Bioacoustics monitoring across multiple ecosystems in biodiversity hot spots

Bates, Naomi S.

Future Generations University

Networks of bioacoustics recording devices in the mountains of Nepal, Bolivia, and the United States allow studies of species population distributions, along with changes over time and elevation. At each project area devices record sound day and night, 365 days per year. Two years of preliminary bioacoustics data are available for some stations. These data are used to help local stakeholders answer questions related to species biodiversity, habitat conservation, land management, or other goals. The long-term dataset will be used to detect evidence of climate change, and results will inform community decision making. As local temperatures, weather patterns, and ecosystems change over many years, a gradual soundscape shift is hypothesized as birds move up elevational transects or to different ecosystems in response to changing climate conditions. Artificial intelligence and machine learning tools are used to analyze the big data and identify specific calls of birds, amphibians, mammals, and insects. Preliminary results in the Himalayas of Nepal show that at least one species of bird is now detected at an elevation 1,000 feet higher than previously observed.

A Threatened Species Index for Australia

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Understanding where and to what extent species populations are increasing or decreasing is crucial for monitoring progress towards global conservation targets, justifying and measuring benefits from conservation investments, stimulating targeted responses and raising the public profile of threatened species. Most national and global indicators report on common species, not on those at greatest risk of extinction. Here we describe a Threatened Species Index (TSX) and showcase it as a tool for tracking and reporting on changes in Australia's imperilled species (threatened and near-threatened). The TSX presently reports on the changes in populations of 65 birds and 57 mammals from over 18,000 locations across Australia. An index for plants is under development. The TSX is based on the Living Planet Index method and uses Essential Biodiversity Variables data of the class 'species populations' provided by over 250 individual data custodians. These data custodians are from the Australian Government, state/territory governments, natural resource management groups, environmental non-governmental organisations, academia and citizen science groups; and the network of the TSX is continuously growing. The TSX indicates that birds have declined by 59% on average between 1985 and 2016, while migratory shorebirds experience the worst declines (72%). The new mammal index shows that the 57 mammals from over 1000 sites included have declined by 38% on average over the last 20 years. The mammals' index allows us to evaluate mammals at sites with and without active conservation management. Mammal populations at sites without conservation management have declined by 60% on average over the last 2 decades while those at sites with targeted conservation management show average increases of 77% between 1995 and 2016. Between 2000 and 2016, populations of 15 threatened mammals at cat- and fox- free sites have increased five-fold, demonstrating the effectiveness of Australia's safe havens network. The TSX addresses requirements set by the Convention on Biological Diversity's Aichi Target 12 by enabling governments, agencies and the public to track changes in threatened and near-threatened species populations. This research received funding from the Australian Government's National Environment Science Program and was developed within the Threatened Species Recovery Hub. We have drawn on the collective efforts of many passionate and dedicated people who champion threatened species monitoring and recovery in Australia. All trends and time-series data can be openly accessed and interrogated at <https://tsx.org.au/>.

Expanding Wallace species distribution modeling software as a BON in a Box tool for national BON assessment and reporting

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1: American Museum of Natural History, United States of America; 2: Pace University, United States of America; 3: Michigan State University, United States of America; 4: Universidad Eafit, Colombia; 5: Okinawa Institute of Science and Technology, Japan; 6: University of Connecticut, United States of America; 7: The Alexander von Humboldt Institute for Research on Biological Resources, Colombia; 8: City College of the City University of New York, United States of America; 9: Graduate Center of the City University of New York, United States of America; 10: The Nature Conservancy, Colombia

Effective policy responses to changes in biodiversity are only possible with adaptable analytic tools, such as the BON in a Box toolset, that leverage the influx of data from biodiversity observation systems. Such analytic tools must also be streamlined and readily mastered by researchers making scientific recommendations. Researchers and practitioners often rely on either software packages that lack flexibility and transparency, or on command-line interfaces that may require additional knowledge of a programming language. Combining positive aspects of both, Wallace is an R-based application with a graphical user interface that supports species distribution modeling (SDM) in an open-source, reproducible, flexible and expandable platform. With rich documentation in the graphical user interface, Wallace guides users from acquiring and processing data through building models and examining predictions. Wallace model outputs characterize environmental suitability for species and can be used to estimate species' geographic ranges —a GEO BON Essential Biodiversity Variable (EBV). We are expanding Wallace's functionality to enable quantifications of species' geographic ranges (by post-processing SDM outputs) and calculations of biodiversity change indicators. Specifically, based on functionalities of two new underlying R packages, users will be able to quantify species' current ranges using in situ observations of species' occurrence and ex situ NASA Earth Science data to determine habitat tolerances. From those estimates, users will be able to calculate biodiversity change indicators such as range size, the upper bound of extent of occurrence, percent suitable land cover, protected area representativeness, or projected trends under future scenarios. Through this expansion and in partnership with the Colombia BON, Wallace will also become a tool for BON in a Box that will facilitate assessment of biodiversity change indicators for national BON assessment and reporting. Our software developments will link Wallace to the Colombia BON through integration with their existing BON in a Box tool BioModelos, which enables expert validation of species' range estimates, to enhance their national biodiversity assessments and decision-making and reporting processes. Overall, we expect this expansion of Wallace to help facilitate responsible reporting on biodiversity by national BONs.

Separating detection from true introduction rates for estimating temporal trends in alien introduction

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1: Tel Aviv University, Israel; 2: Steinhardt Museum of Natural History, Israel

A vital step in predicting future community impacts of alien species is understanding the invasion magnitude. An intuitive way to examine the temporal trends of invasions is by using first records data, which will yield the detection rate – number of new alien species in a region per time step. However, alien species detection rates are subject to methodological pitfalls which strongly bias the true introduction rates. Several statistical models have been proposed to enable the separation between introduction and detection. However, use of these models has been scarce among invasion ecologists, resulting in inaccurate estimates of introduction rates which may dictate policy development.

To demonstrate the problems surrounding the use of first records data, we applied a model to separate introduction and detection for records spanning two centuries of three important taxa: plants, birds, and amphibians. Our results show high variability among the three taxa in introduction rate uncertainty. The uncertainty revolving introduction rate of plants is the lowest, with estimates being close to those achieved by using raw first sighting records. In contrast, for birds and amphibians, introduction rates may be higher than currently estimated and the models suggest there is a large number of alien species yet to be recorded. These results stress the importance of correctly modeling temporal trends in alien species. Separation between introduction and detection should be taken into account in indicators, and used by scientists and policy makers.

A new approach using species accumulation curves to estimate robust absence records for species distribution modeling

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We present a novel approach to infer absence records for species distribution models (SDM) using species accumulation curves (SAC) (Colwell et al., 2012), a method of community ecology to estimate species richness as a function of sampling effort. Firstly, we provided a theoretical demonstration of our approach, termed Species Accumulation Curve informed absences (SAC-absences). Secondly, we evaluated and compared SAC-absences with the traditional approach for inferring absences, pseudo-absences, using as system of study the frog species of the Cerrado ecoregion (Tropical South America). Thirdly, we evaluated and compared SAC-absences against absences estimated in the field (field-absences) using as system of study the tree species of the Appalachian-Blue Ridge forests ecoregion (Subtropical and Temperate North America). For each absence approach (SAC-absences, pseudo-absences, and field-absences), three SDM classification methods were applied: Maximum Entropy (MaxEnt), Random Forest (RF), and Gradient Boosting Machine (GBM). In the study system of frogs, SAC-absences generated good model accuracies (i.e. AUC >0.8 and TSS >0.5) using the RF and GBM classification methods. Pseudo-absences generated models with AUCs above 0.8 using the three classification methods; however, pseudo-absences generated TSSs lower than 0.5 using the RF and GBM classifications and TSSs slightly higher than 0.5 using MaxEnt. In the study system of trees, SAC-absences generated good model accuracies using the RF and GBM classification methods for the all species while field-absences generated good model accuracies in seven of the nine species. SAC-absences and field-absences produced models with accuracies under the limits of acceptance when MaxEnt was used for the all tree species. Our method for estimating absences improves SDM performance, reducing uncertainty and bias compared with pseudo-absence and improve accuracy compare with field-absence approach. SAC-absences can be generalized to any situation where robust SACs can be calculated for target-groups.

Asking the right question with the right data

Hughes, Alice

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In the last decade we have transitioned from being data poor, to data rich and as a consequence our challenges have shifted from how to usefully use the limited available data, to how to sensibly work with ever growing datasets. Unfortunately access to these growing volumes of data, combined with easy to use software packages mean that much of the time data is analysed inappropriately, and in some cases this could lead to poor management outcomes or inappropriate recommendations. Here we take various commonly used datasets for biodiversity analysis including major public biodiversity databases, species distribution maps and climatic data and explore the inherent biases and assumptions within these datasets. We discuss the limits of data use, and how to understand if data is fit for any given scientific question. Understanding caveats and assumptions, and how to assay how data can be used appropriately is a fundamental part of good science, and the excuse of BAD (Best Available Data) analysis when results could have realworld implications needs to be countered by a clearer understanding of data limitations and caveats so outcomes can be used in an informed and appropriate way.

Updated Area of Habitat models to map global biodiversity of terrestrial mammals and birds

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1: Sapienza Università di Roma; 2: BirdLife International

The current rate of biodiversity loss is over 1,000 times higher than background levels, therefore, finding mechanisms to identify where species' suitable habitat is located is an urgent matter to direct conservation action. Conservation depends on the accurate mapping of species distributions. At the global scales, the most comprehensive assessment of species distributions are the IUCN Red List geographical ranges, however, they usually contain areas inside the range that are not occupied by the species, and thus suffer from commission errors (false presence). Area of habitat (AOH; previously known as extent of suitable habitat; ESH) is the 'habitat available to a species, that is, habitat within its range' and is an attempt to reduce commission errors in range maps. The AOH maps are produced by removing the unsuitable habitat from the distribution ranges. To determine the suitable habitat, we used the information on habitat preferences from the IUCN Red List. To map habitats, we developed a novel data-driven crosswalk between the IUCN Red List Habitats Classification Scheme and the Copernicus Global Land Service Land Cover, using a logistic regression model. We presented an updated version of global AOH maps for terrestrial mammals and birds, at 100m resolution. These maps allowed us determining the global distribution of mammals and birds at a finer resolution than what could be obtained using ranges. Having fine-resolution distribution maps can help us to guide conservation action worldwide. AOH maps can be used for site-based conservation and protected areas identification. Moreover, having a clear view of the relationship between habitat and land cover helps us to understand the impacts of land-use change on species.

Predicting the global distributions of bats, a critical source of zoonoses: taxonomic and regional data gaps

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Predicting and mitigating the risk of emerging zoonotic diseases requires detailed knowledge of species' distributions that can be compared to those of human encroachment and exploitation. However, this requires a sufficient volume of geo-referenced occurrence records available in publicly accessible databases. Here, we generate high resolution maps of the predicted distributions of bat species (Chiroptera) by leveraging the facilities of Map Of Life (mol.org), a public web platform designed to integrate large amounts of biodiversity and environmental data from researchers and citizen scientists. Where occurrence data is insufficient for a species we are forced to use range maps that are accurate at much coarser resolutions that limit their suitability. We identify taxonomic and regional data gaps that hinder our ability to generate acceptable models for all species, particularly in some regions associated with a higher risk of zoonoses.

National trends in closing spatiotemporal biodiversity knowledge gaps via complementary data types

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The growing threats to global biodiversity demand understanding species status and trends in order to deploy efficient and effective conservation measures. Doing so requires detailed information on species distributions across large geographic scales, which ultimately falls on individual nations to report. Thus, determining complementarity or redundancy of datasets, identifying biodiversity information gaps, and understanding trends in data coverage over time are priorities to both scientific and political communities. Using 70 years' (1950-2019) worth of digitally accessible species point occurrences, we investigated temporal trends in global data coverage and data redundancy for terrestrial vertebrates at the national level. Further, we demonstrate the potential of camera trapping to contribute to biodiversity science using ca. 4 million publicly available camera trap observations from the newly released Wildlife Insights (WI). We found large heterogeneity in biodiversity data coverage over the previous decade (2010-2019) among nations and taxa. While nearly half of nations (49%) showed significantly increasing coverage for birds over the previous decade, a large majority did not show increasing trends for mammals, amphibians, and reptiles (81-90%). Redundancy in biodiversity data has increased significantly over the previous decade, largely driven by rapid explosion of records collected for bird species. We identified nations, primarily in the tropics, and species, primarily small-bodied mammals, for which camera-trapping observations had the largest contribution to data coverage. Our findings provide a critical assessment of the effectiveness of biodiversity inventories over the past century to understanding rapid changes in global biodiversity.

Species on the Move in the Ocean: Monitoring and Indicators to Inform Policy

Pinsky, Malin

Rutgers, The State University of New Jersey, United States of America

Species distributions around the world are shifting in response to climate and other environmental change, with often profound impacts on ecosystem functioning, economic activities, and human well-being. However, monitoring these shifts and using such information to inform public policy has been substantially more difficult, not least because information on species distributions through time are rarely available. I will discuss efforts through the OceanAdapt project (<http://oceanadapt.rutgers.edu>) that use existing ecological surveys around North America to reconstruct changes in marine species distributions over the past half century. Information is served as animated maps and as biodiversity indicators at scales from species-level to regional and national. Priorities for future development include methods to fill spatial and temporal observational gaps, merge heterogeneous datasets, and develop forecasts to inform near-term management priorities.

Incorporating remotely sensed ecosystem functional attributes into species distribution models to support biodiversity monitoring

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Biodiversity is declining globally at unprecedented rates —and the rate of species extinctions is accelerating. To address this daunting challenge, ecological modellers need to make a step change in our capacity to foresee future environmental changes. Correlative species distribution models (hereafter SDMs, also known as habitat suitability models or ecological niche models) is one of the most widely used toolsets to appraise past, present and future global change impacts on biodiversity, and to support decision-making and evaluate policies. Despite the technical advances and increasing effort of remote sensing community to develop integrative ecosystem functioning attributes (EFA), ecological modellers have yet to make full profit of the most recent developments by integrating them in SDMs. The synergies between the increasingly available open-access satellite images (e.g. Sentinel mission based on a constellation of satellites from European Space Agency) and cloud-based platforms for planetary-scale geospatial analysis (such as Google Earth Engine) offer an unprecedented opportunity for ecologists to incorporate variables related to ecosystem processes and properties that have been so far largely neglected in ecological niche characterization and modelling. Here, we identify a variety of advantages of incorporating remotely sensed EFAs into SDMs. This new type of RS variables is characterized by an increasingly higher spatial and temporal resolution, that can complement traditional environmental variables extracted from interpolated macroclimate data or describing static compositional or structural habitat features —eventually improving ecological niche characterization and the predictive performance of SDMs. In addition, EFAs can be measured and updated systematically and synoptically through Earth Observation data and RS technologies; facilitating a cross-scale, standardized, repeatable and cost-effective biodiversity monitoring. All these advantages confirm that a new generation of SDMs based on such EFAs would offer great perspectives to increase our ability to monitor habitat suitability trends and population dynamics (including short-term stochastic fluctuations, abrupt changes or long-term monotonic trends) and to predict species distributional shifts under global change scenarios. The development of new global datasets supporting the implementation of essential biodiversity variables (EBVs) relevant for monitoring ecosystem functioning is being a priority for the Group on Earth Observations Biodiversity Observation Network (GEOBON; see Working Group Ecosystem function, <http://geobon.org/working-groups/ecosystem-function/>). A coordinated agenda for remote sensing experts and ecological modellers will be essential over the coming years to bridge the gap between remote sensing and ecology disciplines and to take full (and timely) advantage of the fast-growing body of Earth Observation (EO) data and RS technologies —with special emphasis on the development and testing of new variables related to key processes driving ecosystem functioning.

Reverse the Red: Building National Collaborations to Save Species

Rodriguez, Jon Paul

IUCN Species Survival Commission, Venezuela, Bolivarian Republic of

Good news stories about species conservation are uncommon and there is an obvious reason for that, as many threats to species survival continue largely unabated: deforestation and land conversion, pollution and climate change, overexploitation, disease outbreaks, and the overriding threat of growing human demands on nature. The result is that increasingly more species and ecosystems are in peril, as has been laid out in the United Nation's Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) Global Assessment Report, which identified that an estimated one million species are at risk of extinction.

The International Union for Conservation of Nature (IUCN) mobilizes a portfolio of knowledge products aimed at documenting and tracking trends in the status of biodiversity, including: IUCN Red List of Threatened Species, Protected Planet, Red List of Ecosystems, Key Biodiversity Areas, and Environmental Impact Classification of Alien Taxa. The IUCN Species Survival Commission (SSC) leads in many of these initiatives and although they provide a comprehensive global perspective, conservation actions typically occur at regional, national and local scale, so there is often a disconnect between the geographic scope of data sets and the needs of the end users and key stakeholders.

Reverse the Red is an initiative of SSC and a growing network of partners that aims to reverse trends in the red list status of species on the IUCN Red List of Threatened Species. We will achieve this by convening national networks of species survival stakeholders – including experts, conservation practitioners, academics, governments and NGOs. Resources will be mobilized through decentralized institutional partnerships to grow the capacity of national networks to assess species extinction status, develop effective conservation action plans, and catalyze conservation action.

SSC is also exploring changes to the structure of its global expert network, through the creation of national SSC groups which will complement existing taxonomic and disciplinary groupings. We will also work with partners to improve tools for biodiversity monitoring, extinction threat assessment and conservation planning, to support their effective implementation at the national and sub-national level.

Experience shows us that we know how to save species and reverse biodiversity declines. We just need to scale up and coordinate our efforts more effectively to achieve this.

Invasive Species Management Needs Technological Integration

van Rees, Charles Barteld (1); Hand, Brian K. (1); Kimball, John (2); Ferrante, Jason A. (3); Hunter, Margaret E. (3); Luikart, Gordon (1)

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Invasive Alien species (IAS) contribute to one of the worst global environmental crises, causing extinction of native species and billions of dollars of damages annually. IAS impacts are accelerating with climate and landscape change, making their monitoring and management a priority for international agreements like the United Nations Sustainable Development Goals and Aichi Biodiversity Targets. Rapid advances and new technologies in multiple disciplines offer powerful tools to address this crisis, but it is unclear how to fully integrate these into cohesive management strategies. We review recent breakthroughs in fields ranging from earth systems modeling and data infrastructure to eDNA detection and predictive distribution modeling, then synthesize these in a framework for IAS management, drawing inspiration from current research on infectious diseases such as the novel coronavirus. This framework combines new and emerging technologies in a cohesive workflow for Early Detection and Rapid Response, with guidance on occurrence data collection, integration and management, remote sensing of environmental covariates, distribution forecasting, and stakeholder engagement and decision support. We discuss the connections between this workflow and important Essential Biodiversity Variables and show how diverse fields can contribute to a timely and urgently-needed paradigm in invasive species research.

Spatial modelling of abundance for estimates of biodiversity, ecosystem function and services

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Species local abundance is critical to the role species play in their ecosystem, the strength of species interactions, the impact of invasive species, the probability of local extinctions, and the ecological services that species can provide to humans. It is surprising, therefore, that a substantial research attention is focussed on measuring and predicting the spatial distribution of species as species presence or absences given a set of environmental conditions, but that species abundance once present remains relatively neglected. Which factors determine the abundance patterns of individuals across species' ranges remain far less well established, as well as how we can best model spatial abundance patterns, and the benefits of doing so in terms of ecosystem function and services. For the first time, to our knowledge, we provide a comprehensive "Species Abundance Model" comparison of over 100,000 statistical models of >3,000 species: modelling abundance across the geographic ranges of American birds and Australian reef-fishes. We found that random forest algorithms dramatically out performed parametric approaches to modelling abundance in accuracy, discrimination, and precision. However, no models performed well when fitted to novel environmental conditions, suggesting major challenges under novel climatic regimes in application of statistical modelling approaches. Finally, we investigate the spatial deviations in predicted ecosystem function and ecosystem services derived from using Species Distribution Models and Species Abundance Models. Our results develop the foundation for modelling spatial abundance patterns to add another dimension to the consequences of spatial biodiversity changes that are often viewed through the lens of species distributions alone.

Session: Species Populations

Poster presentations

Herpetofauna assemblage in two Watershed areas of Kumoan Himalayas, Uttarakhand, India

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Department of Wildlife Sciences Amu Aligarh

We surveyed for herpetofauna along the poorly-explored region of two watersheds of Kumoan Himalayas, Dabka and Khulgarh. Adaptive cluster method was used to collect forest floor reptiles, and stream transect was used for stream reptiles and amphibians. In total, 19 species of reptiles were recorded in two watersheds, of which 15 and 10 species were recorded in Dabka and Khulgarh, respectively. Forest floor density of reptiles was 87.52/ha in Dabka and 77.71/ha in Khulgarh. In terms of species, *Asymblepharus ladacensis* and *Lygosoma punctatus* density were found highest in Dabka and Khulgarh, respectively. Similarly, 8 species of amphibians were recorded in Dabka with density of 9.38/ha and 4 species in Khulgarh with density of 5.23/ha. In both the watersheds, density of *Euphlyctis cyanophlyctis* was found highest. Reptilian and amphibian diversity of Dabka was 1.519 and 1.227, respectively, and in Khulgarh they were 0.426 and 0.234, respectively. In both watersheds, reptile density, diversity and richness decrease with increasing elevation. Reptile density showed a weak correlation with microhabitat features such as litter cover, litter depth, and soil moisture in both watersheds. Amphibian density was positively correlated with soil moisture, litter cover, and litter depth. Comparison showed that Dabka is richer and more diverse than Khulgarh, presumably because of undisturbed habitat, broad and slow stream, and deeper forest litter of the former.

Spatial predictions of Species Distribution Essential Biodiversity Variables (SDEBV): A bird perspective in the Swiss Alps

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Understanding how and why species are distributed in space and time and understanding the relationship between species and their environment is an important issue of biogeographical research which recently identified as one of the five 'grand challenges' in organismal biology. EBVs Candidates such as Species Distribution can be defined as the presence or absence of species, based on observations with specified spatial and temporal dimensions. EBVs subclass "Species Distribution" allow to build indicators that reflect population trends, extinction of threatened species and biodiversity responses to land use and climate change. We can get such important and essential information in the EBV class 'Species Population'. Species distributions can be estimated by predictive modelling such as species distribution models (SDMs) since they statistically relate the distributions of populations. Modelling habitat suitability (HS) are useful numerical tools to combine the observed abundance or occurrence of species and environmental predictors to predict the species' distribution, environmental suitability (ES) and provide a great opportunities to learn more about past, current and future species distribution and patterns of spatial distribution of species can inform us about rarity and potential extinction risk for species and are essential to effective monitoring.

A major concern that arises from this study is how to build bird SDMs that can be used to derive spatial species distribution for birds under climate change and land use at a regional scale (the bird SDMs can be used as a small part and spectrum from global to subnational and regional) of spatial EBV for birds at a global scale). It has been suggested that in the future lowland area are particularly threatened by climate warming that is related to properties of lowland area such as greater habitat fragmentation and reduced opportunity for short-distance escapes. We can say that this mountain ecosystem will be threatened by climate warming and it will cause upward shifts in optimum habitat of bird species. This study shows the importance of lower temperature at higher elevation and also forest edge for bird species in a mountain area. It seems likely that the changes of species distribution across the three period times (current, future (2050 and 2070) is due to warming air temperature, rather than by land-use changes and bird species need to shift their distribution to high altitude to escape climate warming. Finally, here we showed whether suitability obtained through SDMs in a regional scale can be as a small part and a spectrum from global to subnational indicators of spatial 'Species Distribution' EBV (SD EBV) for bird species.

Session: Species Traits

Flash presentations

Linking in-situ and space-borne observations to study spatial plant functional diversity patterns

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Functional diversity serves as an important link between biodiversity and ecosystem functioning. Satellite earth observation has demonstrated potential to address the lack of information on large-scale continuous patterns of terrestrial plant functional diversity. The spatial extent and pixel-based observations of satellite remote sensing, however, poses challenges to validation and interpretation. This study demonstrates the mapping of functional diversity using Sentinel-2 imagery while offering a validation approach that links leaf and canopy traits and functional diversity from in-situ measurements with satellite remote sensing observations.

Through both traditional field methods and satellite retrieval we measured plant trait data (Leaf Area Index, chlorophyll and carotenoid concentrations, canopy water content and dry matter contents) for 120 plots in 15 locations in the Montesinho National Park, Portugal. Space-borne functional diversity metrics were derived from spectral reflectance data of Sentinel-2 imagery by radiative transfer model inversion. Canopy measurements were taken across the georeferenced plots representative of Sentinel-2 pixels. For both space-borne and in-situ trait data, functional diversity metrics were calculated for each location and compared for validation.

The results allow us to assess the performance of satellite remote sensing to infer multiple individual traits, trait-trait relationships and functional diversity metrics. The validation demonstrates the capabilities to map functional diversity with currently operational satellite imagery while examining the accuracy, robustness and uncertainties of estimates. On the one hand, the demonstrated approach underlines the challenges involved in obtaining field measurements representative of pixel observations. On the other hand, the study highlights the potential of space-borne functional diversity metrics to advance our understanding on macro-ecological patterns without the need for repeated in-situ canopy trait measurement field campaigns.

Session: Species Traits

Oral presentations

Towards an integrated land-surface-phenology monitoring system for Chile: advances on remote sensing based platforms and Phenocam field network

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Monitoring changes in vegetation phenology (or the recurring seasonal life cycle of plants) using remote sensing is the simplest and most efficient way to detect and geographically spatialize the effects of climate change. The increasing temperature of the last decades is altering the Earth vegetation phenological cycles, being the most evident symptom the timing shift of the onset, offset and growing season length of the vegetation phenology. Regional to continental shifts in phenological timing can modify large scale biogeographical patterns affecting biodiversity, forest production, pest dynamics, agriculture and food availability. Several national and international efforts have been made to develop operational remote sensing based phenological monitoring system as well as ground observation networks of time-lapse cameras or “Phenocams”. Particularly in Chile, as it is in most Latin American countries, there are no monitoring programs (remote sensing or ground systems) to assess spatio-temporal phenological changes. The geographical complexity as well as the wide range of climates and ecosystems of Chile, justify fully the implementation of a national biodiversity observatory, being land surface phenology a key variable to report in national and international biodiversity instances. Recently, an alliance between the Pontificia Universidad Católica de Valparaíso, the National Forest Service Conaf and the Ministry of Environment is giving the first steps towards a Chilean land-surface-phenology monitoring system. Following the framework of GEO-BON and the Essential Biodiversity Variables, a remote sensing monitoring platform has been developed using NASA MODIS data for four relevant conservation areas: La Campana National Park, Rio Clarillo National Reserve (mediterranean forest and shrubland ecosystems in Central Chile), Nahuelbuta National Park and Pumalín Douglas Tompkins (Valdivian forest ecosystem in Southern Chile). The web-platforms are based on a flexible non-parametric probabilistic algorithm (the “npphen” R package) capable to reconstruct any type of leaf phenology using remote sensing data and to quantify its inter-annual variation by means of confidence intervals around the most probable annual curve. Phenological anomalies located above 95% confidence interval trigger a “red alert” which is displayed on the web application as soon as the satellite data become available. Furthermore, five Phenocams are being installed in the same protected areas providing the first records of ground phenology. Daily RGB photos are taken and transmitted via wireless to the central server. Phenometrics calculated from the RGB photos are used to calibrate and validate satellite phenological products. In this work, we show the first results obtained from the platforms and Phenocams and discuss future opportunities and challenges to construct a national phenological monitoring network, contributing to global efforts such as GEO-BON or the Global PhenoCam Dataset (<http://explore.phenocam.us/>).

The utility of radiative transfer models derived leaf and canopy traits to assess the response of invasive alien species versus native trees to drought in the semi-arid grassland, South Africa

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1: University of KwaZulu Natal; 2: University of KwaZulu Natal; 3: Council for Scientific and Industrial Research; 4: South African National parks

Climate change and invasive alien plants are major and interconnected drivers of biodiversity loss worldwide. Climate change can result in drought events that increase stress on native vegetation, thus tree mortality. The opening up of vegetation cover consequently makes the ecosystem more susceptible to more tolerant species generally invasive plant species. Increased temperature significantly affects plant physiological functions and morphological characteristics. Thus, it is the most critical factor influencing plant growth and species composition. To understand how drought and invasive species interact, it is useful to first detect the response of native and invasive plant species to drought. Measurements of plant traits based upon reflectance spectra permit the assessment of plant response to stress conditions, such as drought events. In this study, we aimed to assess the adaptability and recovery of native and invasive plants species from the drought stress, with the main hypothesis that invasive plants species physiological and biochemical traits are not affected by elevated temperature resulting from drought. We applied Artificial and Look-up table physical-based driven radiative transfer models for retrieving biophysical and biochemical variables of native and invasive plant species in semi-arid South African grassland. The approach was used on the Sentinel-based optical information of native and Australia native Acacia species. The Sentinel-2 data was acquired during high drought events and post-drought in South Africa. Results show that the radiative transfer model successfully detected and revealed the different response of native and invasive Acacias to drought period. We observed high physiological and biochemical variations between Native and Acacia species during the dries period in South Africa when compared to post-drought. Drought stress affected physiological and biochemical traits of native species compared to Acacia species.

The register of Antarctic (Marine) Species,

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1: Royal Belgian Institute for Natural Sciences, Belgium; 2: Université Libre de Bruxelles, Belgium; 3: University of Salzburg; 4: British Antarctic Survey; 5: University of Genoa; 6: Universiti Sains Malaysia; 7: Alfred Wegener Institute; 8: Universiteit Gent; 9: University of Waikato; 10: California Academy of Sciences; 11: Flanders Marine Institute; 12: University of Tasmania; 13: Centre d'Etudes Biologiques de Chizé-CNRS

The register of Antarctic Marine Species (RAMS) was created during the Census of Antarctic Marine Life. The objective of RAMS is to compile and manage an authoritative taxonomic list of species occurring in the Antarctic for establishing a standard reference for marine biodiversity research, conservation and sustainable management. Here we provide an overview of the development of RAMS over the last 15 years and look towards the future as part of the Lifewatch Species Information Backbone.

From 25-28th November thematic editors of the Register of Antarctic Species and the Register of Antarctic Marine Species met in Ostend to discuss the application of trait data in the Aphia System in the context of the Southern Ocean and the Antarctic region. A mixture of terrestrial and marine expertise was represented from various countries around the world. Further experts provided input through remote participation.

There were discussions on the prioritisation of traits, both in terms of those that should be added to the system as well as those that (thematic) editors should focus on adding. Eight priority data types were determined based on the need for information, the availability of data and, finally, how well these concepts were advanced within the taxonomic backbone. This includes information on habitat, mobility, holotype image and geographical information about type locality, feeding method/type and diet information, size, larval and juvenile development, data on invasive species and Vulnerable Marine Ecosystem (VME) indicator taxa.

Session: Species Traits

Poster presentations

How is *Picea Chihuahuana* Martinez facing the climate change and the increase of CO₂ in the atmosphere?

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Understanding how *Picea chihuahuana* responded to extreme climatic events in the past is crucial for advancing in our ability to predict how recent atmospheric changes of CO₂ will impact this forest ecosystem in the future. *Picea chihuahuana* is a long-lived climate sensitive species thriving in specific habitats along the Sierra Madre Occidental. Currently the species is considered in danger of extinction, and is included under protection of Mexican norm NOM- 059- SEMARNAT-2010. Here, a dual isotope ($\delta^{13}\text{C}$ and $\delta^{18}\text{O}$) approach was combined with standard dendrochronological methods to examine how *Picea chihuahuana* trees has physiologically responded to extreme climatic events over the past 150 years in Chihuahua Mexico. We found that trees recorded extreme dry events in: 1850, 1865, 1880, 1893, 1920, 1940, 1953, 1965, 1982, 2000, 2005, and wet events in 1870, 1885, 1910, 1929, 1951, 1966, 1975, 1987, 1995, 2010. Tree ring $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ recorded shifts in precipitation patterns, as well as physiological adjustments following dry and wet events. A positive relationship between $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ was observed over time, with the highest ^{13}C discrimination and the lowest $\delta^{18}\text{O}$ recorded in tree rings during wet periods. Rising atmospheric CO₂ levels caused increases in water use efficiency (iWUE) but no more growth due to the fertilization effect by the increase of atmospheric CO₂. Tree growth decline and divergent isotopic signals indicated critically low stomatal conductance during dry periods. Therefore, if currently observed precipitation patterns continue in this region will likely cause a widespread increase in forest dieback for this species

Title unknown

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The sand plain along the Brazilian coast was colonized by trees and scrubs, which formed an ecosystem known as restinga, composed by species from the surrounding ecosystems (Atlantic Forest, Cerrado and Caatinga). That ecosystem is strictly related to advances and retreats of sea level during the quaternary period (20000 years ago) when the substrate ("soil") was deposited and colonized. Considering the topographic variation, which is related to the proximity of the water table, different vegetational formations may occur. An interesting one is the Open Clusia Scrub Land (OCSL) that is correlated with areas farthest from the water table, where the species are exposed to water and nutritional deficits that impose a vegetational cluster surrounded by bare sand. The restinga de Jurubatiba National Park is the most extensive and well-protected restinga area of Brazil, which has been being studied for the last 30 years. Clusia is the only CAM species on the neotropics and your metabolism is usually linked to the ecological dynamic on the OCSL, because its biomass productivity, dominance and ability to maintain resources in the system made it a potential facilitative species. In this way, the restinga ecological knowledge has been built on the basis of physiology and population ecology. The current paradigm states that Clusia is a nurse plant to the other C3 species, which only can colonize the system once the harsh environment is attenuated by Clusia canopy. Until now, the researches have not been conducted at broad scales, but only at local sites. We surveyed vegetational patches all over the protected area to test if the taxonomic, phylogenetic and functional diversities are ruled by the Clusia cover. We also correlated the functional diversity with edaphic and vegetational variables. The pattern that emerged matches both niche and neutral theory, although we can not state which process lead to that. The OCSL flora is a convergent evolution scenario and the patches formation diversities are independent of Clusia influence. Finally, we propose a new ecological dynamic approach to the OCSL that harmonizes niche and neutral theory without denying one or another but demonstrating that both, probably, take some part structuring the OCSL, leading to the coexistence of functional equivalent species.

Using species traits to quantify seabird bycatch vulnerability and predict conservation gains

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Fisheries bycatch, the incidental mortality of non-target species, is a profound threat to seabirds worldwide. Reducing bycatch is crucial to encounter declines of species' populations and indirect changes in ocean trophic dynamics and ecosystem functioning. To develop effective fisheries management and conservation goals, identification of the most vulnerable and affected species as well as quantification of the success of mitigation strategies is necessary. Here we combine species' traits and distribution ranges for 341 seabirds with a spatially resolved gear-specific fishing effort dataset to (1) understand spatial variation in seabird community traits; (2) predict whether mitigating bycatch has the potential to conserve community traits; and (3) quantify species vulnerability based on their exposure, sensitivity and adaptive capacity to longline, trawler and purse seine bycatch. We find distinct spatial variation in the community weighted mean of four seabird traits. Furthermore, successful bycatch mitigation will prevent significant shifts in the traits of seabird communities across the globe. Our findings may offer valuable insights into the benefits of bycatch mitigation for ecosystem functioning protection. Finally, we provide suggestions for targeted conservation strategies.

Macrofungi of the Vakh river basin. The first data.

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Surgut State University, Russian Federation

Random forays were undertaken in August of 2011 in remote area of Western Siberia at 6 locations down the Vakh River starting from the Bolshoi Laryak village.

Taiga mixed forests on the territory with sharply continental climate were surveyed.

In total, 115 occurrences of 87 macrofungi species, 52 genera, 29 families, 8 orders, 5 classes were noted: ascomycetes - 2 species, basidiomycetes - 85 species.

Distribution of families by the number of species: Hymenogastraceae - 12, Tricholomataceae – 9, Agaricaceae – 7, Strophariaceae – 7, Boletaceae – 7, Cortinariaceae – 7, Hydnangiaceae – 7, Mycenaceae – 6, Russulaceae – 6, Suillaceae – 6, Hygrophoraceae – 5, Inocybaceae – 5, Amanitaceae – 4, Psathyrellaceae – 4, Marasmiaceae – 3, Entolomataceae – 2, Omphalotaceae – 2, Physalacriaceae – 2, Pleurotaceae – 2, Auriscalpiaceae – 1, Cudoniaceae – 1, Dacrymycetaceae – 1, Gomphidiaceae – 1, Hericiaceae – 1, Hygrophoropsidaceae – 1, Paxillaceae – 1, Polyporaceae – 1, Pyronemataceae – 1, Tremellaceae - 1

For the first time in Yugra region, four species *Cortinarius callisteus*, *C. inolens*, *C. luteo-ornatus*, *Gymnopus aquosus* were reported.

Two regionally redlisted species *Hericium coralloides* и *Chrysomphalina chrysophylla* were found.

Hericium coralloides is relatively rare in KhMAO (Zvyagina, 2018), although its status corresponds to LC according to the Version 3.1 of the IUCN Red Lists and criteria (2000).

Chrysomphalina chrysophylla is extremely globally rare. This occurrence is the second find on the territory of KhMAO.

New chorological data was obtained for *Chroogomphus purpurascens*, *Laccaria nobilis* and *C. luteo-ornatus*.

Session: Genetic Composition

Flash presentations

Distribution and population genetic diversity of the giant clams, *Tridacna squamosa* and *T. maxima* in the Perhentian Islands Marine Park, Malaysia

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1: Bachok Marine Research Station, IOES, University of Malaya, Kelantan, Malaysia; 2: Third Institute of Oceanography, Ministry of Natural Resources, Xiamen, China; 3: Tropical Marine Science Institute, National University of Singapore, Singapore

The distribution and population diversity of giant clams from the coral reefs of Perhentian Islands Marine Park (PMP), Malaysia were surveyed. Two tridacnine species *Tridacna squamosa* and *T. maxima* were encountered. The results of the transect survey covering 11,500 m² revealed the *T. squamosa* and *T. maxima* abundances of 1.62 and 4.08 ind. per 100 m², respectively. The population genetic variation of both species was assessed based on the partial fragment of the cytochrome oxidase I gene from 180 individuals collected from 13 sampling sites. Both tridacnine populations in PMP exhibited high levels of genetic diversity, with the overall haplotype and nucleotide diversities being 0.624 and 3.5% for *T. squamosa*; 0.842 and 6.2% for *T. maxima*. The results also suggested that the PMP populations are highly genetically interconnected (*T. squamosa*, $F_{ST} = -0.05$; *T. maxima*, $F_{ST} = -0.007$) with no significant genetic differentiation. The relatively high genetic diversity and connectivity of PMP populations suggest that the populations of both tridacnine species in PMP are likely to possess sufficient genetic variation to be viable and resilient to various environmental stressors. This information is useful to inform and update spatial planning on biodiversity conservation.

Strong benefit of genetic admixture on survival and reproduction of an endangered fish during restoration of a previously extinct population

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Human-driven environmental change has resulted in unprecedented loss of biodiversity. Many species have been reduced to small and isolated populations, which, in addition to other threats, experience loss of genetic diversity which leads to reduced ability to adapt to changing environment, inbreeding and inbreeding depression (lowered fitness due to inbreeding). These genetic problems elevate extinction risk of small populations and limit their ability to recover after catastrophic events such as fire, flood or drought. Augmenting genetic diversity through assisted immigration can increase population fitness and growth (genetic rescue) and its ability to adapt to changing environments (evolutionary rescue), and thus improve its persistence. Similarly, genetic admixture has the potential to enhance efforts to re-establish previously extinct populations, which usually involve movement of a limited number of individuals. For example, translocated individuals can be sourced from different populations and artificial breeding programs can use parents from different populations. But limited demonstration of benefits of admixture and concerns over negative outcomes, such as fitness loss due to interbreeding between incompatible populations or loss of local adaptation, prevent its widespread uptake.

We assessed the impact of genetic admixture in a population of an endangered Australian freshwater fish, Macquarie perch, re-established in the Ovens River through translocations and stocking from two source populations, Yarra and Dartmouth, using samples collected over three years of Ovens monitoring. For stocking, same- and different-population parents were used. We genetically assigned Ovens fish to their broodstock parents and tested whether genetic dissimilarity between parents is associated with offspring survival. We also tested for recruitment of locally-spawned fish by assessing the genetic ancestry of non-stocked individuals. Analyses of survival and reproduction supported strong benefits of genetic admixture. Offspring of more genetically dissimilar parents— those from different populations and from the more genetically diverse Yarra population— had higher juvenile survival. The presence of non-stocked, admixed Ovens offspring indicates that fish of Yarra and Dartmouth ancestry successfully interbred locally. The Ovens had >10x more recruits with Yarra and admixed genetic ancestry than recruits solely of Dartmouth ancestry, despite 67% of stocked and 98% of translocated fish being from Dartmouth; this suggests superior survival and reproduction of fish of Yarra and admixed origin. We did not observe any evidence of negative effects of admixture. We conclude that admixture between even mildly different stocks can have measurable fitness benefits that are likely to apply to conservation management of many species of freshwater fish and other wildlife. Future management protocols for threatened species should include genetic augmentation between populations, given appropriate risk assessment balancing the benefits of alleviating inbreeding depression plus enhancing evolutionary potential against any envisaged costs of genetic admixture.

Session: Genetic Composition

Oral presentations

Using climate data to gain insight into community-level adaptive genomics in the Atlantic Forest, Brazil

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Investigating correlations between climate and community-level genetic diversity helps us understand patterns of biodiversity, predict biological responses to a shifting climate, and potentially monitor genetic changes in near-real time. To that end, recent studies have attempted to identify correlations between environmental conditions and the spatial or temporal distribution of genetic diversity. This was based on genetic markers assumed to evolve under neutrality. However, we argue that including an adaptive component can be particularly helpful to these monitoring efforts, contributing unique data to models of how species may react to future climatic shifts. To date, including adaptability is rare. To address this gap, we use genome-scale sampling (GBS and RADseq) from 25 taxa distributed throughout the Atlantic Forest domain in Brazil, including plants, amphibians, lizards, birds and butterflies, to investigate if and how climatic gradients correlate with genomic adaptation in individual taxa. Earlier studies in the region found that patterns of neutral diversity are driven by both past and current climate, however, different parts of the forest have been impacted in disparate ways, roughly making a distinction between southern, cold-adapted species and species from the mostly northern lowlands. Here, we ask if present and former climates similarly explain the distribution of potentially adaptive markers in the local biota. To quantify current climatic features, we used three datasets: remote sensing data (MODIS Land Surface Temperature and CHIRPS precipitation), bioclimatic variables derived from remote sensing data, and bioclimatic variable derived from weather station data (CHELSA). We also included projections of historical climate from four different time periods: 1) Last Interglacial (~130 ka), 2) Last Glacial Maximum (~21ka), 3) Heinrich Stadial 1 (~17.0-14.7ka), 4) Late-Holocene/Meghalayan (4.2-0.3ka). To detect signatures of selection, while accounting for species-specific population structure, we used Latent Factor Mixed Models (LFMM2).

Our results indicated that 1 to 15% of the sampled loci per species are potentially under selection. First results suggest that southern, cold-adapted species are more strongly impacted by current climate, whereas the northern, lowland species show a stronger association to historical climate. Although this seems to be apparent across some species, in other taxa it is less consistent. A possible explanation is that some species have changed their distributions more dramatically in response to climatic oscillations over time, therefore losing specific signatures of past climate legacies. Although for species with high dispersal capabilities and dynamic ranges this approach may violate assumptions regarding the historical climate they have been exposed to, this approach is promising when applied in a community wide context. We propose that understanding the adaptive response of species to current and past climate can be a helpful step towards a more effective way of monitoring genetic diversity on a larger taxonomic, spatial and temporal scale.

Implementing an Omic Biodiversity Observation Network (Omic BON)

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Molecular techniques to observe biodiversity have been steadily growing in popularity, effectiveness, and feasibility of deployment. From an early stage, the Genomic Observatories Network - initiated as a collaboration between GEO BON and the Genomic Standards Consortium - has been working to integrate DNA data into Earth observing systems. Since the network's first globally coordinated action (Ocean Sampling Day, 2014), rapid adoption of and advances in eDNA sequencing, metagenomics, metatranscriptomics, and metabolomics (collectively, "omics") have greatly expanded the international community of omic observers; however, the sheer rate of progress has made robust, coordinated, and coherent operationalisation a considerable challenge. As new networks, such as the Global Omics Observation Network (GLOMICON) have emerged to meet these challenges, we see a clear need for a more consolidated network-of-networks strategy to sustainably realise the potential of omics in observatory-grade systems. Thus, spurred by a coordination meeting between representatives of the Genomic Observatories Network and GLOMICON in 2019, a drive to create a thematic "Omic BON" has taken form.

In this contribution, we will describe the status of the Omic BON proposal and seek input from the broader community prior to its finalisation. We focus on its core mission to align existing and emerging omic observation networks in order to realise greater global impact and prepare for a more automated future. We will describe how the Omic BON will help scale the successes of participating networks, drawing examples from multi-national sample exchanges, calibration activities, inter-observatory data exchange, and new publishing models for FAIR omic biodiversity data. Further, we will highlight collective progress, already emulating the spirit of an Omic BON, in omically augmenting 1) national, regional, and international observatory infrastructures and 2) global reporting frameworks, including the Global Ocean Observing System's Essential Ocean Variables. We will also report progress in advancing digital capacities with partners such as the Ocean Biogeographic Information System and the Global Biodiversity Information Facility.

The Omic BON will serve the global omics community through an unprecedented level of open and inclusive coordination: a key element for omics to effectively and sustainably contribute to the global baselines and trusted indicators needed to address pressing threats to the biosphere. We envisage that the Omic BON community will establish decadal strategies and interoperability models, forging sustained links to an ever-growing collection of stakeholders and global programmes, such as the UN Decade of Ocean Science for Sustainable Development and the Decade on Ecosystem Restoration. This fundamental step in mainstreaming omic approaches will help build the collective intelligence needed to address grand scientific and societal challenges of our time: from combating pandemics, to restoring biodiversity in the face of climate change.

Building a Global Genomics Observatory: using GEOME (the Genomic Observatories Metadatabase) to expedite and improve deposition and retrieval of genetic data and metadata for biodiversity research

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Genetic composition data represent a relatively new frontier for our understanding of global biodiversity. The DNA-based genotypic data which underlie essential biodiversity variables such as allelic diversity and differentiation should ideally be linked to the ecological context of where, when and how the genotyped organisms were sampled. Yet most tools and standards for data deposition focus exclusively either on genetic (e.g. Genbank) or ecological attributes (e.g. GBIF; OBIS). The Genomics Observatories Metadatabase (GEOME: geome-db.org) provides an intuitive solution for maintaining links between genetic datasets stored by the International Nucleotide Sequence Database Collaboration (INSDC) and their associated ecological metadata. GEOME facilitates the deposition of raw genetic data to INSDC's short read archive (SRA) while maintaining persistent links to standards-compliant ecological metadata held in the GEOME database as globally unique objects, and also accessioned to GBIF. This approach facilitates findable, accessible, interoperable and reusable (FAIR) data archival practices. Moreover, GEOME enables bespoke data management solutions for large, international, collaborative groups, and expedites batch retrieval of genetic data from the SRA. This talk will describe how GEOME can enable genuinely open data workflows for genetic biodiversity researchers worldwide, drawing on the example of the Diversity of the Indo-Pacific Network (DIPnet; diversityindopacific.net) which aims to promote collaboration and equity among biodiversity scientists working in the world's largest biogeographic region.

Conservation monitoring of genetic variation and management of the Scandinavian wolverine population

Ekblom, Robert

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Maintaining and monitoring genetic variation in natural populations is of crucial importance for conservation and management. Reductions in genetic diversity may have short term consequences in terms of increased inbreeding depression as well as long term effects by reducing the evolutionary potential of the population and decreasing the resilience against environmental change. With the developments in high throughput sequencing and genotyping it has now become possible to identify and monitor adaptive and neutral genetic variation at a genome-wide scale. Genetics has, for example, been intensively used for conservation monitoring of Scandinavian wolverines (*Gulo gulo*) during the last two decades. In particular, genetic analyses have been utilized for individual identification and sex determination of non-invasively collected samples. I will describe recent methodological developments of this work using genomic tools such as whole genome sequencing and high throughput SNP-genotyping, enabling additional applications such as pedigree reconstruction, estimation of historic demography and current effective population size. Our wolverine genome assembly and re-sequencing analyses revealed a genetic diversity among the lowest ever detected in a red-listed population. Demographic analyses indicate that there has been a long-term decline of the effective population size, starting well before the last glaciation. We also found strong genome-wide signatures of inbreeding, but this effect was not observed when analysing a set of highly variable SNP markers for extended genotyping, illustrating that such markers can give a biased picture of the overall character of genetic diversity. Comparing population genetic profiles of samples collected during a 20 year period (over 3 generations), we found a slight but significant increase in genetic variability and a decrease of genetic structure. This could possibly be an effect of gene-flow from neighboring populations. Temporal sampling also allowed us to calculate precise estimates of current effective population size.

Detection and attribution of animal genetic diversity change across scales and taxa: from micro to macroscopic patterns.

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Humans are an evolutionary force. Our impacts on genetic diversity over much of the globe are poorly understood, yet critical to biodiversity conservation. Genetic diversity reflects past and current evolutionary bottlenecks and indicates a population's potential for adaptation to future stressors. Theory predicts that human activities can affect intraspecific genetic diversity via demographic and evolutionary mechanisms. Depending on how human disturbances alter selection, drift, gene flow, and mutation rates, intraspecific genetic diversity may decrease, increase, or remain unchanged over time. Trends in intraspecific genetic diversity are expected to be scale-dependent, just like trends in other dimensions of biodiversity, because human disturbances occurring at different scales may have contrasting effects on genetic diversity. In this talk, I report on the impacts of human population density and intensive land use on animal intraspecific genetic diversity worldwide, at four spatial scales while accounting for effects of geography, time and spatial distance between sequences. We used 175 247 COI sequences collected between 1980 and 2016 to assess the global effects of land use and human density on the intraspecific genetic diversity of 17 082 species of birds, fishes, insects, and mammals. Human impacts on mtDNA diversity were taxon and scale-dependent and were generally weak or non-significant. Spatial analyses identified weak latitudinal diversity gradients as well as negative effects of human density on insect diversity, and negative effects of intensive land use on fish diversity. The observed effects were predominantly associated with species turnover. Time series analysis revealed nearly an equal number of positive and negative temporal trends in diversity, resulting in no net monotonic trend in diversity over this time period. Our analyses reveal critical data and theory gaps and call for increased efforts to systematically monitor global genetic diversity.

A global meta-analysis of genetic change in natural populations

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To develop strategic methods and targets for preserving biological diversity, we must understand how human actions have led to both losses and improvements to the genetic status of species. Over recent decades, we have seen dramatic developments in our genetic tools, analytical methods, and a wide diversity of species examined. As 2020 is the end of the International Decade on Biodiversity, it is timely to gather this evidence onto a common scale and quantitatively ask, “Have we been successful at minimising genetic erosion?” This presentation reports progress on an ambitious effort to answer this question via a global meta-analysis of temporal genetic research. We aimed to quantify the empirical patterns that more than three decades of genetic research have produced, as well as identify understudied areas of opportunity. Our search of the peer-reviewed literature returned 80,271 works, and with sophisticated text mining we narrowed this to 34,346, which were further filtered by topic. During 2019, the project Core Team developed, tested and revised a 40-page screening and extraction protocol, to standardize the data processing process. With the support of COST Action CA18134, 20 researchers participated in a “crash course” workshop in Sweden in March 2020 to begin screening papers and extracting data. By the end of that week, we had processed around one-quarter of the works. The following month, April 2020, the workshop was delivered again – this time online – to 34 new participants to the project. Our 58-strong research team comprises diverse genetic, taxonomic and geographic expertise, and is located across 19 countries; many are members of the GEOBON Genetic Composition working group and the IUCN Conservation Genetics Specialist Group. Data screening and extraction are nearing completion, so we are now beginning to process, validate and analyse our data. Extrapolating from work completed, our final dataset is anticipated to comprise approximately 5,000 temporal genetic comparisons from 600 species distributed widely across the tree of life. In this presentation, I will provide an overview of our goals, report on our progress so far, provide preliminary observations on the dataset we have amassed, and look ahead to the questions and hypotheses we will address. In addition to the Core Team named above, this research is taking place in collaboration with 48 additional contributors.

Developing Essential Biodiversity Variables (EBVs) for the GEO BON Genetic Composition Working Group

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GEO BON's Essential Biodiversity Variables (EBV) are used to harmonize aggregated data sources for improved interpretations of complex biodiversity observations. The EBVs represent a higher-order level than direct observations, but lower than synthetic policy indicators, to provide a bridge between biodiversity monitoring programs, scientific assessments, and decision makers. Genetic composition - the genetic variation that occurs within a species - is a fundamental element of biodiversity. It contributes to the capacity of populations to adapt to environmental changes and defines many biotic interactions. The Genetic EBV class has relevance to global policy instruments including Aichi Target 13, Sustainable Development Goal 2.5 and most other SDGs, Global Strategy for Plant Conservation Target 5 and Target 9. However genetic measurements have not been sufficiently mobilized or integrated into large scale conservation policies to date. Here we discuss four proposed EBVs, which we have identified as the most feasible, scalable, and relevant. These Genetic EBVs are genetic diversity, genetic differentiation, inbreeding, and effective population size. We outline guidelines for their application including: standards, metadata, and data archiving; method and model best practices for translating genetic data into patterns of change across space and time; current challenges in data availability, and informatic standards; and proxies for the proposed EBVs, which do not require genetic data. We emphasize that the routine and robust calculation of Genetic EBVs will depend upon development of standardized field, laboratory, and informatic methodologies, along with F.A.I.R. (Findable, Accessible, Interoperable, and Reusable) archive practices to enable re-use of data and interoperability with analytical tools and other data resources. We conclude with recommendations for improved monitoring and reporting of standardized Genetic EBVs, to allow for more effective conservation of genetic diversity, management of human activities for sustainable development, and enhanced ecosystem services to support long-term persistence of wild and agricultural species.

Using “geospatial genetics” to support global marine biodiversity monitoring and conservation

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The protection of evolutionary processes and maintenance of genetic diversity is necessary for the persistence of biodiversity and the promotion of ecosystem resilience. The importance of accounting for genetic diversity and evolutionary processes has been reflected in a range of marine policy mechanisms, and the genetic “toolbox” has great potential to support marine biodiversity monitoring and conservation at global and sub-global scales. Despite significant scientific advances in the application of genetics in marine protection and management, the systematic integration of genetic information has been generally lacking. One of the primary drivers of this genetics-policy implementation gap appears to be a knowledge and communication disconnect between geneticists and the marine policy and management community. To meet these outstanding needs, we have developed a “geospatial genetics” approach to spatially map genetic data and associated information in a way that can be readily integrated by practitioners into marine monitoring and conservation. The development of techniques to derive geospatial genetic data layers, which can be viewed and mapped alongside other kinds of data commonly used by conservation practitioners (e.g., habitat models, satellite telemetry, survey data), holds promise for increasing the ability of genetic data to more fully support policy decisions. While this approach can be applied to many taxa and habitats, an initial focus was placed on marine mammals, and work was developed and refined through a series of international meetings and published papers, as well as the development of interactive, expert-reviewed case studies hosted on the marine spatial planning tool SeaSketch (humpback whales in the South Atlantic and western Indian Ocean, spinner dolphins in the Hawaiian Archipelago, and common bottlenose dolphins across the Wider Caribbean). Outcomes of the work to date are currently serving in the policy arena by informing the identification of Important Marine Mammal Areas, or IMMAs, an initiative led by the IUCN Marine Mammal Protected Areas Task Force. Through its development, it has become clear that geospatial genetics has great potential to foster increased collaboration and new partnerships among an intersectional community of geneticists, spatial ecologists, and practitioners. This increased opportunity for dialogue and cooperation will serve to advance the field of geospatial genetics and, most importantly, ensure that evolutionary processes are increasingly factored into marine monitoring and conservation, and potentially in freshwater and terrestrial systems.

Suggestions for goals, action target and indicators for genetic diversity in the CBD post-2020 global biodiversity framework

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Genetic diversity within species is recognized as one of the three cornerstones of biodiversity in the Convention on Biological Diversity (CBD) that is to be maintained, monitored and sustainably used. In implementing the CBD, however, the genetic level has long lagged behind. The CBD Strategic Plan for 2011-2020 focus on genetic diversity of domestic species – particularly domestic animal breeds - while targets and indicators for wild species are lacking. Thus, it is highly worrying that the first draft of the new framework for 2021-2050 – which was presented January 2020 – also lacks clear goals and action targets for genetic diversity that includes all species as well as suggestions for indicators to monitor trends in such diversity for all species – wild and domestic. During 2020 over 40 conservation genetics researchers has engaged in highlighting how the CBD post-2020 framework can be improved for genetic diversity. In a Letter in Science the need for a strong goal and an initial suggestion for indicators were highlighted and in an upcoming paper proposed goals, action target and indicators are elaborated further. It is important that indicators for genetic diversity within the CBD framework are possible to apply regionally as well as nationally and worldwide. The suggested indicators are: 1) the number of populations with effective population size above versus below 500, 2) the proportion of populations maintained within species, 3) the number of species and populations in which genetic diversity is monitored using DNA-based methods. Here, the proposed goals, action targets and indicators are presented and the urgent need for spread and strong support for genetic diversity in the upcoming CBD work to finalize the post-2020 global biodiversity framework is highlighted.

The Ira Moana Project: enabling stewardship of marine genetic data at a national scale

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The safeguarding of genetic diversity and monitoring the genetic composition of populations is recognized as crucial in several international commitments and national strategies regarding biodiversity. Yet it remains difficult to access and synthesize genetic data at a national scale to inform monitoring and the reporting of progress toward these commitments. Equally, the calculation and interpretation of Essential Biodiversity Variables (EBVs) for genetic composition is contingent on the accessibility of genetic data with crucial metadata, such as geo-references, habitat, and date of sampling. The 'Ira Moana – Genes of the Sea – Project' (www.massey.ac.nz/iramoana) is working to enable better stewardship of genetic and genomic data for Aotearoa New Zealand's marine biodiversity providing a proof-of-concept for the consolidation of genetic data at a national scale. In partnership with the Genomic Observatory Metadatabase (GEOME, www.geome-db.org), the Ira Moana Project is establishing an ecosystem of interoperable data infrastructures and tools that help researchers follow international best-practice and standards in genetic data and metadata curation and deposition, in line with the F.A.I.R. Principles (Findable, Accessible, Interoperable, and Reusable) and C.A.R.E. Principles for Indigenous Data Governance (Collective benefit, Authority to control, Responsibility, and Ethics; <https://www.gida-global.org/care>). Over 90 researchers from 25 institutions have participated in Ira Moana Project workshops and datathons to build a national resource of genetic and genomic data for Aotearoa's marine biodiversity. This dynamic national resource has created opportunities for data synthesis, will now inform future research priorities, and can be continuously updated to facilitate national monitoring and reporting of genetic composition EBVs for marine populations of Aotearoa. In this talk, I will present an overview of the Ira Moana Project 'ecosystem' and invite others to participate and use the data infrastructure and tools toward their own objectives.

Genomic resources for Australian mammal conservation: The Oz Mammals Genomics Initiative

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Genetic diversity is a key component of biodiversity. There is increasing recognition of the need to understand, monitor, and manage, the genetic diversity of threatened species. However, the availability of genetic and genomic resources for such monitoring varies considerably among even relatively well-studied taxa, and coordinated efforts are needed to develop genetic tools and datasets for conservation. Australia is famous for its unique mammals, but in the last 200 years around 10% of Australian mammals have become extinct and many others are now threatened. Further, many mammal populations declined so rapidly following European colonisation that we are left with a poor understanding of historic species distributions and natural patterns of population connectivity. Genetics provides valuable tools that advance our understanding of Australian mammals, for example by revealing species and population boundaries, characterising genetic diversity within populations, and monitoring the effects of management actions. The Oz Mammals Genomics Initiative (OMG) has adopted a novel collaborative strategy to develop genomic resources for Australia's mammals. OMG brings together researchers, museums, data specialists, and wildlife management agencies, to comprehensively tackle rodent, bat and marsupial genomics at a continental scale. We combine three approaches to developing genomic resources for threatened species: whole genome sequencing, phylogenomics, and conservation genomics. There are relatively few published whole genomes of Australian native mammals. We are preparing well-assembled genomes from 14 species, including a phylogenetically representative range of 11 marsupials. These are already providing reference data and new genetic markers for population-level conservation studies. Our understanding of evolutionary relationships among many mammal species, subspecies, and populations remains incomplete, but this often impedes effective conservation. Robust taxonomy allows delineation of management units and informs actions such as translocations and reintroductions. OMG is generating comprehensive phylogenies of all extant and recently-extinct terrestrial mammals native to the Australo-Papuan region, by sequencing over 1000 genes from hundreds of marsupials, rodents, and bats. This work has already resolved relationships among marsupial families and given new insights into extinct rodents. Ongoing work will clarify taxonomic boundaries for many species and subspecies of conservation concern. Genomes and phylogenies provide a solid base for conservation genomics. OMG projects focused on 17 threatened mammal species are now directly contributing to management and monitoring efforts: by characterising genetic diversity and inbreeding in wild and captive populations; by evaluating the effects of serial translocations on genetic diversity of managed populations; and by identifying appropriate source populations for reintroductions and genetic rescue. Incorporation of DNA from museum specimens, including from extinct populations, will allow extant genetic diversity to be placed in an historical context. These projects have been prioritised to ensure that genomic data are contributing directly to urgent management decisions.

Towards globally applicable genetic indicators for fisheries management

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The rapidly advancing field of genomics is a rich reservoir of tools for conservation and management of wild fish populations. For instance, population structure and local adaptation of stocks can help to identify management units to indicate if which populations should be regulated jointly or separately. Insight into ecological resilience of these units can be gained through indicators of evolutionary potential, e.g. effective population size and the amount of adaptive genetic variation. One of the hardest challenges in this field is the translation of genomic data into indicators that can be readily produced, communicated to and interpreted by policy makers, creating a gap that only grows as genomic technology progresses. Given the lack of usable indicators for the genetic aspects of various internationally agreed targets (such as Aichi target 13 – the safeguarding of genetic diversity), we will investigate which information and indicators stakeholders would consider most helpful in the management of commercial fish stocks. We will specifically compare the needs and expectations of stakeholders between the Global North and South, and between people involved in genetic research and fisheries or conservation policy. We will compile a list of possible indicators based on a review of scientific literature and policy documents, and select the most promising ones based on questions posed to a panel of North and South stakeholders on the desirable characteristics of an ideal indicator. We will then create a prioritization of the selected indicators using a multi-round Best-Worst-Scaling approach, leading to a consensus ranking of the indicators. We will highlight differences in opinion – if any – between stakeholders in the North and South, and between stakeholders of different professions and backgrounds. In dialogue with the stakeholders, we will identify concrete management needs and explore methods of comprehensively communicating the indicators (e.g. visualization). The integration of effective genetic indicators with the views of end-users regarding their user-friendliness will contribute to a higher applicability of genetic indicators in fisheries management and conservation biology in general.

Developing a method to assess genetic diversity – the Scottish approach

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Biodiversity is recognised at the ecosystem, species and genetic levels. International and national reporting for the conservation of genetic diversity have been governed by the Convention on Biological Diversity Aichi Biodiversity Target 13 and will be incorporated in future targets and indicators.

Understanding levels and change in genetic diversity is important. Loss of genetic diversity can reduce fitness and elevate extinction risks of varieties, populations and species. Genetic diversity loss impedes adaptive responses to environmental change (e.g. to climate change or new pests and pathogens) and loss of genetic diversity in key individual species can have wider impacts on diversity in other species. Furthermore, genetic diversity loss reduces the genetic resources available to enhance species traits for human use.

Tackling the Aichi Genetic Diversity target has proved challenging. At national levels, the heterogeneity of the target (encompassing the agriculture, forestry, horticultural and environmental sectors) creates an ownership challenge, as the component parts of the target transcend sectoral, institutional and discipline boundaries. Thus, although data are available for some individual elements (e.g. for crop wild relatives), no cohesive and comprehensive national plans existed for any country.

Bringing together specialists from biodiversity conservation, forestry, agriculture and horticulture, we reviewed existing data and developed a world-first robust national framework and assessment of genetic diversity to promote long-term conservation of genetic diversity. It tackles a major policy challenge in biodiversity science. At a national level, it enables Scotland to address its Aichi Genetic Diversity Target, which was hampered by knowledge gaps. At an international level, by providing a world-first comprehensive national assessment of genetic diversity, we hope the work will be of significant interest as a model for other countries.

Pitfalls and best practices when estimating wildlife genetic diversity in macro-genetic studies

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For decades, population and conservation geneticists have lagged behind population and community ecologists regarding the amount and the range of data they were able to compile and analyze. The number of species/populations, as well as the spatial and temporal scales investigated was limited over this period because of the time and cost required for molecular analyses. Transitioning to a global or 'macro-genetic' scale is a significant step for the conservation genetics field. However, caution is necessary for undertaking this new upscaling of population and conservation genetics, due to inherent caveats and analytical challenges of analyzing genetic data at large spatio-temporal scales.

An increasing number of pioneer studies have recently attempted to explore patterns and drivers of intraspecific genetic diversity across taxa at broad spatial (continental or worldwide) and temporal (e.g. >30 years timespan) scales using massive amounts of repurposed molecular data (predominantly, mitochondrial haplotype sequences) from open databases like Genbank or BOLD. These studies often conclude with broadly drawn, and potentially controversial (and conflicting) findings, such as the absence of consistent effects of human activities on animal genetic diversity worldwide or the global positive relationship between genetic diversity and sea surface temperature in marine species. However, major idiosyncrasies and pitfalls in these macro-genetic studies can compromise the reliability and soundness of their results and interpretations.

We identified important limitations in such studies that may strongly constrain their capacity to reliably characterize worldwide patterns of intraspecific genetic diversity and their drivers at large spatio-temporal scales. These constraints are multiple and include statistical and conceptual constraints (e.g. conflation between spatial and temporal scales in assembled genetic datasets), as well as constraints related to the public archiving of molecular data (e.g. misrepresentation of intraspecific genetic diversity due to inconsistent data-archiving practices). These are all relevant to macro-genetic studies, which are increasing in number. The aim of this presentation is to provide context on these limitations: (i) to prevent future studies from reproducing them (ii) to avoid unintended consequences for biodiversity conservation due to misinterpretations and (iii) to initiate constructive discussion on best practices for future macro-genetic studies.

G-BiKE (Genomic Biodiversity Knowledge for resilient Ecosystems) network: rationale and activities

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Under predicted climate scenarios, maintaining healthy, intact ecosystems will become increasingly important to avoid the severe impacts of climate change. A recent review of 46 independent scientific studies showed that biodiversity increases ecosystem resistance to a broad range of climate events. In particular, genetic diversity is the basis of biological differences, both between species and among individuals of the same species. Several studies have demonstrated that higher genetic diversity provides insurance for coping with future environmental change because the more gene combinations available, the greater the resilience options in an uncertain future. In spite of these solid evidences, genetic diversity, especially across EU, is being overlooked and not explicitly taken into account when implementing conventions and directives for biodiversity conservation and climate action. Explicit consideration of genetic variation and functioning gene flow in species is needed in the post-2020 work. G-BiKE is a scientific network funded by EU H2020 research Program through COST (European Cooperation in Science and Technology) which includes more than 120 researchers and practitioners from 42 countries. Its main scope is to create a large community of conservation practitioners and scientists for bringing genetic diversity to the forefront of future biodiversity policy and practice. G-BiKE's overall activity is broken down into five different Working Groups: Implementing genetics into management; Monitoring of genetic diversity; Genomics and ecosystem services; Biotechnological assessment and Knowledge sharing. With specific Workshops, Training Schools, Short Term Scientific Missions and Policy Briefs G-BiKE aims at firmly installing genetic diversity into policies, monitoring and management integrated into the EU Biodiversity Strategy, Habitats Directive and CBD post-2020 strategy. The latter has been the focus of a recent publication, drafted as a joint effort of many G-BiKEs and other researchers worldwide (Laikre et al, 2020).

Session: Genetic Composition

Poster presentations

Drinking at the last chance saloon – conservation genomic strategies for an endangered plant species

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The persistence of endangered plant species is threatened by a reduction in adaptability caused by loss of genetic diversity and inbreeding. Genomic analysis can reveal levels of diversity and inbreeding, which in turn can inform conservation management decisions. Here we apply a conservation genomics approach to make evidence-based management recommendations for the endangered *Acacia whibleyana*.

A. whibleyana is a wattle, endemic to the Tumbly Bay area of Eyre Peninsula, South Australia. We used population genomic analysis of all known stands of this species to assess levels of genetic structure, diversity, and historical inbreeding. We sampled remnant stands, revegetated stands of unknown origin, plus a post-fire seedling cohort. We identified clear genetic structure across the remnant stands, which fitted a pattern of isolation-by-distance. Remnant stands had low genetic diversity and high levels of inbreeding, which was as expected for this extremely restricted and isolated species. We were able to confidently identify a likely donor of the revegetated stands in all cases. The seedling cohort showed evidence of admixture from two genetic clusters.

Our results indicate a degree of historical connectivity across the landscape, but habitat loss and/or pollinator community disruption are likely causes of the almost zero contemporary connectivity revealed by the genomic data. Greater genetic diversity in admixed seedlings provides hope that genetic rescue through prescribed admixture could be an effective management technique for the species

Session: Freshwater BON

Oral presentations

Development of multi-platform remote sensing framework for peat degradation monitoring

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Peatlands are a rare and unique wetland type in Southern Africa. The fact that they exist in water deficit environments (evaporation > precipitation) makes them especially vulnerable to changes in the hydrology and water sources that sustain them in semi-arid countries such as South Africa. Peatland ecosystem services ranging from carbon sequestration to water purification and hydrological regulation. They regulate water flow and enhance groundwater recharge. Besides the fact that peatlands store over 30% of the world's terrestrial carbon, peatlands also host 10% of the world's freshwater. Peatlands, in general, exist in areas with high water abundance: high rainfall areas, such as coastal areas and areas characterized by available groundwater such as primary aquifers in the coastal areas and karst. Peat accumulates under, permanently inundated conditions. Once the hydrological conditions change, peatland degradation begins. Peat degradation occurs when the water table drops, the peat subsequently dries out, forms cracks and becomes oxidized due to its exposure to the air. Peat degradation results are the release of CO₂ gas to the atmosphere which contributes to climate change. This is the ideal condition for subsurface peat fires to occur. Peat fires can burn and smoulder for a long period causing health risks to the communities, their livestock and wildlife. Sub-surface peat fires are difficult to detect with remotely sensed sensors and characterised by lower temperatures than surface fires. Therefore, this study aims to develop a national multi-platform remote sensing framework for peat fire detection and degradation monitoring.

Monitoring framework was developed corresponding to different monitoring scales, ranging between national and local scales. The system was targeting three major peat characteristics which are: 1) Groundwater level, 2) peat moisture/inundation, and 3) thermal anomalies. These characteristics were assessed at the three monitoring scales. The hydrological indicators coupled with thermal information and vegetation indices were used to assess peat system stress and dryness. The developed framework has various components that range between ground measurements, low altitude sensors, and satellite-based indicators. Peat fires are a set of complex processes and factors that interact to make peatland systems susceptible to fire. At the national scale, anomalies detection can be used to differentiate between healthy and degraded systems. This is by analysing time series data that represent the land surface temperature, vegetation conditions and groundwater levels. The annual and seasonal analysis of the groundwater level showed a high association between groundwater levels and peat degradation levels at the three tested study sites.

Monitoring global change effects on mountain aquatic ecosystems: strengths and weaknesses

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Global change has important implications for human societies, including the availability of food and water, the increase of environmental hazards, the loss of biodiversity or the appearance of new pathogens and diseases. Identifying and quantifying the impacts of global change within the biotic and abiotic elements of the ecosystems is critical to predict future scenarios and consequently, promoting reliable adaptation measurements to reduce its negative effects. In this regard, ecosystems of mountain areas, and especially aquatic ecosystems within them, are recognized as “sentinels for environmental change”, as they show patterns that are often more readily identifiable than in any other location of the globe. Monitoring aquatic ecosystems of mountain areas is essential to 1) understand and quantify the effects of global change, 2) anticipate measures to face impacts of global change 3) improve and address conservation actions to improve freshwater biodiversity. In this work, we have compiled information describing the monitoring programs that are currently carried out in mountain freshwater ecosystems, aiming to evaluate their quality, extent and usefulness to assess the impact of global change. We have address this objective at three level of detail from the worldwide scale using the ILTER network data to the European scale, based on the monitoring programs carried out in selected Mountain National Parks. Our results highlight that monitoring programs are far from agreeing a common strategy. Even at the continental and national scales, contrasting strategies and level of detail have been historically applied. Water physico-chemistry, physical habitat and biodiversity are commonly used in many monitoring programs, while variables dealing with biological community structure and especially ecosystem functioning are especially scarce. The assessment carried out in the Spanish Mountain National parks (the most complete and rich in the whole EU) evidenced, in addition, a contrasting level of monitoring according to the targeted aquatic ecosystem. In this regard, rivers account with most of the attention and the largest amount of resources, while wetlands are rarely considered in the monitoring programs. We consider that greater international efforts must be done to provide an integrated and coordinated strategy to monitor mountain aquatic ecosystems at national, continental, and global scales. A coordinated monitoring program from local to worldwide scales is needed to improve our understanding on the effects of global change at several levels of biological organisation.

Application of a socio-ecological approach to the selection of indicators and design of freshwater monitoring programs in a large and complex tropical watershed

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The Magdalena-Cauca basin exhibits a high variability of climates and ecosystems, and therefore a great ecological offer, which is reflected, for example, in having 76% of the endemic fish species in Colombia. This basin is also the axis of socioeconomic development in Colombia, housing 77% of its population, producing 86% of its GDP, 75% of hydraulic energy, 70% of agricultural crops and 50% of freshwater fishing. The convergence of ecological complexity with anthropic pressures has led to the deterioration of fishing resources, alterations related to energy production, mining, agriculture and infrastructure development; and general trajectories of degradation in ecosystem health, with the consequent alteration of ecosystem services which are key for the sustainability of communities inhabiting the basin. We took a socio-ecological system approach to understand interactions between functional biodiversity, social domain, and land use. First, we carried out a historical reconstruction of territorial changes, together with different stakeholders, such as authorities, NGOs, and communities. Then, through a combination of expert knowledge and participatory analyses, we built a conceptual model of the main positive and negative relationships of the socio-ecological system, using the Response-Pressure-Status-Benefit model as a guide. Finally, potential indicators that were expected to result from monitoring trends were assigned to each of the identified relationships. With all this, the construction of socio-ecological narratives were made, and allowed us to prioritize present strategic ecosystems, environmental services, drivers of change, and information needs. Subsequently, we analyzed the roles or governance for the capture and reporting of potential indicators, as well as the articulation and strengthening requirements to implement comprehensive monitoring of these socio-ecological systems. As a result, a series of guidelines were obtained for the development of monitoring programs and systems with a socio-ecological focus, that contemplated implementation routes according to the roles performed by different actors. With the application of this approach towards the constructions of monitoring programs, and their resulting information systems, as well as in the selection of indicators, and the design of workflows for their reporting, we aimed to guide decision-making and management actions to address environmental problems of water bodies in a comprehensive manner.

An ecological integrity index for páramo lagoons based on biological indicators and habitat: a case study of La Virginia lagoon, páramo Sumapaz, Colombia

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Jorge Tadeo University, Colombia

Ecological integrity shows ecosystem structure status and functioning in relation with pristine ecosystem reference conditions or ecosystems with high conservation status. There aren't ecological integrity index for lentic ecosystems of páramo. Páramos are high mountain biomes (elevation 2900-4700 m), characteristic of the Andes mountains of Colombia, Venezuela and Ecuador, with extensions in Costa Rica and Panama. Objective is to development and validation of an ecological integrity index for lentic ecosystem of páramo using three multitemporal ecological status indicators: Biological integrity, aquatic habitat integrity and habitat quality considering cover changes in lagoon landscape. Biological integrity assessment is made through formulation and implementing of a biological integrity composite index (BICI) based on macrophytes biological integrity, macroinvertebrates, and birds. Habitat integrity assessment is performed by formulating the aquatic habitat integrity index (AHII) considering water surface availability, types of substrates and physical-chemical factors. Habitat quality at landscape scale assessment is done by considering changes in landscape lagoon cover and using InVest quality model. BICI and AHII have a score 0.63 (good integrity) and 0.54 (acceptable integrity), respectively. At landscape level, habitat provision is good (89.7% – 90.3%) in the lagoon, but it decrease (9.7%) close to a rural road. Even though aquatic biodiversity is high, the habitat is subject to continual alterations, including effects of ENSO and climate variability, which compromises the ecosystem conservation and drinking water supplement, the most important ecosystem services of this páramo.

The link between human activities, water quality and benthic macroinvertebrates in the headwaters of Lake Edward Basin, Uganda: Management lessons

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The Greater Virunga Landscape forms part of the Lake Edward Basin in South western Uganda and is one of the highly populated landscapes. We therefore investigated variation in water quality and benthic macroinvertebrate diversity along a protected area-human settlement landscape as indicators of human impacts on water provisioning to surrounding communities. Physicochemical parameters of water quality were assessed onsite using electrochemical methods while other water samples were analysed in the laboratory for heavy metals, nutrients and faecal contamination. Benthic macroinvertebrates were sampled using kicknet samplers at suitable locations within the streams. The results showed that water quality and benthic macroinvertebrates were relatively pristine inside and near protected area boundaries, although in some parts of Echuya Central Forest Reserve, water quality was highly degraded due to the nature of forest management practices. The results show the importance of protected area systems in maintaining the flow of ecosystem services to surrounding communities. The findings are being used to identify water sources that can be harnessed and supplied to local communities for better human wellbeing. In terms of policy implications for managing degraded water resources outside protected area systems, we recommend restoration of degraded riparian vegetation or replanting of vegetation along stream banks to reduce degradation and or pollution of freshwater resources.

Status and trends in Arctic freshwater biodiversity: Highlights of the first circumpolar assessment by the Arctic BON (CBMP)

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Across the Arctic, variation in warming rates, development, and biogeography may be expected to contribute to changes in biodiversity of freshwater organisms. Critical to detecting such changes is the quantification of existing biodiversity patterns across the Arctic region. The Circumpolar Biodiversity Monitoring Program (CBMP, part of the Conservation of Arctic Flora and Fauna working group of the Arctic Council) is the Arctic BON, an international network of scientists, government agencies, Indigenous organizations and conservation groups that is working to facilitate more rapid detection, communication, and response to biodiversity-related trends and pressures in the Arctic. The freshwater group of the CBMP (CBMP-Freshwater) has completed the first circumpolar assessment of freshwater flora and fauna to determine the state of biodiversity in Arctic freshwaters. CBMP-Freshwater compiled and harmonized biodiversity data from all Arctic countries, including data from both historical (paleolimnological data and records from 1800 to 1950) and contemporary (post-1950) time scales to develop a circumpolar freshwater database. Assessments compared and contrasted the regional state of Arctic freshwater ecosystems in North America, Iceland, Greenland, Fenno-Scandia, and Russia. In addition, circumpolar assessments for specific focal ecosystem components, namely fish, benthic invertebrates, benthic algae, macrophytes and plankton, provided novel analyses of how climate change and associated environmental drivers affect these biological components. This group of studies represents the first circumpolar assessment of trends in Arctic freshwater biodiversity. In this presentation, we outline the major findings of this international effort, and highlight multiple-stressor scenarios that act on the biodiversity and biogeochemistry of Arctic freshwaters and cause change in biological communities of lakes and streams.

Essential Biodiversity Variables: how soil information can help

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Soil provides a variety of goods and services and is a key natural resource to realise a number of UN Sustainable Development Goals. Quality-assessed soil information is required to underpin a large range of global assessments, such as soil and land degradation, sustainable land management, and environmental conservation. Soil is also fundamental for supporting biodiversity and influencing directly many indicators of essential biodiversity variables, such as productivity, nutrient retention, vegetation species distribution and habitat composition. In this work, we use SoilGrids maps to show the relevance of soil for modelling essential biodiversity variables as a source of information on erosion risk, carbon sequestration potential, productivity and water content, among others. SoilGrids is a source of consistent, medium-resolution derived soil properties to support global modelling. We used an updated version of SoilGrids that considers a larger set of standardized and quality-assessed soil observations, an updated set of covariates and improved machine learning models. It provides global assessments of prediction uncertainty, quantified with a 90% prediction interval, and has an improved validation procedure providing more realistic metrics of map accuracy. We highlight some of the challenges of assessing soil information at global scale. The geo-computational framework developed offers great flexibility to apply a diverse set of models to generate soil information products tailored to specific applications. We present simple indices that can support or integrate the set of Essential Biodiversity Variables, in particular for Ecosystem Function and Ecosystem Structure classes.

The Freshwater Information Platform: an online network facilitating the work of FWBON

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Species distribution data are crucial for understanding biodiversity dynamics and the underlying drivers. This is especially the case for freshwaters, which are among the most endangered ecosystems globally. However, a huge body of data gathered by scientists and water managers is currently difficult to access: systematic data publishing practices have not been fully adopted yet and data embedded in scientific papers and research project websites are often challenging to extract. At the same time, data and knowledge generated through publically-funded research or monitoring programmes are considered a common good.

The Freshwater Information Platform (FIP) aims at pooling freshwater related research information from multiple projects and initiatives to make it easily accessible for scientists, water managers, conservationists and the interested public. The FIP consists of several major components, three of which form its “data publication unit”: (1) the Freshwater Metadatabase with the connected Freshwater Metadata Journal, (2) the Freshwater Biodiversity Data Portal as base of the “GBIF Freshwater Network” and the (3) Global Freshwater Biodiversity Atlas with its interactive online maps. Here, we focus on introducing these components as tool to streamline open access freshwater data publication, arguing it will improve the capacity to protect and manage freshwater biodiversity in the face of global change.

Additionally, we shortly introduce another component of the FIP, namely the Freshwater Species Trait Database as it is a valuable tool to support the Essential Biodiversity Variables concept.

Hatch of Hope? Survival Estimate and Habitat Association of Re-introduced Critically Endangered Royal Turtle of Cambodia

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Reintroduction of head started species is a widely applied management approach for conserving endangered species, especially for those having minimal or lack parental care. However, its conservation value is often challenged for its unknown success. Survival estimate is one of the vital demographic measures to inform the performance of released species, and in turn evaluation of the project's efforts. Here, we estimated the first-ever survival rate of reintroduced individuals of Critically Endangered Southern river terrapin, *Batagur affinis edwardmollii* at Sre Ambel River, Cambodia. We used detection histories of 21 released individuals obtained from both active and passive acoustic telemetry for the year 2015-2016. We applied the Cormack – Jolly - Seber model in the Bayesian framework combining both data from both monitoring methods to estimate the annual apparent survival rate. We also modeled the possible habitat parameters influencing their occurrence in the river. We estimated an average apparent survival of 0.24 (CI: 0.10 - 0.44). This low survival estimate could be attributed to probable high emigration rates, which is not separated from mortality in the current model. Our assessment of the physio-chemical parameters of river water found that the turtles prefer slightly acidic water with moderate conductivity during the months of April – June.

The place of freshwater reptile monitoring in global assessments of freshwater biodiversity

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Recent global assessments show that 270 turtle species, 237 snakes, 101 lizards, and 23 crocodilians may be attributed to freshwater. Hence monitoring of this group could play an important role in tracking changes in global freshwater biodiversity. We examined global patterns in species sighting records in GBIF made between 2013 and 2018. There were records for a majority of known species of crocodilians and freshwater turtles for this period but only about one in three freshwater lizard species and one in ten freshwater snake species were sighted. Of the 426 Freshwater Ecoregions of the World (FEOW) freshwater reptiles were recorded in only 265 regions and there was a strong correlation between the number of sightings made in an Ecoregion and the number of species recorded. Monitoring efforts would need to improve substantially across the world before freshwater reptiles can be used widely to assess changes in freshwater biodiversity at sub-national to Global scales. However, even with the current level of observations, this group could be useful in tracking biodiversity in some environments. We examined records for the same five year period in and near 3525 cities across the world with a population exceeding 100000 and found records of freshwater reptile sightings from 1327 cities with more than five species in 311 cities. The ability of some species to survive urban pressures together with the high sensitivity of other species mean that freshwater reptiles could be particularly useful in urban biodiversity monitoring and conservation. However our analysis showed that even cities that have the greatest species richness probably do not support enough taxa for freshwater reptile assemblages to be used in measures of community composition in a similar way to freshwater macroinvertebrates, fish or birds.

Remote sensing of lacustrine and palustrine wetlands under climate change in the Grassland Biome of South Africa

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We report on the result of a study which assessed the use of Sentinel–1 and –2 images for the monitoring of palustrine wetlands in the Grassland Biome of South Africa. Remote sensing are particularly crucial for monitoring and informed decision making related to wetlands in arid to semi-arid Africa. Climate change impacts have shown an increase in the frequency and intensity of drought for sub-Saharan Africa where many communities are highly dependent on rivers and wetlands. The global monitoring of open water systems with remote sensing are in place, yet in semi-arid countries such as South Africa, open water constitute only a tenth of wetland cover types.

The use of the freely available Sentinel-2 satellite images of the European Space Agency was compared to the proprietary WorldView-3 images for separating wetland and upland vegetation in the grassland biome of South Africa. We tested whether wetland vegetation communities can be mapped and whether above ground biomass (AGB) of the wetland vegetation, and soil moisture content of the wetland, can be quantified. In addition, we evaluated the capabilities of the Sentinel-2 sensor in characterizing the maximum extent of inundation and the hydroperiod of predominantly open water depressions in the grassland biome.

Spectra of wetland vegetation were found to be highly separable from upland vegetation in the Grassland Biome for two study areas, including Tevredenpan (Mpumalanga Province) and Hogsback (Eastern Cape Province). Sentinel-2 attained high accuracies for mapping wetland vegetation communities, comparable to, or slightly less than those attained by using proprietary WorldView-3 images.

The Sentinel sensors were able to predict the AGB of wetland vegetation with accuracies comparable to those of WorldView-3. This means that large changes in AGB can potentially be detected and monitored at a site scale for vegetated wetlands in the Grassland biome. AGB is an important contributor to the process and health of peat wetlands. Climate change is expected to reduce the amount of AGB in wetlands: seasonal monitoring of the amount and phenology will provide early warning of vegetation loss.

The Sentinel optical and Synthetic Aperture Radar (SAR) sensors both showed potential for estimating soil moisture content (SMC) across a wetland-upland gradient in the Grassland Biome.

The higher temporal frequency of Sentinel–2, compared with Landsat, improves the determination of the maximum extent of inundated depressions. This is important information for SDG 6.6 reporting, and for characterising hydroperiod classes for the inventory of wetlands.

Although remote sensing has contributed primarily to the monitoring of open waterbodies over the past fifty years, the new sensors, such as Sentinel, enabled improved capabilities for monitoring both lacustrine and palustrine wetlands. Having free access to these big datasets are important for African countries to enable informed decision making for wetlands.

Assessing the threat status and protection levels of South African river and wetland ecosystem types

van Deventer, Heidi

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South Africa uses two headline indicators for assessing and tracking the status of biodiversity. The Ecosystem Threat Status (ETS) and Ecosystem Protection Levels (EPL) of inland aquatic ecosystems, including rivers and inland wetlands, and freshwater species, were assessed as part of South Africa's third National Biodiversity Assessment of 2018 (NBA 2018).

The diversity of inland aquatic ecosystem types are primarily represented by (i) river ecosystem types as a line shapefile, and (ii) wetland ecosystem types as a polygon shapefile. The ecological condition of rivers were determined through monitoring and expert ranking, while those of wetlands were modelled primarily from the land cover spatial data. The ecological condition was then used, combined with a biodiversity threshold of 20%, to determine the threat status, and then combined with the protected areas layer to assess the protection levels. The red list assessment was done for seven freshwater taxa, the red list index and back casting applied for trends, while a novel protection level was tested for the taxa too.

Wetland and estuarine ecosystems were found to be the most threatened and least protected ecosystems in South Africa, with 88% of wetland area and 99% of estuarine area threatened. The Aichi Target was not reached, with only 14% of rivers and 7% of inland wetlands found to be within protected areas.

Freshwater fishes are the most threatened species group assessed in South Africa. One-third of South Africa's native fish species and two-thirds of endemic species are threatened. Predation by invasive alien fishes and habitat degradation are key pressures on native freshwater fish. Freshwater fish showed the highest extinction risk and steepest decline in their Red List Index, compared to seven other taxonomic groups. Freshwater fish are poorly protected and affected by pressures upstream of their habitats.

Biological invasions threaten biodiversity and human wellbeing, and are expected to increase under climate change impacts.

Climate change impacts have resulted in more intense droughts and fires, and combined with an increase of water abstraction in a semi-arid country, have led to the dying of riparian forests and burning of 17 peatlands over the past decade.

Intervention programmes proves successful, including species breeding programmes for critically endangered frogs, the use of piscicide in the eradication of invasive fishes, and the return of dragonflies after the removal of invasive trees. 27 Taxa of Conservation Concern are prioritized for species management plans.

Healthy ecosystems can help us adapt to climate change, and therefore restoration of rivers and wetlands in the next decade is crucial. Cooperative governance and a catchment-based approach to management needs to be adopted. The development of water-efficient technology under the 4th industrial revolution is important for water-scarce countries.

The structure of fish and macroinvertebrate communities in the Karun River system, Iran

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The Karun River, western Iran, is the largest (catchment area of 57'059 km²) and the only navigable river system in Iran. It flows westwards out of the Zagros mountain range (max. altitude 4409 m.a.s.l.), traverses the Khuzestan plain, and joins the Shatt al-Arab, which then enters the Persian Gulf. The freshwater ecosystems of the Karun are affected by various uses of its water and catchment (i.e. agriculture, rural development, aquaculture and hydropower facilities) but the impacts of these activities on fish and macroinvertebrate communities is largely unknown. This is particularly problematic because the Zagros mountain range is the heart of the Irano-Anatolian Biodiversity Hotspot. As part of a collaborative project between Iranian and Swiss research groups, we investigated fish and macroinvertebrate communities and the abiotic conditions at 53 lotic sites in the entire river system in spring and summer 2019. Sites ranged from small high-altitude creeks to large lowland rivers, the latter often affected by various anthropogenic pressures. Pristine abiotic conditions were mainly restricted to small high-altitude sites, which had low chemical pollution and excellent habitat features (in particular with low fine sediment deposition, natural channel morphology and intact riparian vegetation). Fishes were sampled in all habitats of the respective sites by backpack electro fishing and benthic macroinvertebrates on ten transects per site using kick-netting and surber sampling. Samples were preserved in formaldehyde and transferred to the laboratory for identification. We identified 36 fish species and 77 macroinvertebrate families. Fish communities were dominated by cyprinids (65.2%; mainly *Capoeta coadi*, *Garra rufa*, *Capoeta aculeata*) and macroinvertebrate communities by chironomids (46.4%), both taxa being relatively insensitive to habitat degradation. Overall, we observed significant correlations between fish and macroinvertebrate communities in terms of various diversity indices (based on species richness and evenness) and overall abundance, suggesting similar community responses of both organism groups to the anthropogenic and natural gradients in the Karun. Specifically, we measured highest fish diversity in large lowland river reaches despite being rather polluted, thus pointing at positive effects of connectivity and habitat heterogeneity, but probably also of introductions, for biodiversity. Rare endemic fish species (e.g. benthic species such as *Sasanidus kermanshahensis*, *Oxynoemacheilus freyhofi*, *Turcinoemacheilus hafezi* and *Turcinoemacheilus saadii*) were restricted to relatively clean headwater sites characterized by coarse sediment and high flow velocity. We measured highest macroinvertebrate diversity in sites with excellent habitat features albeit moderate chemical quality. In particular, we observed highest EPT diversity (the orders Ephemeroptera, Plecoptera, Trichoptera, comprising many sensitive species) in riffle sites characterized by cobble sediment and high flow velocity. Findings from our project will contribute to the management and conservation of freshwater biodiversity in this region, which currently undergoes major environmental changes due to human population growth, increasing resource demands and climate change.

Session: Freshwater BON

Poster presentations

Fish diversity and resources in the Yangtze River

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The Yangtze River, China, is one of the longest river in the world (about 6,300 km) and also is the aquatic biodiversity hotspot with more than 400 fish species. We have monitored the fish diversity and resources in the Yangtze River since 1997 in order to understand the situation and changes on the river ecosystem. The monitoring area covers the upper-middle Yangtze basin. We collect 194 fish species, including 51 species endemic to the upper Yangtze and 23 exotic species. The resources of the symbolic fish, such as four major Chinese carps, Chinese sturgeon, Yangtze sturgeon, and Chinese paddlefish, also are monitored. Four major Chinese carps only reproduce 19.3 billion eggs on average, which is reduced to 16% in the 1960s., in the middle Yangtze. The natural populations of the three sturgeon have been extinct or near extinction. It is evident that the fish diversity and resources in the Yangtze have been declined sharply due to human activities, especially overfishing and damming. The Chinese government is implementing a series of policies for protecting the Yangtze ecosystem. The ten-years fishing ban, which will eliminate completely the effects of the fishing, is considered the starting point or turn point to restore the Yangtze. However, the more difficult problems, such as habitat destruction, fragmentation, flow regulation, caused by construction of dams currently have not been solved. These native and endemic fish still will be under threat.

Phytoplankton biodiversity in the context of ecological and trophic states of the lakes

Napiórkowska-Krzebietke, Agnieszka

Inland Fisheries Institute, Poland

It is generally well known that biodiversity refers to the variety and variability of species living on Earth, and taxonomy provides the “key to life”. Climate changes with global warming and unusual phenomena (such as heat waves, droughts, violent storms), as well as human activities, this all has recently put the biodiversity at risk in many ecosystems including freshwaters. This research focused on describing the variability in phytoplankton biodiversity caused by changes in ecological and trophic states of temperate water bodies in Poland, as a case study. In general, the lake ecological and trophic conditions significantly affect the species biodiversity. Present findings suggest that species richness increases along with the increase of a lake trophic level from mesotrophic to eutrophic, while its significant decrease is usually found in hypereutrophic waters. By assessing the lake ecological status according to Water Framework Directive can be also found that lower species richness is often noted in lakes having a high or good ecological status (at least good water quality) whereas higher species richness in lakes with poor ecological status (poor water quality). Similar trends can concern the values of biodiversity indices, for example the Shannon index or evenness.

Additionally, species richness and biodiversity indices can be resulted from the other factors, for example the degree of heating the waters, water exchange time, competition or allelopathy. Present studies suggest that warmer waters, faster water exchange and frequent lack of a winter ice cover in the lake included into water-cooling system were favorable to diatoms, euglenoids and chlorophytes. In other case, higher species richness and biodiversity indices were generally recorded during the turbid-water state than the clear-water state of a lake. It was confirmed that strong competition and allelopathic effect of *Chara* species significantly helped to stabilize better water quality on the one hand, but negatively influenced the phytoplankton biodiversity on the other hand. Therefore, it is recommended that each case should be analyzed separately.

Session: Marine BON

Flash presentations

Integrating data from researchers, industry, and environmental licensing: SIMMAM a success case for marine mammals in Brazilian waters

Barreto, Andre Silva; Cabral, Alencar; Taufer, Renata Maria; Almeida, Tito Cesar Marques de
LIBGeo, EMCT/UNIVALI, Brazil

In the past, researchers have been traditionally reticent to share data, especially if it was regarding species that are difficult to be found, such as marine mammals. Even though this situation has changed in the last decades, large numbers of sightings still sit in private data collections. Added to that, environmental licensing processes usually require the acquisition of new data that, at least in Brazil, usually end only in unpublished reports. This data, even being classified as 'public access', has little or no availability to researchers. If all this data could be integrated into larger and public repositories, they could provide new insights into marine mammal distributions. To minimize this problem, since 2005, an effort has been underway to aggregate data on strandings and sightings of marine mammals in Brazil. The development of a data management system built specifically for marine mammal data (SIMMAM - Sistema de Apoio ao Monitoramento de Mamíferos Marinhos), has allowed gathering information from these three sources. Since 2010 it has been widely used by the oil and gas industry to record data collected by Marine Mammal Observers (MMO), as part of the environmental licensing of seismic exploration for offshore oil. In parallel, researchers have been using SIMMAM as a repository for data collected in specific research projects, both along the shore and in open waters. At the moment, SIMMAM holds almost 45,000 records of strandings (44%), sightings (55%), and incidental captures (1%), of 59 species of aquatic mammals (Mustelidae = 2; Pinnipedia = 7; Mysticeti = 9; Odontoceti = 39; Sirenia = 2). As there was also an effort to collect records from the scientific literature, it now spans 109 years of data (1911 to 2020). Analysis of the diversity within the SIMMAM database indicates that as a whole it has reached the total richness of cetacean species, but not of pinnipeds. SIMMAM data shows that while data from scientific sources provide records with better taxonomic details, data from the oil industry has a wider geographical scope. This study indicates that integrating data from multiple sources seems to be the best option to sample marine mammal biodiversity where resources dedicated to research are scarce.

Stratifying ocean sampling to optimise monitoring of biodiversity

Costello, Mark J. (1,2); Jefferson, Tamlin (2); Zhao, Qianshuo (2)

1: Nord University, Norway; 2: University of Auckland, New Zealand

Sampling is always biased, geographically, temporally and taxonomically. Every sampling method brings its own biases and limitations. Thus, our view of the world is biased. Yet we know the world is not homogenous, and patterns of environmental variability and biodiversity vary geographically and taxonomically. We now have a rich collection of global environmental and biological data that provides a rational basis for a stratified sampling of the oceans. Not everything can be cost-efficiently sampled, but any such triage of what is sampled should be justified.

In this talk, we show where there is more and less environmental variability, biodiversity (from genes to ecosystems), threatened species and fishery productivity. These data indicate where a greater density and frequency of sampling is needed to monitor trends in biodiversity. Maps like these may help justify and obtain funding to sample these areas.

The study of photosynthetic parameters of microalgae from Penang intertidal areas using Water-PAM and Pocket-PAM

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Pulse Amplitude Modulation (PAM) fluorometer is a powerful tool in microalgae studies as it can provide useful information on photosynthetic activity of microalgae. However, different types of PAM available in the market may lead to a variety of outputs. To overcome this problem, we would have to determine the differences of photosynthetic parameters using two fluorometers (Water-PAM and Pocket-PAM) in field studies. Field samples were collected at Teluk Bahang and Pantai Jerejak, both locations in Penang, Malaysia. The maximum quantum yield (Fv/Fm), maximum relative electron transport rate (rETR_{max}), photosynthetic efficiency (α), and photoacclimation index (E_k) in these samples were measured. Nutrients and chlorophyll a data were also presented to determine the nutrient conditions and biomass in the field samplings respectively. Water-PAM displayed significantly ($P < 0.05$) higher Fv/Fm and rETR_{max} compared to those of Pocket-PAM in sediment and seawater samples. The output differences of Fv/Fm, rETR_{max}, α and E_k values might be due to the unequal ability of the cells to absorb light at different wavelengths as Water-PAM and Pocket-PAM had red and blue light LEDs respectively. In addition, the technical characteristics of the different types of PAM, in particular the approximate detection limit of Water-PAM (0.025 $\mu\text{g chl a L}^{-1}$) is lower compared to that of Pocket-PAM (500 $\mu\text{g chl a L}^{-1}$). Our findings suggest that Water-PAM is more suitable for use in field studies compared to Pocket-PAM.

Observing life in the deep-ocean with National Geographic's deep-sea camera system; a low-cost and scalable approach

Giddens, Jonatha; Turchik, Alan; Delaney, Denley

National Geographic Society, United States of America

National Geographic Society's Exploration Technology Lab developed a low-cost deep-sea camera system in 2009 that has since been deployed opportunistically across the world's ocean. From these exploratory expeditions, we are assessing the abundance and diversity of bathyal demersal scavenging fauna through image analyses, generating biodiversity indices, and characterizing deep marine biogeography to help inform conservation planning. Here we demonstrate an emerging approach to fill critical biodiversity observing gaps in deep-ocean by extending the depth range of low-cost deep-sea imaging technologies. Our Deep-Sea Research Project is currently defining our science strategy for the future to best meet global ocean observing needs. We aim to form partnerships for sustained multidisciplinary ocean observing, and to refine our data process to best serve the Global Ocean Observing System and GEO BON in the Decade of Ocean Science for Sustainable Development.

Tracking ecosystem sentinels: identifying marine megafauna hotspots for biodiversity conservation

Hammerschlag, Neil (1); Black, Chelsea (1); Herrera, Enrique Montes (2); Ogburn, Matthew (3); McKinzie, Megan (4); Woodward, Bill (4); Muller Karger, Frank (2)

1: University of Miami, Rosenstiel School of Marine & Atmospheric Science; 2: University of South Florida; 3: Smithsonian Environmental Research Center; 4: U.S. Animal Telemetry Network

When considering biodiversity conservation, information beyond type, abundance and distribution of species is required for protection, forecasting and mitigation against anthropogenic and other impacts. Sentinel species are long-lived, highly migratory marine megafauna that integrate trophic information across multiple spatiotemporal scales. They provide unique insight into ecosystem processes and change. They are sentinels of an ecosystem's response to environmental variability and change. We demonstrate a framework for coupling telemetry data from tagged marine megafauna (e.g. sharks, turtles, tunas, whales, manatees) with remotely sensed environmental data on multiple Essential Ocean Variables and thematically classified "seascapes" to identify and characterize areas of overlapping migratory pathways and shared highly suitable habitats. These marine megafauna hotspots provide opportunities for prioritizing spatial protections, planning for multiple use of ocean spaces, and monitoring for ecosystem responses to environmental change.

Assessing the diversity of marine phytoplankton across the South China Sea and Malacca Strait using metabarcoding approach

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Phytoplankton serves as the primary producer in the coastal ecosystem, supporting the basal of the marine food web and mediating biogeochemical cycles of the planet earth. However, the proliferation of selected phytoplankton taxa in the eutrophic water has caused oxygen depletion and subsequently lead to the mortality of marine life. Some species are biotoxins producers that caused a tremendous impact on public health. In this study, the phytoplankton community assemblages across Peninsular Malaysia covering the waters of the South China Sea (SCS) and Malacca Strait (MS) were investigated by the mean of genetic metabarcoding. A total of 72 sub-surface water samples were collected during the research cruise in July-August 2019 using a 16 µm-mesh size plankton net, followed by filtration onto a 0.2 µm nylon filter membrane. The samples were preserved in buffered-saline ethanol and kept at -20 °C. DNAs were extracted, the 18S rDNA V9 region was amplified, and analysed by Illumina Miseq platform. The results revealed a total of 386 phytoplankton species: 166 Bacillariophyta, 154 Myzozoa, 24 Ochrophyta, 15 Chlorophyta, 15 Chrytophyta, and 12 Haptophyta from 19,847 Operational Taxonomic Units (OTUs). The number of OTUs that annotated as harmful algal bloom species was 28, with seven new records of occurrence in Malaysian waters. The predominant Thalassiosiraceae, Coscinodiscophyceae, Hemiaulaceae, and Chaetocerotaceae were observed with high OTU abundances, particularly the near-coast sampling stations of Malacca Strait, this was likely influenced by high nutrient loading in the region. High species diversity was documented at the offshore sampling stations, especially in the northern part of Malacca Strait, with the alpha diversity (Shannon index) ranged 1.040-5.469. This study provides valuable baseline inventory of marine phytoplankton diversity, which is crucial for future monitoring of the coastal ecosystem health and biodiversity observations in Malaysian coastal waters.

Cold or warm? That is the question: EOVS monitoring in the Galapagos Marine Reserve by a citizen science observation network

Moity, Nicolas; Ramírez-González, Jorge

Charles Darwin Research Station, Charles Darwin Foundation, Santa Cruz, Galapagos, Ecuador

Ocean observations provide the information necessary to detect and understand changes in marine ecosystems. They serve to inform management, governance, and policy decisions to enhance the protection and conservation of Marine Protected Areas. With a protected area of 138,000 km², traditional monitoring actions of the Galapagos Marine Reserve (GMR) requires challenging logistics and expensive resources. As a result, current monitoring schemes are scarce in time, space and ecological representativeness, limiting our understanding of the biodiversity trends and ocean dynamics in this unique archipelago. Sea temperature has been identified as an Essential Ocean Variable due to its importance in biophysical patterns and processes. To continuously measure sea temperature, we started the Galapagos Islands Climate Change Observation Network project. The aim is to implement an affordable, low-maintenance, automated monitoring system of the sea temperature in the GMR with the help of a network of citizen scientists. We use small and affordable temperature loggers that communicate with smartphones via an app to set mission parameters and data retrieval. Loggers are placed underwater, at visitor-tourism sites. The data collection is enabled by a network of naturalist guides who visit the sites every week as part of their guidance. After some months of data gathering, loggers are retrieved by the guides, data is downloaded on board and the loggers are placed back underwater. Data is sent to and collected by the Charles Darwin Research Station where it will be stored, analysed and summarized in publicly accessible on-line dashboards. So far, we placed 18 temperature loggers in rocky intertidal and subtidal habitats (sampling every hour) covering all Galapagos' bioregions at depths ranging from 0 to 43 m. This reproducible, scalable and affordable system will significantly enhance the data collection capability of stakeholders in the GMR and will continue beyond the lifetime of the project with minimal financial investment required once established. Once proved successful, a similar system could be replicated in other MPAs where human activities take place (e.g. fishers, local community and tourists recreation) to expand the geographical coverage of the temperature observations. The data collected will enable the detection of sea temperature variability and its association to ecosystem changes related to climate change and to find patterns that explain the spatial-temporal dynamics of the GMR biodiversity in the long term. Analysis on temperature data will be related to biological variables such as abundance of charismatic and indicator species, artisanal fisheries landings, and others. This information will have direct use in zoning and conservation-oriented management of the GMR.

MBON: Addressing the Need for Best Practices for the Complementary Essential Ocean Variables (EOVs) and Essential Biodiversity Variables (EBVs)

Muller-Karger, Frank (1); Miloslavich, Patricia (2); Bax, Nicholas (3); Costello, Mark (4); Sousa Pinto, Isabel (5); Montes, Enrique (1); Soares, Joana (6); Soccodato, Alice (6); Best, Ben (7); Canonico, Gabrielle (8); Klein, Eduardo (9); Appeltans, Ward

1: University of South Florida, United States of America; 2: Scientific Committee on Oceanic Research (SCOR); 3: Institute for Marine and Antarctic Science, University of Tasmania; CSIRO; 4: Nord University; 5: Centre for Marine and Environmental Research, University of Porto; 6: Atlantic International Research Centre (AIR Centre); 7: EcoQuants, LLC; 8: NOAA U.S. Integrated Ocean Observing System (IOOS); 9: Universidad Simon Bolivar; 10: Ocean Biogeographic Information System (OBIS); 11: US Geological Survey (USGS); OBIS; 12: IEEE; Fourbridges; 13: National Aeronautics and Space Administration (NASA); 14: Akkeshi Marine Station of Hokkaido University

The status and trends of species population distribution, abundance, and production in coastal and ocean waters are required to inform policy and management in the context of growing human uses of marine resources, coastal development, and climate change. They are fundamental to develop coastal economies, to create and sustain jobs, and to conserve resources. Over the past decade, two synergistic efforts have identified priority variables to support the developing Blue Economy. The Global Ocean Observing System (GOOS) is implementing Essential Ocean Variables (EOVs). The Group on Earth Observations Biodiversity Observation Network (GEO BON) is implementing the Essential Biodiversity Variables (EBVs). Such efforts are important because they help guide efforts to increase the density and frequency of observations around the world. They emphasize the need for data collected using best practices and standards, and managing information in an interoperable manner. This allows comparisons from one place to the other and over time. Linking databases, and effective information management and delivery, are critical to develop practical and useful regional and global assessments. These assessments are fundamental to report to international conventions and treaties. They are important to guide planning and implementation of the UN Decade of Ocean Science for Sustainable Development (2021-2030). They are needed by policy-level assessments (e.g., the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services or IPBES), and to track progress toward international development goals (e.g., Convention on Biological Diversity post 2020 targets and the United Nations Sustainable Development Goals).

The Marine Biodiversity Observation Network (MBON), a thematic component of GEO BON, is collaborating with the GOOS, the Ocean Biogeographic Information System (OBIS), the Integrated Marine Biosphere Research (IMBeR) project, and the OceanObs Research Coordination Network (OceanObs RCN) to ensure that EBVs and EOVs are complementary, representing alternative uses of a common set of scientific measurements. This open community of technical experts helps international coordination on best practices for observing, data management and services, combined with capacity development. The EOVs and EBVs incorporate observations from traditional and molecular taxonomy (such as eDNA), animal tagging and tracking efforts, passive and active sounds, ocean biogeochemistry, and ocean observatory initiatives that use in situ to satellite remote sensing tools. The scope spans terrestrial floodplain to ocean interior habitats, from the surface to the bottom of the deep ocean. The strategy requires a coordinated strategy for capacity development. MBON is helping coordinate such efforts through the Ocean Teacher Global Academy (OTGA).

The ultimate objective of these efforts is to support the development and retention of jobs and to stimulate the economy while advancing conservation as a key element to enable sustainable development.

Marine Biodiversity Observation Network (MBON) Contributions From the US

Muller-Karger, Frank (1); Montes, Enrique (1); Runge, Jeffrey (2); Iken, Katrin (3); Kavanaugh, Maria (4); Chavez, Francisco (5); Miller, Robert (6); Canonico, Gabrielle (7); Price, James (8); Coon, Catherine (8); Blythe, Jonathan (8); Weise, Michael (9);

1: University of South Florida, United States of America (USF); 2: University of Maine, Gulf of Maine Research Institute (GMRI); 3: University of Alaska Fairbanks (UAF); 4: Oregon State University (OSU); 5: Monterey Bay Aquarium Research Institute (MBARI); 6: University of California Santa Barbara (UCSB); 7: NOAA, U.S. Integrated Ocean Observing System (IOOS); 8: Bureau of Ocean Energy Management (BOEM); 9: Office of Naval Research (ONR); 10: MarineGEO, Smithsonian Institution

Observing life in the sea is one of the most significant challenges facing the scientific and resource management community. The Marine Biodiversity Observation Network (MBON) links groups that collect observations in the world's ocean and provides advice on how to track marine species, their abundance and biomass, and how marine habitats are changing. MBON is working with the Global Ocean Observing System (GOOS) and the Ocean Biogeographic Information System (OBIS), both under the Intergovernmental Oceanographic Commission (IOC), to define the Essential Biodiversity Variables (EBVs) and Essential Ocean Variables (EOVs) that need to be measured. The information is needed locally and by each State, for UN assessments, to meet the UN Sustainable Development Goals, and to address targets and goals defined under the Convention on Biological Diversity. It will provide guidelines for the International (UN) Decade of Ocean Science for Sustainable Development 2021-2030.

Six projects constitute the core of the U.S. MBON network:

Central California MBON: quantifies relationships between climate, the ocean environment (physics, chemistry) and marine food webs (from microbes to fish and top predators), to provide predictive understanding of marine ecosystem responses to environmental change. PI: Francisco Chavez, Monterey Bay Aquarium Research Institute.

Arctic MBON: Unprecedented changes are occurring in the Arctic and affect all components of Arctic marine ecosystems, including humans. AMBON works towards a sustainable approach to observing biodiversity in the Chukchi Sea. PI: Katrin Iken, University of Alaska – Fairbanks.

Northern California Current MBON: Understanding patterns and drivers of biodiversity and ecosystem functioning from plankton to seascapes using biological oceanographic time series, surveys, and local expertise. PI: Maria Kavanaugh, Oregon State University.

Southern California Bight MBON: Provides a picture of biodiversity in the Southern California Bight using a transferable system that integrates and augments existing monitoring programs. PI: Bob Miller, University of California - Santa Barbara

Gulf of Maine MBON: Seeks to understand long-term change in plankton biodiversity drivers of key fisheries and marine mammal populations in the Gulf of Maine. PI: Jeffrey Runge, Northeastern Regional Association of Coastal Ocean Observing Systems (NERACOOS)

South Florida MBON: Provides biodiversity information developed from integrated ground and satellite observations in and around the Florida Keys National Marine Sanctuary and the Rookery Bay National Estuarine Research Reserve. PI: Frank Muller-Karger, University of South Florida.

The Marine Global Earth Observatory (MarineGEO) of the Smithsonian Institution is a global network of partners focused on understanding coastal marine ecosystems. PI: Emmett Duffy.

MBON works with private, academic, and government partners to advance Ecosystem-Based Management. Projects contribute to the global MBON community of practice with products (satellite maps, species abundance patterns, indicators, best practices, information and knowledge) that support operational and science goals. They provide standardized, open data to international databases like OBIS.

Development of Asia-Pacific Marine Biodiversity Observation Network (AP MBON)

Nakaoka, Masahiro (1); Yamakita, Takehisa (2); Costello, Mark J. (3)

1: Hokkaido University, Japan; 2: Japan Agency for Marine-Earth Science and Technology (JAMSTEC); 3: Nord University, Norway

The Asia-Pacific region has the highest density of marine species on Earth, notably in the Coral Triangle. This region is home to about 60% of the world's human population and faces numerous threats including pollution, overfishing, mining, shipping and many other ocean uses that affect life in the sea. There is an urgent need to know what is happening to marine biodiversity in this region for marine food security to support human health, plus the effects of climate change and natural disasters (e.g., typhoons and tsunami), and how these effects interact. Marine scientists participating the global Marine Biodiversity Observation Network (MBON) and APBON (Asia-Pacific Biodiversity Observation Network) agreed to organize a subgroup called AP MBON (Asia-Pacific Marine Biodiversity Observation Network), and started activities in 2019. The AP MBON community of practice will provide the scientific expertise, data and knowledge to determine the facts about the state of marine life and ecosystems, and to predict how this will change in the future. This knowledge will enable scientists to provide evidence-based advices to governments and society on how to restore fisheries and health of ecosystems, and sustainably use the oceans for the long-term benefit of society and nature. Proposed future activities of AP MBON include (1) building effective biodiversity monitoring system along the major coastlines of Asia-Pacific, (2) conducting various thematic research topics, such as detecting changes in marine biodiversity along a latitudinal gradient of this region, which could be compared with the findings of the "Pole to Pole" (P2P) MBON in the Americas, (3) developing new tools and methods for marine biodiversity observations based on recent innovative technologies, such as in remote sensing, eDNA, new statistical and modelling methods, (4) capacity building, i.e., developing the next generation of the AP MBON membership, and (5) planning effective outreach programs by building partnerships with citizens, stakeholders and policy-makers to disseminate our findings toward establishing better practices and policies for marine biodiversity conservation and promoting sustainable use of ecosystem services.

A Marine Biodiversity Observation Network Pole-to-Pole of the Americas (MBON Pole to Pole) in support of conservation post 2020.

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The Marine Biodiversity Observation Network Pole to Pole of the Americas (MBON Pole to Pole) is a regional program of collaborating research institutions, marine laboratories, parks, and reserves, aiming to provide data and information to decision-makers for the conservation of marine biodiversity and sustainability of its ecosystem services. The network seeks to support the development of a framework for policy and best practices for stakeholders that integrate knowledge, biodiversity protection, human well-being and sustainability in marine and coastal areas, beginning with rocky intertidal shores and sandy beaches. Over the past three years the network has collected biodiversity observations in the coastal zone across 12 countries using standard methods and contributed over 15,000 new records to the Ocean Biogeographic Information System (OBIS). The program has carried out capacity building workshops to develop field protocols and train scientists and managers in open source technologies for data visualization and mapping, aligning data according to agreed standards (i.e. Darwin Core), and sharing data via OBIS. The training and research also include satellite remote sensing observations, from which seascapes are derived and used to evaluate changes in biogeographic provinces over time in each sampling area. The network is applying machine learning methods to survey rocky shore communities using photo-quadrat imagery gathered at monitoring sites to expand the spatial and temporal coverage of the surveys. Coordinated monitoring of the MBON Pole to Pole provides a unique opportunity to develop marine Essential Biodiversity Variables (EBVs) that allow to compare patterns of biodiversity throughout the region and examine how marine communities are changing. The network seeks to contribute to GEO BON by generating Species Population and Ecosystem Composition EBVs to better understand how natural and human pressures affect marine habitats and predict their responses to future environmental change.

A versatile and user-friendly interface for computing, plotting and analysing biological metrics from various monitoring protocols

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Assessing the state of ecosystems is central to many environmental policies, in particular in coastal areas where monitoring and assessment is mandatory in contexts involving Marine Protected Areas or, in Europe, the Marine Strategy Framework Directive. Coastal monitoring is achieved from various field observation protocols. To date, there are very few off-the-shelf tools for producing and analysing biological metrics from data sampled using the most common monitoring protocols in coastal ecosystems, such as Underwater Visual Censuses, Catch-effort data and underwater video.

This paper presents an R-based user interface enabling easily computation and plotting of a large array of ecological indicators and analysing their spatial and temporal variations as a function of sampling station-related factors. The interface can deal with monitoring data obtained from various observation protocols provided that data are framed into two files following a standardized format. The first file describes the observation units and their geographical, environmental and temporal descriptors, while the second file contains the ecological data sampled at each observation unit. A third file containing a reference list of species together with their taxonomy, traits and other characteristics allows to compute metrics based on combinations of species characteristics. Plots, statistical test results, metrics values may be easily exported for reporting or for further statistical analyses. The software was extensively tested and applied to varied datasets.

It is illustrated here by two examples from distinct ecosystems and sampling protocols in the case of Marine Protected Area Management Effectiveness Assessment: i) the Côte Bleue Marine Park located in the French Mediterranean, monitored by Underwater Visual Censuses (UVC); and ii) New Caledonian MPAs located in the southwest Pacific, monitored by underwater video.

The Temporal Changes in Abundance & Distribution of Jellyfish along the Coastal Area of Northern Penang, Malaysia

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Jellyfish blooms have been a threat to mankind over the decades. Jellyfish pose risks to human health and socioeconomical activities which include severe stings, death, collapse of fisheries industries and aquatic systems. Monitoring of jellyfish diversity and abundance in the coastal waters of Penang, Malaysia was conducted for 25-months period started July 2017 until July 2019 using observation (scooping) and towing methods. In-situ water quality parameters were also recorded and its correlation with jellyfish abundance was determined. Eight jellyfish species were identified in this study namely *Chrysaora chinensis*, *Phyllorhiza punctata*, *Aurelia* sp., *Rhopilema hispidum*, *Acromitus flagellatus*, *Cyanea capillata*, *Chiropsoides buitendijki*, and *Morbakka* sp.. A specimen of *C. capillata* or lion's mane jellyfish (with bell diameter of 60cm) was first recorded in Malaysian waters. No occurrences of significant jellyfish bloom but their presence were observed throughout the whole sampling periods. The most abundant and dominant species was *C. chinensis*. Water off Tanjung Bungah had the highest diversity of jellyfish species. Abundance of jellyfish showed a very weak positive correlation with water temperature, salinity, dissolved oxygen & pH level. Other factors such as effect of currents, concentration of chlorophyll-a, and abundance of mesozooplankton should be taken into considerations for future researches on abundance of jellyfish.

Analysis of marine fisheries statistics in Benin and potential links between fisheries variability and sea surface temperature

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Marine fishing in the Republic of Benin is a fishery gathering activity that is mainly carried out on the continental shelf. It consists of artisanal and industrial maritime fishing.

Upwelling is almost absent on the Beninese coast. Despite the narrowness of the continental shelf, the fish fauna has more than 257 species of fish including 43 selacians and 214 teleosts.

The fishing sector affects 15% of the total active population and 25% of that of the primary sector. It contributes to the GDP of 3%. The individual consumption is 8,50 Kg/year; which ensures nearly 31% of proteins of animal origin (PADPPA 2010).

The present study aims to retrospectively report on the marine fishery in Benin in the light of available data and a critical analysis of the potential correlations between changes in fishing quantities and sea surface temperature over the same periods. A relationship between different coastal upwelling index parameters and catch per unit effort was highlighted.

Seasonal variations in catches (t) of artisanal marine fishing are more pronounced from September to January with a marked peak in November and another high in February. The fishing effort seems to be responsible for this fluctuation because it presents a temporal evolution similar to that of the catches but this result is immediately put in question because to the weak fishing efforts are not always associated with strong CPUE (index of abundance of biomass).

MBON: Marine Biodiversity Observation Network: Current status and action plan

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Biodiversity is essential to the functioning of marine and coastal ecosystems that are co-responsible for food, feed, medicine and other biomass uses for billions of people around the world. It provides also recreational, inspirational and health needs and has a vital role in climate and nutrient regulation. Despite its importance, and the evidence that it is increasingly threatened directly and indirectly by human activities, its changes and the mechanisms responsible for the changes, including effects of management actions, remain major gaps in ocean observing. Implementing operational, sustained programs to observe marine biodiversity and to integrate these observations with environmental information at the different spatial and temporal scales is critical to understand changing patterns of biodiversity in the face of increasing and accumulated stressors and changing ecosystems, and to determining impacts on natural capital, ecosystem services and on people's well-being.

The Marine Biodiversity Observation Network (MBON), a thematic network from GEO BON, is working in partnership with the Global Ocean Observing System (GOOS), the Ocean Biogeographic Information System (OBIS), and other global, regional and national partners to make available the marine biological and ecosystem observations needed to ensure living marine resources are sustainably conserved and managed and are able to support essential human needs now and in the future.

Efforts to date include developing new advanced methods to evaluate marine biogeographic provinces (seascapes), advancing 'omics methods, catalyse the development of regional and thematic networks, including citizen science and promote capacity building to integrate existing and new field data into global clearinghouses like OBIS and GBIF following agreed standards. New developments include the set-up of new regional nodes, new projects and a new secretariat set up in the Azores that will allow the increase of its activity in the next years.

Information from a community of practice like MBON is critical for the assessments that IPBES is conducting. We will review and engage with participants of the GEO BON All Hands meeting in a dialogue about this process and how to make it more effective

Where Marine Protected Areas would best represent 30% of ocean biodiversity

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The IUCN (the International Union for Conservation of Nature) World Conservation Congress called for the full protection of 30% of each marine habitat globally and at least 30% of all the ocean. Thus, we quantitatively prioritized the top 30% areas for Marine Protected Areas (MPAs) globally using global scale measures of biodiversity from the species to ecosystem level. The analysis used (a) Ecosystems mapped based on 20 environmental variables, (b) four Biomes (seagrass, kelp, mangrove, and shallow water coral reefs) plus seabed rugosity as a proxy for habitat, and (c) species richness within each biogeographic Realm (indicating areas of species endemism), so as to maximise representivity of biodiversity overall.

We found that the 30% prioritized areas were mainly on continental coasts, island arcs, oceanic islands, the southwest Indian Ridge, the northern Mid-Atlantic Ridge, the Coral Triangle, Caribbean Sea, and Arctic Archipelago. They generally covered 30% of the Ecosystems and over 80% of the Biomes. Although 58% of the areas were within countries Exclusive Economic Zones (EEZ), only 10% were in MPAs, and < 1% in no-take MPAs (IUCN category Ia). These prioritised areas indicate where it would be optimal to locate MPAs for recovery of marine biodiversity within and outside country's EEZ. Our results thus provide a map that will aid both national and international planning of where to protect marine biodiversity as a whole.

Session Marine BON

Poster presentations

The “Effort Gap” Metric: Assessing Countries’ Uneven Conservation Effort Towards Habitats and Biodiversity Protection

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The establishment of Marine Protected Areas (MPAs) have become a common conservation measure worldwide. The percent of global marine area protected is used an indicator to assess progress toward habitat protection, but this indicator does not consider the nuances of the distribution of these protected areas. Here, we propose a novel indicator to evaluate conservation efforts across marine habitats by using measurements of central tendency, the mean and the median, to describe the percentage of habitats protected globally. The gap between these measures highlights the differences in effort countries put towards habitat protection, we define this as the Effort Gap. We discovered that there is an uneven distribution in conservation efforts. In all the habitats assessed there is a large Effort Gap revealing how even though some countries are contributing towards achieving a “total conservation target”, the majority of countries are under-performing. Additionally, we found that biodiversity is not a significant factor in predicting MPA coverage and the wealth of the country (GDP) is a weak predictor of MPA area. Overall, a solution to fill this Effort Gap is for wealthier countries to cooperate with, and compensate for, less wealthy countries. To reach international goals and properly protect habitats and biodiversity strong international cooperation through capacity building, financial support, and creation of economically viable alternatives for employment are urgently needed.

Survey on the diversity of benthic macrofauna in seagrass bed, Middle Bank, Penang, Straits of Malacca.

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Seagrasses would be one of the most productive aquatic ecosystems in coastal areas where it provides shelter and food for a wide range of species. Malaysia lying within the global biodiversity hotspot is considered to have high species diversity. However seagrass bed along the northern Straits of Malacca is poorly understood due to high sedimentation, which causes the water to be turbid on this side of the peninsular Malaysia. To fill up the knowledge gap, a survey was carried out to describe the diversity of benthic macro fauna from a seagrass bed. Samples were collected using a core sampler and also from the sediment surface at Middle Bank, north Straits of Malacca. A total of 71 species from 6 phyla was collected. Highest species rich group were Mollusca (52 species), Arthropoda (7 species) and Echinodermata (5 species). 71.15% of all the molluscs recorded were gastropods, and family Nassariidae and Potamididae dominated the assemblage with respect to abundance. Genus Nassarius and Cerithiidae were the two dominant gastropods found in the seagrass bed. Bivalves were represented by only 15 species from 13 genera of the samples, with *Modiolus nitidus*, *Atrina pectinata*, and *Meretrix* sp. being the most dominant species among all the bivalves. Compared to other studies locally and regionally, the diversity of benthic macrofauna in the current survey area was low. However long term monitoring for species diversity is crucial for a sustainable development of marine resources in a seagrass bed.

Fisheries diversity and environmental variables in the waterways of the eastern Sundarbans mangrove forest, Bangladesh

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This study will identify the seasonal ecosystem structure in terms of fisheries diversity and different environmental parameters in the waterways of the eastern Sundarbans mangrove forest (hereafter, Sundarbans), specially the Dublar char region. Dublar char is coordinated as 21.774151 N, 89.561821 E and hub of the fish business specially dry fish inside the Sundarbans. Total of 172 species of fishes including varieties of local fish, 20 species of prawn and 44 species of crabs including two edible crabs caught from inside the Sundarbans and from the coastal water of the Bay of Bengal are landed in this island. So, this place represents the rich fish and fisheries diversity among the other Sundarbans regions. Also, as this place is used as the hub of fisheries business, anthropogenic impact is quite high than any other places of Sundarbans. However, there is no such current information on the effect of anthropogenic pressure on fish and fisheries diversity in this region. So, in this research project, we will identify firstly, the richness of fish and fisheries diversity and find out the anthropogenic activities (i.e., major pollution trend) over the year round.

Session: BON Development

Oral Presentation

Implementation of a community based monitoring scheme of Essential Biodiversity Variables in Montes de Maria, Caribbean Region of Colombia

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Tropical dry forest (TDF) is an important part of the cultural and economic development of human populations. About 92% of the TDF in Colombia has been transformed into agricultural production or urban areas. Montes de Maria region at northern part of Colombia where is located one of the most threatened TDF in the country, has been strongly affected by the violence period. Rural communities in this area have developed projects that have contributed to the sustainability of this ecosystem. Humboldt Institute has supported community based monitoring processes for approximately 4 years in the Montes de Maria region. Community based monitoring is a continuous process where local communities record information about their natural resources, generate more precise knowledge about its conditions and implement management actions in response to what they have learned in the process.

During 2019 and 2020, the PEER project “Implementation of Essential Biodiversity Variables (EBV) for biodiversity assessment and monitoring at the subnational level in Colombia”, a monitoring scheme was developed with the communities to generate community-based EBV at a local scale in Montes de Maria. Three farmers community associations of men and women victims of violence participated in this project, and a set of indicators for monitoring EVB were identified. In this project the first protocol for monitoring EVB at local scales is being developed, and it includes a whole cycle composed of eight steps: 0) understand the problem, 1) raise scenarios, objectives and actions, 2) identify the monitoring question and variables to answer it, 3) define how to monitor and collect data, 4) systematize and send the data, 5) analyze and calculate indicators, 6) evaluate progress towards the stated objective and 7) communicate and publish progress.

This PEER project has had the possibility of implement the cycle until step 3 and we look forward to keep up to step 7. Based on community perceptions the main problems around the TDF were grouped in: water regulation and offer, direct uses of the forest and production systems. Based on these, communities built desired futures, defined goals and proposed actions to implement to reach these goals. Each association proposed a monitoring question and eight EBV and indicators were selected to be monitored and calculated to answer these. The EBV selected belong to four of the five classes proposed by GEO BON. This approach empowers the community since it provides them with tools to be an active part of the transformation of their territory, and enables the sustainability of this methodology over time. With a wide implementation of this methodology there is a potential to increase global observation networks at a local scale that eventually could give information that can be used to take decisions at larger scales.

Machine learning applications to monitor marine Essential Biodiversity Variables in rocky shore communities

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Monitoring marine ecosystems and biodiversity are necessary to understand ecological patterns and processes but also to detect natural or human induced changes such as those resulting from climate change or coastal pollution. A standard technique used in rocky shores is the estimation of cover of benthic organisms. Photoquadrats are becoming standard practice for surveying biodiversity of intertidal and subtidal habitats. They allow to collect large volumes of reliable data efficiently and rapidly in addition to provide a permanent record of the sample. Despite known limitations in taxonomic resolution (insufficient accuracy and low representativeness of marine biota), photoquadrats have demonstrated to perform well when estimating coverage of functional groups. However, man-work for processing photoquadrats is normally time demanding, rendering them impractical. Cutting-edge machine learning tools are now being used by marine ecologists to annotate species records from photoquadrat imagery. They allow the automatic identification of species, or functional groups, to examine community composition and biodiversity of rocky intertidal and subtidal habitats with high certainty. The use of these tools can significantly reduce the processing time of photo-quadrat imagery and optimize biodiversity survey programs. In this study we present results from visual versus photoquadrat assessments of rocky shores from Argentina, Galapagos Islands (Ecuador) and the Pacific Colombian coast using the CoralNet software. Photoquadrat imagery was collected during visual surveys carried out at these sites following the protocol implemented across the continent by the Marine Biodiversity Observation Network of the Americas (MBON Pole to Pole) program. We applied an ad hoc standardized list of benthic biota and substrata (i.e. CATAMI) as a common label set to enable the comparison between locations. Preliminary results show that CoralNet is able to identify key benthic species and substrate types with high levels of confidence (Pearson correlation coefficient (ρ) from computer vs visual annotations: Substrate Consolidated, $\rho = 0.91$, Molluscs Bivalves, $\rho = 1$, Macroalgae filamentous, $\rho = 0.79$, Macroalgae sheet-like $\rho = 0.87$). We conclude that the CoralNet software can be used to estimate presence and cover of CATAMI categories. Temporal changes (Nov/2018 and Nov/2019) in coverage of bivalves at 3 sites in Puerto Madryn, Argentina, was successfully detected with an unsupervised configuration of CoralNet. This method brings together two programs that are already working to facilitate data analyses over large latitudinal gradients. We suggest the suitability of this method to establish a protocol to rapidly describe rocky shore biodiversity and to detect changes in the biota in the time frame of the MBON Pole to Pole project along the American continent.

Functional characterization of Peruvian ecoregions based on remotely sensed Ecosystem Functional Types

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Ecoregions are in the highest organization levels used in biogeography to delimit ecologically similar territorial units. Traditionally ecoregions have been defined in terms of environmental conditions and the structure and composition of biodiversity. However, such information shows some limitations to assist more effective conservation and monitoring efforts: 1) it mostly depends on complete biodiversity inventories; 2) rarely it is useful to monitor ecosystem response against environmental changes; 3) it does not directly relate to ecosystem services as a basis to understand the coupled human and natural systems. To overcome these limitations, new regionalization schemes that shift from ecological patterns to ecosystem functions and from observational to an explanatory approach are required. An easy-to-develop way to implement such functional ecoregions schemes is the Ecosystem Functional type (EFT) concept, that has been noticed as a robust approach to identifying large spatial units based on their ecosystem functioning. Here, we move towards ecological regionalization based on the ecosystem functioning using as proof of case Perú, a megadiverse country. For this purpose, we followed an approach based on: 1) the identification of Ecosystem Functional Types (EFTs) based on remote sensing; 2) the characterization of ecoregions from their composition and abundance of EFTs; and 3) generating a hierarchical classification of such ecoregions into new units, we call functional biomes. As a result, we have obtained a functional characterization of Peruvian Olson's ecoregions, and an updated biome scheme that could be used in ecosystem conservation and monitoring programs.

EBV Workflows for the Design of Sustained Biodiversity Observation Systems

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The Essential Biodiversity Variable (EBVs) concept serves as an effective framework for the design and implementation of interoperable and sustainable Biodiversity Observation Networks. One key challenge to ensuring sustained production of updated and continually refined biodiversity observation outputs and products, is to ensure a repeatable workflow that runs from data to decision (data collections, data management and curation, data analytics and mainstreaming application). These workflows allow for all essential aspects of a biodiversity observation system to be accounted for and ensure that these components are interoperable. They also serve as a 'recipe' by which institutions and national governments can then use to ensure consistent, repeatable production of the biodiversity outputs and ensure continued investment in the underlying data, curation and analytics required to sustainably produce these outputs. We used the EBV workflows in the context of two countries (Ghana and Uganda) to produce a sustainable and repeatable production pathway for identified biodiversity information products. This involved a structured mapping process by which existing data (both within country and external) along with an assessment of required technical capacities and needed tools and platforms for the production of these products identified was placed along a 'data to decision' workflow. The process and the outputs of this structured workflow mapping process was used to design a repeatable solution for the production of these Biodiversity Information Products and will be profiled in this presentation.

SoilBON: A vision for a global soil biodiversity observation network

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In the last two decades, the world has seen an unprecedented increase in the awareness of the importance of natural systems for human wellbeing and for the maintenance of critical biogeochemical cycles at both global and local scales. This awareness coincided with significant changes in the way that society aims to protect and make use of these natural systems and resulted in a significant increase in the extent and type of conservation areas. It also resulted in a significant increase in the extent and type of nature conservation, allowing for more informed policy design and development, and prompting the establishment of nature conservation goals. Amid the failure to achieve the 2020 conservation targets and paving the way for nature conservation post-2020, recent articles suggest that new nature conservation goals require not only an expansion of current protected areas, but also the definition of more targeted and effective conservation objectives. However, to date, the bulk of this literature focuses on the impacts of human development and the beneficial effects of protected areas on aboveground systems, almost completely missing the major terrestrial biodiversity pool residing under our feet. Moreover, little is known about the effects and actual protection value for soil ecosystems of current conservation policies. Here we present a vision for the future of global soil monitoring and the pathway for large-scale integration of soil biodiversity and ecosystem function data.

Integrated cloud infrastructure system for characterizing and reporting biodiversity change at the national and regional levels

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The consolidation of a global biodiversity observation network that can inform both research and policy at both the national and global scales is an aim and also a challenge for the successful implementation of Essential Biodiversity Variables (EBVs). In recent years there has been a substantial advance in the development of global products that facilitate the monitoring of biodiversity change in a spatially and temporarily consistent manner. In parallel, some national and regional Biodiversity Observation Networks have made important progress in their capacity to produce data infrastructures for monitoring biodiversity change. That is the case of Colombia where there have been substantial advances in the elaboration of data products for characterizing ecosystem types, species distributions, and other variables relevant for the production of EBVs and the derivation of Spatial Biodiversity Indicators (SBI). We present an integrated system aiming to harness the potential of both national and global spatial data products to assess biodiversity change and inform decisions on biodiversity management and planning. The system combines 1) a cloud storage data catalog and processing infrastructure that harmonizes both national and global products to produce SBI derived from EBVs 2) a user-friendly graphical interface that assists decision-makers and other relevant stakeholders to retrieve spatial EBV products and SBI 3) a suite of software applications that streamlines the production of new spatial data products and metrics with the potential to further expand the functionality of the system. Currently, the system hosts circa 30 Gb of data that enables it to provide metrics for 18+ SBI within pre-defined areas or user-defined areas of interest, covering the extent of Colombia. These SBI will facilitate the reporting of advances in fulfilling national and international biodiversity conservation commitments in Colombia, including five goals for the Convention of Biological Diversity, two Sustainable Development Goals, and six goals contained in the national development plan. The software applications correspond to the production of two packages in the open-source R programming environment. The first package produces time series maps and indicators of change in EBVs related to the distribution of forest and inland water ecosystems, forest structure, and species populations. The second package consists of a semi-automated workflow for the preprocessing of satellite images and their combination with other spatial datasets to produce and validate time series thematic maps representing changes in ecosystem extent. The modular design of the system allows for the expansion of the functionality as new datasets and software applications are developed while the encapsulation of the system in docker containers offers the opportunity to adapt it to the conditions and needs of other BONs worldwide.

Mapping landscape restoration opportunities in Amazonian forest in Colombia

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The Colombian Amazon currently concentrates more than 50% of the country's deforestation, but despite being the most extensive and preserved natural area, it presents high rates of degradation. In order to address established global commitments and effectively recover extensive degraded areas, the context of landscape restoration requires a variety of strategies that include not only the ecological but also the socio-economic aspects. An assessment was conducted for the planning of landscape restoration opportunities that included: 1) an analysis of the integrity (structure, size, shape, composition and forest fragmentation), functionality of the landscape (connectivity) and provision of ecosystem services for the entire region (pollination, water supply and regulation, carbon stocks). 2) identification of disturbances through exercises with cartography and local communities to prioritize areas. 3) Evaluation of successful experiences in the region that included production modes typical of the Amazon, their cost-benefit, and analysis of the sustainability of current land use. As results we highlight that it is necessary to reactivate the connectivity between the areas of the lomerio towards the mountain, which currently refers to a few patches present in Putumayo and Guaviare. Additionally, those areas whose soils are degraded and have eroded areas were identified as priorities, as well as the flood valleys, these also affect the productivity of the communities. The strategy proposed here seeks to improve the livestock production mode, diversify production on the farm and restore degraded areas, with a view to stopping deforestation and encouraging the production of well-being for communities. However, activities such as illegal mining, cocaine production crops, lack of clarity in legal land tenure and armed conflict represent the greatest challenge for the region, since it requires higher impact government strategies.

Towards the network of national biodiversity observatories – the Finnish Ecosystem Observatory

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To respond to the information needs of the Convention on Biological Diversity, in its Beijing call, GEO BON secretariat proposed that development of sustained operational national biodiversity observation networks should be included in the planned set of post-2020 targets. In this presentation we introduce the Finnish Ecosystem Observatory (FEO), which aims to create a coherent, all-encompassing biodiversity monitoring and indicator network for Finland. It will achieve this by creating a national level co-operation model for biodiversity monitoring, harmonizing data sources, filling in data gaps and designing a technology platform to strengthen the existing biodiversity related data flows, deploy new ones and to manage documentation of the whole data-to-information processes.

FEO draws together and complements different monitoring and indicator frameworks that are currently hosted by various institutions. In addition to national CBD targets, indicators and monitoring networks are developed for example to serve needs of red lists of ecosystems and species, essential biodiversity variables and ecosystem accounting, but also for mainstreaming biodiversity information to decision-making at all levels. Data needs and monitoring methods of these approaches share a lot of common ground.

FEO makes use of this common ground by facilitating co-operation in data management and processing. The core tool of FEO is an information management system that allows documenting data-to-information flows from raw monitoring data to different indicator products that are used in policy processes. The system increases transparency, reproducibility and credibility of the indicator frameworks, facilitates reuse of old code, data and outputs, and helps to disseminate best practices. FEO also aims to harmonize commonly used data sources and facilitate accessibility of less commonly used data. Possibilities to implement emerging technologies, such as eDNA, remote sensing and artificial intelligence, in operative BD monitoring will be studied to fill possible critical monitoring gaps.

FEO is currently in early development phase and is being set up step by step during the next few years. Budget for the first year is 1,4 M€ and the total costs of establishment is expected to be approximately 6 M€. The system is planned to be up and running by 2024. Once operating, FEO will help guiding and evaluating progress toward the national biodiversity targets, but also building possible scenarios of future development and identifying measures that are needed for reaching the “living in harmony with nature” vision for 2050.

Essential Mountain Variables for monitoring mountain social-ecological systems: progress and prospects

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Mountains worldwide host rich biodiversity, are home to millions of people and provide upland and lowland inhabitants with vital ecosystem services and resources. However, mountain regions are highly dynamic environments and undergo constant changes in response to biophysical drivers such as climate, but also in response to other processes of change such as natural hazards, land use, and political and socio-economic contexts. Consequently, addressing the impacts that arise in response to these changes require effective policies and management approaches that not only account for these changes, but also have adequate monitoring schemes in place that are fit-for-purpose. Safeguarding mountain natural assets that underpin human wellbeing and ecosystems along elevational gradients, require effective monitoring frameworks that offer relevant, regular, timely, and harmonized data to generate information that responds to reporting and management needs. Incorporating Essential Variables (EVs) into monitoring frameworks offers a means to integrate different sources of data and harmonize the collection of data pertaining to drivers and processes of change that are context-relevant, in this case through the in situ and remote monitoring of relevant climate, biodiversity and societal variables from the local to the global scale. However, given their remoteness, their steep environmental gradients, diverse habitats and microclimates, diverse socio-cultural contexts, and complex social-ecological systems interactions, mountains are particularly difficult to monitor. To facilitate harmonised data compilation, Essential Mountain Variables need to be identified that fulfil a set of criteria that includes scalability, temporal sensitivity, feasibility, and relevance for global change processes in mountains, specifically.

Through initial rounds of expert consultations and two subsequent workshops, the Group on Earth Observations (GEO) Initiative – the Global Network for Observations and Information in Mountain Environments (GEO-GNOME) has outlined the identification of relevant Essential Variables (EVs) as a key activity and objective in its previous (2017-2019) and existing (2020-2022) Implementation Plans under the respective GEO Work Programmes. The specific goal is to identify sets of Essential Mountain Variables that so far include considerations for Essential Climate Variables (ECVs); Essential Biodiversity Variables (EBVs) and Essential Societal Variables (ESVs), that jointly would respond to systems-oriented monitoring and data needs. In this presentation, we summarize the preliminary outcomes of these workshops, presenting the climatic and social-ecological processes identified as particularly important and relevant in mountain environments along with the variables allowing for their knowledge and understanding. We also present our preliminary ideas on integrating these sets of variables in a framework of Essential Mountain Variables addressing information and monitoring needs of full mountain social-ecological systems.

The Asia-Pacific Biodiversity Observation Network: 10-year achievements and new strategies to 2030

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The Asia-Pacific Biodiversity Observation Network (APBON) was launched in 2009, in response to the establishment of the Biodiversity Observation Network under the Group on Earth Observations in 2008. APBON's mission was to increase exchange of knowledge and know-how between institutions and researchers concerning biodiversity science research in the Asia-Pacific region and thereby contribute to evidence-based decision making and policy-making. Here we summarize APBON activities and achievements in its first 10 years. We review how APBON has developed networks, facilitated communication for sharing knowledge, and built capacity of researchers and stakeholders through workshops and publications as well as discuss the network plan.

Key findings by APBON members include descriptions of species new to science, mapping tropical forest cover change, evaluating impacts of hydropower dams and climate change on fish species diversity in the Mekong, and mapping "Ecologically and Biologically Significant Areas" in the oceans. APBON also contributed to data collection, sharing, analysis, and synthesis. A highlight was contributing to the "Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services" regional report.

New strategic plans target to promote national level BONs in AP region and interdisciplinary research to address the data and knowledge gaps and increase data accessibility for users and for meeting societal demands. Strengthening networks in AP region and capacity building through APBON meetings will continue. By promoting monitoring and scientific research and facilitating the dialog with scientists and policy makers, APBON will contribute to the implementation of conservation and sustainable use of biodiversity in the entire AP region.

The MRV capacity-building approach: promoting the use of biodiversity data for decision-making in Africa

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In the framework of its activities to enhance capacities in its African partner countries, the CEBioS program organises training workshops about the 'Measurement, Reporting and Verification' (MRV) concept for biodiversity. It offers an approach to valorise scientific data and translate them into policy-relevant biodiversity indicators that can be communicated to decision-makers. Such indicators help measuring the impact of policies and projects, supporting decision-making, and monitoring the implementation of biodiversity strategies.

The MRV training workshops, with an audience mainly consisting of biology professors, researchers and representatives of the national and regional administration of environment, park managers and some representatives of NGO's, address subjects that are relevant for the adequate formulation of MRV projects. The MRV concept is explained in depth, together with basic principles regarding the development of biodiversity indicators or the Science-Policy interface. Topics as 'Biodiversity governance' and 'Mainstreaming of biodiversity monitoring in policy sectors and development plans' are treated and illustrated with case studies. A comparison of online biodiversity data portals and training about data quality and database management related to biodiversity indicators are also part of the program. The participants have the opportunity to present their project proposals and improve them following discussions with resource persons from different fields. Project Cycle Management and the Theory of Change are introduced to facilitate the conceptualisation and evaluation of the project.

These workshops are also an opportunity to discuss the main challenges scientists and authorities are coping with. The use of the 'world café' method facilitates the selection of recommendations regarding the development of policy-relevant biodiversity indicators, and their communication towards decision-makers, in order to help bridge the Science-Policy gap.

Together with a more in depth study of the implemented MRV projects, the workshops discussions stress data availability and data accessibility as critical steps in indicator development. Tools like GBIF and other portals are often poorly known due to limited internet access, poor knowledge of English, lack of sufficient capacity for database management and software availability.

For the development of an adequate national biodiversity monitoring system, especially in an African context, the involvement of stakeholders is also considered to be essential. In particular a more structured, continuous collaboration and a more intensified communication between scientists and policymakers is demonstrated as a high priority.

Moreover, there is a need for more understanding and a wider application of the indicator concept itself. Hence, training of key actors both in the policy and science spheres is needed to operationalize indicators and ensure their continuity and sustainability.

With a special focus on DR Congo, a country that is very rich in biodiversity while facing huge (national) biodiversity monitoring challenges, key subjects discussed during the workshops with participants from nine African countries, will be presented.

South Africa's biodiversity monitoring strategy and the development of South Africa BON.

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South Africa has exceptional biodiversity, characterised by high species richness, high levels of species endemism and a wide variety of ecosystems. Identified as one of the world's 17 megadiverse nations South Africa also holds three of the world's 35 biodiversity hotspots. Robust foundational biodiversity observation data and clear indicators are required to monitor and report on biodiversity trends; and this information is crucial to support biodiversity policy development, national and global reporting, and to promote defensible decision making and strategic conservation planning.

South Africa has a long history of undertaking coordinated environmental research and observation, and national scale biodiversity assessments. There are also national institutions with broad mandates that include biodiversity observation (including the South African National Biodiversity Institute & South African Environmental Observation Network), and there are national data portals for sharing biodiversity data. These attributes, combined with existing southern African regional observation systems such as SASSCAL, a relatively strong university research network and a series of well-established annual biodiversity forums demonstrate that a partly formed national biodiversity observation network already operates in South Africa.

As part of an emerging national biodiversity monitoring framework, there is an opportunity to further develop / formalize the existing biodiversity monitoring systems into a "South Africa BON", by meeting the GEOBON requirements for BON development. In this presentation the strengths and weaknesses of the current South African network will be discussed, and the steps and resources required to form "South Africa BON" will be outlined. The development of national, thematic and regional BONs around the world are likely to build on existing efforts and networks; understanding the key steps and challenges in formalizing BONs globally is essential for building GEOBON into the future.

Session: BON Development

Poster presentations

Bioacoustics and Machine Learning for Avian Species Presence Surveys

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1: Future Generations University, USA; 2: Microsoft; 3: Future Generations University, Nepal

The complex realities of changing climate and biodiversity are imperfectly understood. Bioacoustics is a conservation tool, going where human ears cannot stay and listen. Locally-informed machine learning analysis leads to big data insights, empowering informed decision making. Networks of bioacoustic recorders in some of Earth's most biodiverse and vulnerable regions (near Everest in Nepal, Madidi National Park in Bolivia, and the Chesapeake Bay watershed in the United States) are bearing witness to a changing climate. More than 1850 days of audio data already collected provide a powerful dataset for studying species distributions. Machine learning (ML) turns this data into information to understand climate change and biodiversity. ML models are being trained for a dozen species in Nepal, Bolivia, and USA. Analyzed data show location and time of species vocalization. Modeling can expand rapidly as labeled data is collaboratively created by local experts. Preliminary results from Nepal show that a rare bird species was identified 1,000 feet higher in elevation than previously recorded: probable proof of concept that bird species are migrating uphill with changing climate. Bioacoustics is a valuable tool for species population surveys and biodiversity monitoring.

Session: Policy Support

Flash presentations

Marine governance in Costa Rica: a perspective to the marine conservation and marine spatial planning

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Marine governance is a dynamic tool for the conservation of coastal and marine ecosystems and for the sustainable development to make decisions in marine spatial planning. There are ten important elements to marine governance from the Costa Rican experience in marine and coastal management, these include the territorial identity; the role of stakeholders, scientists, politicians and sectors; the political relationships between economic sectors and communities; the public policy making process and its methodology (different points of view aimed to a common goal); effective institutions as important factors in the ocean public action; cooperation; blue economy; and local key action for SDG implementing. Costa Rica has a high biological diversity, hosting 90.000 species (Obando, 2008), in the marine component or EEZ (577.731 km², this is ten times more than the mainland), and coastal line (Caribbean 212 km, Pacific 1016 km). With mangroves, coral reefs, seagrasses, mudflats, rocky beaches, cliffs, a seasonal upwelling area, an oceanic thermal dome, an oceanic trench more than 4.000 m deep, a submarine mountain range with 800 km length (Coco Ridge), many coastal islands and one oceanic island (Cocos Island), and marine cold seeps (Alvarado, et al., 2012), some of these ecosystems are located in more than 22 marine protected areas (2,65% of the EEZ) and responsible fishing marine areas.

A call for international coordination to realize the potential of technology in biodiversity conservation

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With global climate systems changing at unprecedented rates (Intergovernmental Panel on Climate Change, IPCC, 2014), land-use intensification commandeering primary production, and continuing biodiversity loss thrusting us into the sixth mass extinction event, salvaging ecosystems and species has never been more challenging (Intergovernmental Science Policy Platform on Biodiversity and Ecosystem Services, IPBES 2019). Advancing technology represents an unprecedented opportunity to enhance our capacity to conserve the Earth's biodiversity. However, this great potential is failing to materialize and rarely endures. I contend that unleashing the power of technology for conservation requires an internationally coordinated strategy that connects the conservation community and policy-makers with technologists. I argue an international conservation technology entity could (1) provide vision and leadership, (2) coordinate and deliver key services necessary to ensure translation from innovation to effective deployment and use of technology for on-the-ground conservation across the planet, and (3) help integrate innovation into biodiversity conservation policy from local to global scales, providing tools to monitor outcomes of conservation action and progress towards national and international biodiversity targets. This proposed entity could take the shape of an international alliance of conservation institutions or a formal intergovernmental institution. I will share experiences from the climate change community and explore how a similar mechanism would benefit biodiversity conservation.

Session: Policy Support

Oral presentations

Creating the pathways towards biodiversity conservation for transformative change in China

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Global biodiversity has been experiencing rapid past and ongoing loss in terms of species extinction and ecosystems degradation. Biodiversity loss poses a threat to the sustainable future for mankind. The international community has appealed urgent transformative change to conserve biodiversity. Among the mega-biodiverse countries, China is confronted with a plethora of anthropogenic and environmental threats as elsewhere in the world, such as natural habitat degradation, over-exploitation of natural resources, environmental pollution, land use change and climate change. To mainstream biodiversity conservation for the national or even global human well-being, China has put forward “Ecological Civilization - Building a Shared Future for All Life on Earth” as the theme of the coming 15th meeting of the Conference of the Parties to the Convention on Biological Diversity. It is a golden period to develop guidance for the implementation of transformative change to realize global biodiversity targets. Here, we create the pathways towards biodiversity conservation for transformative change across technological, economic, and social circles in China through comprehensive analysis of possible impediments and solutions from multiple sectors to cause biodiversity loss. Our study of China’s transformative change of biodiversity conservation can inform other’s nations to make similar research and practice on the track towards the global biodiversity targets.

GEO BON Evolution Is Entering Its Next Major Phase

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The GEO BON concept document, completed in October 2008, laid out the outlines of a global biodiversity observation network to “cooperate in understanding changes in biodiversity by monitoring its state and trends, as a basis for collaborative actions.” GEO BON has made tremendous—remarkable, really—progress since then while keeping its Mission and Vision consistent with the original concept.

What progress has GEO BON made? Broadly, it has created the informational, organizational, and social infrastructures required to fulfill its Mission to “Improve the acquisition, coordination and delivery of biodiversity observations and related services to users including decision makers and the scientific community.” More specifically, it has established key national and thematic observational networks as well as a focused conceptual framework for biodiversity observations that works across scales of space, time, and biological organization. In the last year, a cornerstone of this framework--the Essential Biodiversity Variables (EBVs)--has reached a level of maturity that constitutes a major GEO BON milestone. EBVs, in conjunction with the basic infrastructure GEO BON has built, now enable the next major phase in GEO BON’s evolution.

What is that next phase? Because EBVs are the key data needed for GEO BON to fulfill its Mission, operationalizing them and their derivatives as actual data products and making these products available for decision makers and scientists are a core element of the next phase. Scientific algorithms, product generation software, and platforms to run that software and provide access to the products are essential enabling factors. The “GEO BON in the Cloud” conceptual platform could support these and provide “delivery of biodiversity observations and related services” as called for in GEO BON’s Mission; so, advancing this cloud-based concept is important. The foundation for these products--and upon which GEO BON is built--is the science needed to understand the natural world. That foundation supports the BONs by guiding what, where, and how they collect their measurements, and expanding and enhancing BONs will continue to be a priority in this next phase.

GEO BON’s future will unfold within a radically changing technological context. The quantity and types of data will continue to accelerate, as will the practical applications of artificial intelligence. The rapidly expanding computer processing capabilities that enable AI applications also enable new data analysis techniques and products, and new types of sensors will provide data never before available. GEO BON’s next phase will utilize many of these advancements.

However, it is essential that this next phase address the data and information needs of the international community. The needs of governments are key because they manage most of Earth’s land and water, and GEO BON’s long-term success depends on meeting those needs with operational data products.

A review of National Reports to the Convention on Biological Diversity- genetic diversity and Aichi Target 13

Hoban, Sean (1,24); Campbell, Catriona (2,24); da Silva, Jessica (3,4,24); Ekblom, Robert (5,24); Funk, W. Chris (6,24); Garner, Brittany A (7,24); Godoy, José (8,24); Kershaw, Francine (9,24); MacDonald, Anna J (10,24); Mergeay, Joachim (11,12,24); Minter, Melissa (13, 24); O'Brien, David (14,24); Paz-Vinas, Ivan (15,16,24); Pearson, Sarah K (17,24); Perez-Espona, Silvia (18,24); Potter, Kevin M (19,24); Russo, Isa-Rita M (20,24); Segelbacher, Gernot (21,24); Vernesi, Christiano (22,24); Hunter, Margaret E (23,24)

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The Convention on Biological Diversity (CBD), established in 1992 and currently signed by 196 states, is the premier instrument for guiding and measuring global conservation. Signatories to the Convention are required to submit National Reports every four years on their national-level progress towards the CBD Targets and other biodiversity information (threats, trends, values, etc.). CBD National Reports offer one of the only global sources of information on country level monitoring and conservation actions, and provide context on their consideration of the importance of biodiversity.

Although the CBD is committed to conserving ecosystems, species, and genetic biodiversity, the Targets for genetic diversity have been less well developed and have emphasized primarily genetic diversity within species of direct human use, especially agricultural ones. Evaluation and improvements to National Reports can help develop better targets and measures in the future, including how best to recognize and assess genetic diversity. In this context, and to assist with the post 2020 planning period, we systematically assessed the consideration of genetic diversity in a large representative sample of 5th and 6th CBD National Reports from 2014 and 2018. We aimed to understand how countries are assessing and protecting genetic diversity in both agricultural and natural ecosystems in the context of CBD Targets and indicators. Our specific aims are to analyze the 5th and 6th National Reports to: (1) assess Targets pertaining to genetic diversity, and indicators used to assess status (present state) and trends (change) in biodiversity; (2) quantify the reporting of genetic diversity actions (e.g. management interventions, policy, funding, etc.), threats (e.g. concerns or drivers of change), and values (e.g. utility or benefits); (3) quantify the frequency with which different types of species are mentioned; (4) determine if these results change across time and across socioeconomic categories.

We found for both reports that, while most countries identify the importance of genetic diversity, they primarily reported status, actions and species relating to agricultural genetic diversity, likely due

to the emphasis of Aichi Target 13 as well as the socioeconomic importance of agriculture for many countries. The most frequently used indicators are unfortunately not well connected to genetic diversity. Very few reports mentioned genetic monitoring, in situ genetic conservation, and genetic diversity relating to indigenous and local communities. Domesticated species were mentioned more frequently than crop wild relatives, forestry and fisheries species and species of conservation concern. There are even fewer mentions of “other socio economically important species” such as wild harvested plants and animals, species providing ecosystem services, horticultural species, and culturally valuable species. We close with recommendations for future research and actions that may improve the quality and level of genetic diversity reporting in National Reports for improved conservation actions.

EKLIPSE- The European Science-Policy-Society Interface on Biodiversity and Ecosystem Services

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EKLIPSE is an innovative, ethical and self-sustaining mechanism that supports evidence-informed decision-making on biodiversity and ecosystem services related issues at the European level. EKLIPSE fulfil its aim by launching regular Calls for Requests where policy and other societal actors identify topics or evidence needs requiring in-depth analysis and a consolidated view from science and other knowledge holders. Since 2016, EKLIPSE has opened five calls for requests, received 40 applications to provide trustworthy evidence, often on contentious policy-relevant issues. EKLIPSE has now processed 13 requests on a range of topics linked to biodiversity and ecosystem services, from a wide variety of policy and societal actors such as the European Commission, IUCN, the French Ministry from the Environment, Buglife and many more. The outputs are a set of ethical, credible, transparent, and jointly developed evidence reports (and other targeted outputs), addressing specific topics in response to societal and policy needs. To reach this goal, EKLIPSE uses a proven and robust process that responds to the evidence needs of requesters by synthesising the best available knowledge, facilitating actionable policy recommendations. Knowledge synthesis refers to a set of methods used to review, collate and communicate the best available knowledge on a specific topic or question, including explicit scientific knowledge, but also indigenous and local knowledge, or tacit technical or opinion based knowledge held by stakeholders (Dick et al., 2017). EKLIPSE's Method Expert Group (MEG) has identified and described 21 different methods to synthesise the different types of knowledge needs requested. On this basis, EKLIPSE identifies and tailors a set of methods for each specific request from policy makers and societal actors. EKLIPSE has five main functions; 1) to answer critical questions from policy and/or society by mobilising and synthesising the best available knowledge and experts, 2) to identify current and future emerging issues of policy makers and citizens related to biodiversity and ecosystem services, 3) to create a responsive and active network of experts and knowledge holders across Europe that get acknowledged for providing their knowledge, 4) to improve citizens engagement in SPI activities and finally 5) to link up with international SPIs such as IPBES, SBBSTTA-CBD. EKLIPSE has a strong focus on networking through building the Network of Networks and organising capacity building events, and all EKLIPSE activities are built on a robust ethical infrastructure. From August 2020 onwards, the EKLIPSE mechanism will be managed by the ALTER-Net Network, a network of 28 European research institutes which aims to enhance biodiversity and ecosystem services knowledge in Europe through high-level multi-disciplinary science integration

FAIR but Inequitable: The impacts of data governance on participatory biodiversity science

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There are growing international efforts to globalize biodiversity data to address the problem of increasing rates of species extinctions and population declines. Predominantly these efforts focus on pooling and standardizing data into centralized infrastructures, which themselves differentiate multiple kinds of actors in terms of rights to contribute, curate, and revise the data. Who benefits and who doesn't from these efforts? Biodiversity scientists have increasingly advocated for adopting the FAIR principles in this context, which advocate for data to be findable, accessible, interoperable, and reusable. While the FAIR principles improve the value of pooled data as a form of capital for key stakeholders (data users, funders, publishers, and industry), their implications are less clear for inclusive participation and governance in collective data pooling projects. Recently, the Indigenous Data Governance Working Group has noted that these efforts don't guarantee, and may in fact forestall, equity of benefits for, and the sovereignty of, different stakeholders, especially indigenous groups. The Working Group has proposed a complementary set of principles based on Collective benefit, Authority, Responsibility, and Ethics (CARE). We present two contrasting types of governance regimes for pooled biodiversity data repositories, analyze how the regimes assign rights to different kinds of participants, and use this to show the regimes vary in how well they satisfy the FAIR and CARE principles. We illustrate these differences using iNaturalist and the Global Biodiversity Information Facility (GBIF) as examples of the centralized regime, and a group of data portals using the Symbiota software platform as an example of a decentralized regime. We conclude that a decentralized governance regime can help address structural vulnerabilities in the FAIR principles, including the potential for exploitation and failure of collective benefit through data sharing.

Are Global Indicators Adequate for Monitoring Invasive Alien Species Targets?

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Current declines in biodiversity are primarily the result of a small number of large-scale key processes, one of which is the impact of invasive alien species. The recognition of the impacts and costs associated with invasive alien species has placed biological invasions at the core of major global policy initiatives, e.g. CBD (Article 8h) and the 2030 SDG's (Target 15.8). However, invasion policy targets remain largely unmet (Aichi Target 9) mainly due to slow progress is inadequate investment in the interventions necessary to slow the spread and reduce the negative impacts of invasive alien species.

However, at question is also the adequacy of available information and the indicators used to assess and monitor progress. Biodiversity policy indicators should have three basic but desirable properties: Policy relevance; Scientific relevance; and the ability to be Effectively communicated. This includes, inter alia, that they are reproducible and convey information on the certainty (and uncertainty) associated with the quantified status or trend.

Multiple indicators for monitoring biological invasions have been developed and implemented at various scales, but the extent to which the existing indicators have been applied to assess, report and monitoring on invasion targets is still under-investigated.

We performed a systematic literature review to evaluate the extent to which existing indicators have been applied to invasion targets, using the criteria of Policy relevance, Scientific relevance, and Communication. We conducted a comprehensive review of published literature considering invasion indicators, analysed their focus and objectives (invasive alien species as well as their impacts, pathways of movement and spread, and policy and management responses) and also evaluated them against Essential Biodiversity Variable design features. Results from this study provide insights about the type and characteristics of the indicators that need to be developed to inform important global environmental policy regarding monitoring of invasive populations. Thus, it is timely to assess the effectiveness and adequacy of current invasion indicators to help inform future developments, in particular as the IPBES Assessment on Invasive Alien Species and their Control is underway.

How Spatial Data Inform Actionable National Policies

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Spatial data is critical to support Parties to the UN Convention on Biological Diversity (CBD) in reporting on their achievements and to inform their conservation decision making. In this study, through sorting out the application of spatial data in the Sixth National Report that Parties to the CBD, we summarized and analyzed the application, existing problems, and challenges in the availability of spatial data that allow for a visual representation of national contribution to the CBD targets, conservation efforts related to the NBSAP and post-2020, and global biodiversity reporting and monitoring. On this basis, we proposed the main approach of integrating spatial data into decision making, including (i) identify the linkage between the spatial data and the conservation targets to evaluate the potential and domain of spatial data for national policy development; (ii) maintain and ensure spatial the data availability at multiple scales to support the biodiversity reporting and monitoring at the national and below scales; (iii) improve the application and demonstration of the spatial data that will contribute to target design and scenario analysis for biodiversity conservation at different levels in future.

Session: Policy Support

Poster presentations

Impact of Drought and Desertification on the Livelihood and Health of the Wayuu Indigenous People of La Guajira, Colombia

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It is well acknowledged that indigenous groups suffer high rates of poverty due to isolation and marginalization, low levels of education and high rates of disease, and addressing such gaps is part of the UN Sustainable Development Goals. This empirical research focuses on the Wayuu people living in the northernmost region of La Guajira, Colombia, and investigates how drought and desertification impact agriculture and food security, and its effect on the rates of malnutrition and childhood mortality.

With a mixed-methods approach, we use databases and questionnaires to assess the environment, livelihood and health of the Wayuu people living in areas that experience different levels of desertification: low, medium and high desertification areas, as defined by Colombia's Institute for Environmental Studies (IDEAM). Perception data are gauged against factual data.

Results show socio-economic and health disparities among Wayuu people living in regions with different desertification levels. Individuals living in regions experiencing high desertification have the lowest population education and accessibility to income, water scarcity and lowest capacity for agricultural practices. Subsequently, results also show high desertification areas present the highest levels of food insecurities, childhood malnutrition, disease and mortality in comparison to individuals living in regions experiencing medium or low levels of desertification.

In conclusion, Wayuu people living in areas with the highest levels of desertification are at an increased risk for extreme poverty, food and water insecurities and childhood mortality. This research is a call for government and private entities to be aware of this crisis and hopes to motivate such institutions to establish effective policies and interventions in order to reduce poverty, food and water insecurities, childhood malnutrition, disease and mortality among Wayuu people.

Session: EBV Data

Flash presentations

MBON: Interactive Infographics and Automated Workflows for Marine Ecological Indicators

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In order to inform timely management and communicate to a wide audience, indicators of marine ecological status and trends should be made available in a readily accessible format and updated as soon as newer data becomes available. Initially as a Marine Biodiversity Observation Network (MBON) project serving the Florida Keys and Monterey Bay National Marine Sanctuaries, we developed an interactive infographic framework (using D3 JavaScript, R and Rmarkdown software) to link elements (e.g., species, climate and human) in an ecosystem illustration to popup windows of interactive maps and time series, which are automatically updated based on the latest available data. The websites are hosted by Github and updated using the Travis continuous integration web service – all of which is free for a reasonably sized website (< 1 GB) and minimal computation for updating (< 1 hr). We are expanding this product to other sanctuaries and NOAA's Integrated Ecosystem Assessment program. All software is free to use and code is open-source.

Using the Darwin core standard for EBV estimated records

Body, Guillaume (1); Mousset, Mathilde (1); Chevallier, Emmanuelle (1); Scandura, Massimo (2); Pamerlon, Sophie (1,3,4); Blanco-Aguiar, Jaso Antonio (5); Vicente, Joaquin (5)

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The development of Essential Biodiversity Variables is an essential step between field data and high level biodiversity indexes. It is necessary, for the best use and understanding of EBV to agree on a common data standard. The Darwin Core Standard is a widely shared data standard within the ecological community. Despite recent developments on sampling events and abiotic records, the Darwin core only allows recording raw data, while EBV data are often statistically estimated data. Within the Enetwild consortium, financed by the European Food and Safety Authority, we face this issue while aggregating data across European countries on wildlife monitoring: occurrences, abundances and hunting bags. Abundance of wildlife is an EBV on species population. We therefore propose a development of the Darwin Core Standard, through the nested extended measurement or fact extension, to be able to record estimated densities with their confidence intervals or other precision measurements. It consists in allowing a measurement (the confidence interval, the variance) be linked to another measurement value (the punctual estimation). We also organise information in metadata to record the useful statistical procedure information to best evaluate and use these data. We believe this development will be useful for the international EBV community.

Earth Challenge 2020: Bringing together citizen science biodiversity data

Bowser, Anne; Meloche, Metis; Long, Alex

The Wilson Center, United States of America

April 22, 2020 was the 50th anniversary of Earth Day. In recognition of this milestone the Wilson Center, U.S. Department of State, Earth Day Network, and other partners launched Earth Challenge 2020 as the world's largest coordinated citizen science project to date. The overall goal of this project is to increase the amount of open and interoperable citizen science data while engaging and activating a global citizenry. Developments to accomplish this goal include work on a data and metadata standard in partnership with the Open Geospatial Consortium (OGC), an open, API-enabled data integration and processing platform, an open data portal, and a new mobile application framework with different data collection widgets. Earth Challenge 2020 looks across six major research areas: One of them is insect populations.

Work on insect populations focuses on integrating data from three different data collection initiatives: iNaturalist, World Bee Count, and the Earth Challenge 2020 app. Each of these projects allows volunteers to collect and share pictures of insect species, with World Bee Count and Earth Challenge 2020 focusing specifically on different types of bees. The use of open data standards and supporting technical platforms allows for integration across these three data sets, and the creation of a much larger information resource than would otherwise be possible. In addition, by working with two machine-learning partners, the project is able to leverage both human and automated intelligence for genus ID.

Presenting on this work is important for a few reasons. First, we hope to share information on our data integration and collection activities as a proof of concept for how citizen science data collected by different projects and communities, at local to global scales, can be brought together for re-use in international monitoring and assessments. Second, we hope to discuss the value of citizen science for contributing data under the EBV framework, and opportunities to work with the citizen science community to bring different data sets together. While initial efforts are focused on species populations, we are also interested in exploring other EBV areas. Lastly, efforts to mobilize legacy citizen science data can help create a baseline data set that is currently lacking for many areas under the EBV framework.

BioTIME: project development and updates

Brambilla, Viviana (1); Antão, Laura (2); Bates, Amanda (3); Fontrodona Eslava, Ada (1); Magurran, Anne (1); Moyes, Faye (1); Richards, Cerren (3); Dornelas, Maria (1)

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Biodiversity data mobilisation plays a critical role in the quantification of biodiversity change across the planet. BioTIME is an open access biodiversity time series database, mobilising assemblage-level data from across the world. BioTIME allows quantitative analysis of biodiversity temporal patterns in the Anthropocene. Active since 2010, BioTIME is currently working towards the expansion of its more than 12 million records of over 45 thousand species to cover and represent as thoroughly as possible all realms (marine, freshwater and terrestrial) and geographic regions of the world. We are also targeting the recruitment of specific taxonomic groups that are under represented in BioTIME.

Moreover, we are working towards making BioTIME increasingly accessible. We are developing online tutorials to show how to interact with the database and give examples of the ecological questions that the database can help answer. Additionally, we are developing a web app that summarises and aids visualisation of the data available. In parallel, we are building an R package that facilitates access to the database records and statistical analyses that can be performed with BioTIME data. These resources will be the backbone of workshop materials to bring BioTIME to broader audiences.

We acknowledge the importance of monitoring biodiversity and the effort scientists put into it, so we are celebrating people collecting biodiversity data by sharing their stories from the field with our new StoryTIME project. This project involves the weekly publication on our web and social media pages of first-hand stories of researcher field adventures.

The ultimate objective of BioTIME in developing all these initiatives is to be an active member in the network of scientists and policymakers who work on the study and quantification of biodiversity change in the Anthropocene.

Biospytial: spatial graph-based computing for ecological Big Data

Escamilla Molgora, Juan; Sedda, Luigi; Atkinson, Peter

Lancaster University, United Kingdom

In this talk I will present Biospytial, a modular open source knowledge engine designed to import, organise, analyse and visualise big spatial ecological datasets using the power of graph theory.

The engine uses a hybrid graph-relational approach to store and access information. A graph data structure uses linkage relationships to build semantic structures represented as complex data structures stored in a graph database, while tabular and geospatial data are stored in an efficient spatial relational database system.

As an application, we built a knowledge graph of the Tree of Life embedded in an environmental and geographical grid to perform an analysis on threatened species co-occurring with jaguars (*Panthera onca*). Our approach reduces the complexity of joining datasets using multiple tabular relations, while its scalable design eases the problem of merging datasets from different sources. Its modular design makes it possible to distribute several instances simultaneously, allowing fast and efficient handling of big ecological datasets.

The provided example demonstrates the engine's capabilities in performing basic graph manipulation, analysis and visualizations of taxonomic groups co-occurring in space. The example shows potential avenues for performing novel ecological analyses, biodiversity syntheses and species distribution models aided by a network of taxonomic and spatial relationships.

Article:

Juan M Escamilla Molgora, Luigi Sedda, Peter M Atkinson, Biospytial: spatial graph-based computing for ecological Big Data, GigaScience, Volume 9, Issue 5, May 2020, g1aa039, <https://doi.org/10.1093/gigascience/g1aa039>

The bdverse: an infrastructural and modular toolkit for biodiversity data quality in R

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Biodiversity data is growing in size, complexity, and type. In parallel, the timely need for monitoring Essential Biodiversity Variables (EBVs) demands broader spatial, taxonomic, and temporal scales than before. Moreover, the development and usage of species distribution EBVs is inherently bounded to the development of biodiversity data quality (BDQ) infrastructure. Developing BDQ standards, tools, and methodologies to untangle the multilayered complexity of data fitness for use, will not only improve the quality of biodiversity data but will also impose a more appropriate use of such data within a case-specific EBVs framework.

In Ecology, the R platform has become the most dominant programming language for biodiversity data science. Today many new and impressive R packages and functionalities are available. However, the skillset required to harness the R ecosystem's synergetic value is far-reaching for most ecologists. Therefore, the development of R packages that integrate existing functionality and add crucially missing one to simplify user-level BDQ exploration and assessment can greatly serve the scientific community.

The bdverse (biodiversity data universe) is a BDQ toolkit constructed as a family of R packages (<https://bdverse.org/>). We build it to serve as a sustainable and agile infrastructure that enhances the value of biodiversity data by allowing users to conveniently and coherently employ R for data exploration, quality assessment, data cleaning, and standardization. The bdverse supports users with- and without programming capabilities. It includes a collection of unique R packages in a hierarchical structure — representing different functionality and dependency. Its core functionality aspects are:

1. `bddwc`: a user-friendly Shiny app and a set of simple functions to standardize data field names in compliance with the Darwin Core (DwC) format, which facilitates data inclusiveness from any biodiversity data aggregators.
2. `bdchecks`: a holistic system for performing, filtering, developing, and managing various biodiversity data checks, aligned with the latest standards developed by TDWG's Biodiversity Data Quality Task Group.
3. `bdclean`: a user-friendly data cleaning workflow system for the inexperienced R user, built to support agile questionnaires (to collect user's specific needs) and various data cleaning reports.
4. `bdvis`: an interactive biodiversity data visualizations and dashboards system (under construction).
5. `bdtools`: an agile and modular tools framework for biodiversity data exploration and analysis (under construction).
6. `bdverse`: main installation package (one to roll them all) that also stores the Shiny apps launcher.

At this moment, bdverse contains five Shiny apps, and under the hood, it is comprised out of 11 R packages. We established our development team using mainly the Google Summer of Code program (<https://summerofcode.withgoogle.com/>).

EBVs require the rethinking of traditional approaches to producing knowledge products. The development of the bdverse demonstrates this by laying down the conceptual, methodological, and technical foundations for an agile, modular, reproducible, and hopefully, sustainable open-source infrastructure for biodiversity data.

IPBES goes FAIR! Data Management Policy Adapted

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The Multidisciplinary Expert Panel and the Bureau of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), at their 13th meeting in January 2020, has approved the IPBES data management policy. This is an important step for IPBES to further improve the accessibility of its products and the transparency of the underlying procedures.

The IPBES data management policy is based on the principles of Open Science and FAIR data. It provides a framework to make the products (e.g. statements, maps, and tables) traceable from the original data layers, through the processing steps, and up to the final status in the product. The IPBES data management policy also provides guidelines on long-term repositories, metadata, and file formats. Management, handling, and delivery of the materials from the indigenous people and local communities are also covered by the policy. The IPBES data management policy will pave the road towards reproducible assessments over time and scalable at the national or regional scale. In this contribution, we aim to inform the community with the highlights of the policy and to present an outlook of projects emerging from the implementation of the policy.

Here is the link to the IPBES data management policy: <https://doi.org/10.5281/zenodo.3551078>

R-Package ecochange: Integrating freely available geospatial data and deriving EBV candidates and indicators in predefined regions of interest

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The effectiveness of Essential Biodiversity Variables for informing biodiversity decision-making requires efficient integration of geospatial biodiversity data sources and the development of workflows for calculating biodiversity indicators that are relevant for decision-making. We introduce a new open-source package, developed in the R programming environment named *ecochange*. This package integrates heterogeneous spatial data sources, structures, and formats to produce spatial metrics, statistics, and EBV indicators for user-defined Regions Of Interest (ROI). The package is designed using a modular approach that enables it to process a wide variety of global change data to produce EBV candidates and indicators. The current implementation of the *ecochange* package integrates readily available global products on Global Forest Change (GFC; Hansen et al., 2013), Global Continuous Tree Cover data (GCTC; Sexton et al., 2013), Surface Water (GSF; Pickens et al., 2020; Pekel et al. 2016), with data produced for national or regional domains including species Areas of Occupancy (AOO) to derive EBV metrics and indicators related to horizontal ecosystem extent, forest fragmentation, disturbance regimes, species distribution ranges, among others. We illustrate the functionality of *ecochange* by studying the effects of forest degradation between 2000-2015 in the northern Amazon region of Colombia, on the AOO of Black-mantled tamarin (*Leontocebus nigricollis*). Recent studies indicate that this species is vulnerable to changes in forest extent and canopy structure. Forest loss increased during the 15 years of the study, especially in the north and along the rivers. Forested areas decreased between 2000 and 2015 from 8064.99 km² to 6791.19 km², respectively. Patterns in marginal entropy (H) (an indicator of degradation in terms of landscape fragmentation) across the AOO suggest that areas with higher ecosystem disturbances ($H > 1.2$) had high levels of degradation with percentages of canopy covers lower than 60%. Degradation was higher in the north ($H > 1.2$) and along the rivers ($H = 0.6 - 1.2$), following a similar pattern found for deforestation. The results revealed an increase in the level of disturbance over time, as indicated by an increment in the number of cell values with $H > 1.2$ during the 15 years. We conclude that if the deforestation observed in the last 15 years continues, it can result in local extinctions of the species and a corresponding migration toward forests in the southern Amazon. Therefore efforts to preserve the species should focus on conserving the southern forests. These results can assist in the understanding of drivers of forest change and the effectiveness of the environmental policy on tamarin conservation in the region. This example demonstrates how the functionality of *ecochange* can assist users in the derivation of workflows for processing EBV candidates and indicators related to ecosystem change for the support of biodiversity monitoring and decision-making.

Introducing POLAAAR, an online portal to discover microbial polar 'omics data

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With few long-term monitoring schemes that look at polar microbial communities, standardizing and archiving data from individual studies is currently our best approach to assess changes over broad temporal and geographical scales. However, microbial ecological research typically generates highly complex multi-faceted 'omics datasets that combine indirect sequence-based species observations with geographical and environmental context data as well as indispensable laboratory protocol metadata. This poses serious challenges for data archiving on commonly used open access biodiversity data repositories (e.g. Global Biodiversity Information Facility; GBIF). At the same time, sequences that are made publicly available through the International Nucleotide Sequence Database Collaboration (INSDC) are often poorly annotated with environmental data and are difficult to find and query. Consequently, it is challenging for microbial data to be completely FAIR (i.e. Findable Accessible Interoperable and Reproducible). Therefore, we introduce the Polar 'Omics Links in Arctic-Antarctic-Alpine (A3) Research online platform, or POLA3R for short, which is a thematic portal that focusses molecular biodiversity data resources from polar regions. Our approach is based on enriching public datasets with the associated metadata and environmental information. These data are made publicly accessible through POLA3R and are also linked to the associated publications and the sequences on INSDC. To allow interoperability with other systems, the portal is designed to operate between different data archiving standards, such as the Minimum Information on any (x) Sequence (MIxS) as well as DarwinCore. Datasets that are listed on POLA3R are also registered on GBIF to increase their discoverability. As such, POLA3R aims to provide a hub for the polar scientific community, where they can discover high quality and complete molecular biodiversity data.

Session: EBV Data

Oral presentations

Virtual laboratories for biodiversity modelling – Australia introduces the EcoCommons program

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Recent technologies have enabled consistent and continuous collection of ecological data at high resolutions across large spatial scales. The challenge remains, however, to bring these data together and expose them to methods and tools to analyse the interaction between biodiversity and the environment. These challenges are mostly associated with the accessibility, visibility and interoperability of data, and the technical computation needed to interpret the data. The EcoCommons program was recently funded under the Australian Research Data Commons Platforms initiative to provide solutions to these challenges. The EcoCommons program includes initiatives such as the Biodiversity and Climate Change Virtual Laboratory (BCCVL) and the ecocloud Platform which together support more than 5000 researchers based at over 400 different organisations in more than 30 countries worldwide. The program will pave the way for paradigm-shifting breakthroughs by providing a springboard for collaboration between researchers and decision-makers concerned with biodiversity including ecosystem services, biosecurity, natural resource management and climate-related impacts and responses.

Here we present two platforms that support researchers and decision-makers through easy access to global biodiversity, climate and environmental datasets integrated with a suite of analytical tools and linked to high-performance cloud computing infrastructure. The Biodiversity and Climate Change Virtual Laboratory (BCCVL) is a point-and-click online platform for modelling species responses to environmental conditions, which provides an easy introduction into the scientific concepts of models without the need for the user to understand the code behind the models. For ecologists who write their own modelling scripts, we have developed ecocloud: a new online environment that provides access to data connected with command-line analysis tools like RStudio & Jupyter Notebooks as well as a virtual desktop environment using Australia's national cloud computing infrastructure. ecocloud is built through collaborations among key facilities within the ecosciences domain, establishing a collective long-term vision of creating an ecosystem of infrastructure that provides capability to enable reliable prediction of future environmental outcomes. Underpinning these tools is an innovative training program, ecoEd, which provides cohesive training and skill development to enhance the translation of Australia's digital research infrastructures to the ecoscience community by educating and upskilling the next generation of environmental scientists and managers. We will also discuss the next steps for these platforms and how we are moving towards a best-practice microservice model, which allows for complete flexibility, scalability and stability in a cloud environment.

This presentation will showcase the tools, services, and underpinning infrastructure alongside our training and engagement framework as an exemplar in building platforms for next generation biodiversity science.

Building the Next-Generation EBV Analyzer

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University of Marburg, Germany

Essential Biodiversity Variables (EBVs) become increasingly important for researchers as well as governments to decide on appropriate actions with respect to climate change and biodiversity loss. The management of such EBVs in a common data format (e.g., NetCDF) is not only crucial for broad accessibility, but it is relevant for researchers to offer modeling and analysis results in a verifiable and reproducible manner. GEO BON strives towards a catalog that manages all public EBV data from many scientists and gathers important metadata. In addition, it is of utmost importance for users to explore and visualize EBVs in a flexible manner.

In this presentation, we introduce the Next-Generation EBV Analyzer as a service where EBVs are offered to users in an easy, exploratory, and interactive way. It extracts information out of NetCDF files and views the underlying hierarchical data with customized search capabilities. The EBV Analyzer is built upon VAT, the Visualization, Analysis and Transformation System that provides a modular way for customizing analytical building blocks on top of a powerful spatio-temporal information system. In addition, it offers an interactive user interface as well as workflows built in the background for the purpose of reproducibility of results.

In our future work, we aim at improving the analytical capabilities of the EBV Analyzer by making better use of the full capabilities of the VAT system, e.g. for combining multiple data sets and computing advanced analyses.

A self-described data format and standard for the Essential Biodiversity Variables.

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A key requirement for boosting the adoption of the Essential Biodiversity Variables (EBVs) framework in science and policy is facilitating access to multiple EBV data products organized under a consistent data structure and with a standardized annotation across all the EBV classes. The development of new conventions is also required for disseminating EBV data products under the GEO BON Data Portal, following best data management practices. We will present the state-of-the-art in the development of data structures and the minimum information conventions adopted for documenting, organizing and distributing EBV data products. The EBV-NetCDF format specifies how biodiversity datasets can be hierarchically structured in a way that is consistent with the concept of EBV data cubes. The proposed approach integrates this hierarchical organization of the data with EML-adapted terms conforming the Minimum Information Standard for an EBV dataset. Both the data structure and the metadata conventions are also consistent with the requirements of the EBV Data Portal and will be proposed as a standard to be adopted by GEO BON in support of interoperable, self-described biodiversity data products.

Rapid mobilization of evidence to improve decision-making on invasive species

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Invasive alien species (IAS) represent a major environmental and economic problem. Prevention, risk analysis, management planning and policy evaluation all require open, rapidly mobilized data from fragmented sources. These include essential biodiversity variables for invasions needed to inform decision-making, maximise the benefits of available resources, anticipate future threats, use the most up-to-date evidence and to do this all in a rapidly changing environment.

The TriAS project has built a semi-automated data-driven workflow in support of IAS policy that covers a full suite of instruments. Checklist and occurrence data-publication pipelines provide the raw data. Aggregation workflows generate both a unified, annotated, alien species inventory. Using the Global Biodiversity Information Facility as a central data hub, we ensure openness and sustainability, and from this is built an occurrence cube of species, location and year, based upon the checklist. These data products are then used to feed indicators of species invasion, including occupancy trends within and outside protected areas and pathways of introduction. The occurrence cube is also the basis of risk models and maps, used to forecast the establishment risk of IAS in response to climate change.

The unified checklist is published as the Belgian contribution to the Global Register of Introduced and Invasive Species (GRIIS) and all products are communicated to a wide range of stakeholders, including citizen scientists, researchers, invasion managers and IAS decision-makers. These results also support risk assessments performed by taxon experts, which will integrate expert opinion into policy advice.

All of these workflows have been built on the principles of Open Science, which means that anyone can rerun or adapt this workflow, including running them for any other country or region. The TriAS workflow and results definitely constitute a significant improvement towards evidence-based decision making that is transparent, repeatable, adaptable, and supported and endorsed by stakeholders.

Galaxy for Ecology: An open source platform on academic cloud to produce and share EBV data products and EBV workflows

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1: French national Museum of Natural History, France; 2: Sorbonne University, France; 3: IFREMER, France

Assessments based on periodic biodiversity monitoring are fundamental for understanding and reporting changes in biological life forms. In this context, many "tools" developed by French initiatives offer to researchers and/or areas managers and/or naturalists and/or citizen practical ways to calculate, plot and model a biodiversity indicators based on in situ monitoring. Among those, one can mention

1/ Vigie-Nature <http://www.vigienature.fr/>, a national French program gathering 17 biodiversity monitoring schemes targeting a wide range of taxa (birds, plants, pollinators, bats, snails, etc.) and a wide range of public (from skilled naturalists to students and land managers). Among those, STOC-EPS (a bird monitoring scheme started in 1989 <http://www.vigienature.fr/fr/suivi-temporel-des-oiseaux-communs-stoc>) and Vigie-Chiro (a bat monitoring scheme started in 2006 <http://www.vigienature.fr/fr/chauves-souris>) gather millions of species records and abundance measures, collected by hundreds of skilled participants.

2/ PAMPA a project dedicated to researchers and MPA (Marine Protected Areas) managers to facilitate creation of a wide range of marine biodiversity indicators.

These initiatives implies a diverse and complex need for data visualisation and analysis, not only by the research lab coordinating the scheme but also by the partners/participants themselves. However this desire to involve collaborators to get rich information from their data is impeded by the complexity of statistical methods and software processes (e.g. to produce temporal trends).

Here, we propose an intermediate progress assessment on on-going projects aiming at creating FAIR (Findable, Accessible, Interoperable, Reuseable) data, tools and workflows which would yield a pilot system for the production of EBV once completed. Decomposing the STOC-EPS, Vigie-chiro and PAMPA tools into a chain of Galaxy-E tools <https://ecology.usegalaxy.eu/>, we are currently working on building whole workflows that fulfills most EBV key steps outlined by Kissling et al. in 2017. First versions of tools from this workflow are now scripted and functional:

- A community metrics calculation tool computing specific richness, Simpson, Shannon, Pielou and Hill indexes
- A Generalized Linear Model tool computing a GLM to test the effect of year, location and habitat on any biodiversity variable computed from field measurements.
- A csi (community specialization index), cti (temporal) and ctri (trophic) per year and site tool who can compute and plot time variation of indicator or mean trait values of communities

Making more out of it: The SinAS workflow for standardising and integrating databases in invasion ecology

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Large amounts of biodiversity data have been made accessible in recent years. These data often provides valuable information beyond the initial scope they were collected for. Combining data becomes particularly relevant at large spatial scales, where comprehensive sampling is not feasible. Thus, addressing the current challenges of global change necessitates the integration of multiple – often numerous – data sets. In the field of biological invasions, however, the integration of databases remains a major challenge, as different concepts associated with terminologies and categorisations of the invasion status of species invasion status are applied in invasion biology itself and across countries and regions. This presents a significant hurdle to the the process of integration. The integration of alien species data from different sources has become a common problem in many projects, and published articles often do not provide sufficient information on the applied standardisation and integration process. As a consequence, research lacks transparency and is not reproducible, and time is wasted as the standardisation and integration has to be repeated for each new project . Here, we introduce a new workflow for standardising and integrating alien species data (SinAS). Based on lists of alien species occurrences, the SinAS workflow standardises 1.) terminologies using Darwin Core standards, 2.) location names based on a spatial resolution widely used in studies in invasion ecology, 3.) taxon names using the GBIF Backbone Taxonomy and 4.) dates of first record based on published rules on treating date entries. The workflow provides a large degree of flexibility, which allows the user to adapt it to user’s needs, and at the same time provides a way to readily report modifications. We illustrate the application using a case study of the integration of five common global databases of alien species occurrences. We show that the overlap between databases is still surprisingly low, which indicates different scope and objectives of each database and the potential to improve the coverage of individual databases. However it also demonstrates that that the application of different concepts and classifications of alien and invasive species data may result in different research outcomes. We recommend using such publicly available workflows, or making study-specific data integration workflows available on publication, as it will improve the reproducibility and transparency of invasion research that relies multiple data sources. This will increase the confidence and trust in data, study results and conclusions in invasion science.

NextGEOSS's Biodiversity Community Portals for Generating Remote Sensing-enabled Essential Biodiversity Variables and Habitat Suitability Maps

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Earth observation data is an ideal platform for capturing change in biodiversity at various resolutions, both spatially and temporally, while GEOBON creates an explicit structure for monitoring biodiversity by proposing EBV candidates. It is not only important to generate remote sensing (RS)-enabled biodiversity products using high-resolution data, but more than ever, it is necessary to address the biodiversity loss at the global scale from satellite acquisitions. In this regard, under the biodiversity pilot of the NextGEOSS initiative, the ITC biodiversity community portal (<http://nextgeoss.itc.utwente.nl/ebv/>) provides a self-service framework to generate RS-enabled biodiversity products for better understanding of biodiversity loss and ecosystem changes for the remote sensing and biodiversity communities. In addition, the WENR Biodiversity community portal (<https://www.synbiosys.alterra.nl/nextgeoss>) applies the RS-enabled biodiversity products as predictors, as well as in situ vegetation plot data for EUNIS habitat suitability modelling. Different users, including research and development institutions, public and private stakeholders, and decision-makers, are also making use of these resources. Currently, users can access the ITC Biodiversity community portal to generate Leaf Area Index as an RS-enabled biodiversity product in GEOBON EBV class 'Ecosystem Function', and also as one of the most important vegetation biophysical variable on a global scale using high-resolution satellite data (Sentinel-2, 20m) processed online using Cloud services (Terradue Cloud service). Also, under the EuroGEOSS project, additional remote sensing biodiversity products (Net primary productivity, chlorophyll content, habitat type, and fragmentation) are being moved and mirrored from the ITC biodiversity community portal to the GEOBON biodiversity portal, where they will be permanently available for use by the biodiversity and remote sensing communities.

The SCAR Antarctic Biodiversity Portal, an online ecosystem for linking, Integrating and Disseminating Antarctic Biodiversity Information

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The SCAR Antarctic Biodiversity portal (www.biodiversity.aq) is a gateway to a wide variety of Antarctic biodiversity Information and tools. Launched in 2015 as SCAR-MarBIN and the register of Antarctic Marine Species (RAMS) the system has grown in scope from purely marine to also include terrestrial information.

Biodiversity.aq is a SCAR product, currently supported as one of the Belgian contributions to the European Lifewatch-ERIC (European Research Infrastructure Consortium). The goal of lifewatch is to provide access to: Distributed observatories/sensor networks;

Interoperable databases, existing (data-)networks, using accepted standards; High Performance Computing (HPC) and Grid power, including the use of the start-of-art of the so-called Cloud and Big Data paradigms technologies; Software and tools for visualization, analysis and modeling.”

Here we provide an overview of the most recent advances in the biodiversity.aq online ecosystem, a number of use cases as well as an overview of future directions. Some of the most notable components are:

The Register of Antarctic Species (www.marinespecies.org/RAS) provides an authoritative and comprehensive list of names of marine and terrestrial species in Antarctica and the Southern Ocean. It serves as a reference guide for users to interpret taxonomic literature, as valid names and other names in use are both provided.

IPT.biodiversity.aq allows disseminating Antarctic biodiversity data into global initiatives such as the Ocean Biogeographic Information System (OBIS) as Ant-OBIS (formerly also known as SCAR-MARBIN) and the Global Biodiversity Information Facility (GBIF) as AntaBIF. Data that can be made available includes metadata, Species checklists, species occurrence data and more recently event based data. Data from these international portals can be accessed through data.biodiversity.aq.

Biodiversity.aq, provides a strong and tested platform for sharing, integrating, discovering and analysing Antarctic biodiversity information originating from a variety of sources into a distributed system.

Session: EBV Data

Poster presentations

The fraction of land cover classes; derived variables from ESA CCI Land Cover time-series (1992 - 2018)

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GEOEssential project (<http://www.geoessential.eu/>) is built on an end-user-driven approach to first identify environmental policy indicators, then their associated Essential Variables (EVs), and finally the appropriate Earth Observation data sources. In the context of the GEOEssential project, we developed a workflow to aggregate the ESA CCI Land Cover time-series (<https://www.esa-landcover-cci.org/>) in a more end-user friendly format and structure.

The ESA CCI Land Cover time-series describe the land surface with 22 classes at a spatial resolution of 0.002778° (~ 300 m) annually from 1992 to 2018. We calculated the fraction of each class at two windows of 10 x 10 pixels and 100 x 100 pixels for the entire time-series. As a result, we produced 22 layers corresponding to each of the classes, per year, presenting the fraction of each class in ~3 km and ~30 km globally from 1992 to 2018. This provides the end-users with the possibility to explore the changes in a fraction of a single land cover class, e.g. urban areas, and easily employ the ESA CCI Land Cover time-series in their works with a significantly less computational cost at the global scale.

Furthermore, we merged the three classes of cultivated areas, forest areas, and urban areas, and calculated the fraction of each class following the classification used by the IPCC Assessment Report 5 and the IPBES Global Assessment. These derived variables could be used to monitor ecosystem structure and changes of specified land cover classes extent in time and space.

In this contribution, we aim to inform the community about the availability of such derived variables and to present some example applications. To download the latest version of the dataset visit <https://doi.org/10.5281/zenodo.3730469>.

Essential geodiversity variables to complement EBVs

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In the face of accelerated anthropogenic and natural change of biotic and abiotic aspects, appreciation of the interaction diversity between all spheres of the Earth is urgently needed. Yet, to date, the vast majority of studies only account for the effect of climate and, potentially, soils on biodiversity, ignoring interactions (e.g. the effect of biodiversity on soils) and other aspects of geodiversity (the range, value and dynamics of geological, geomorphological, pedological and hydrological aspects and features of the Earth's surface and subsurface). This applies to both, primary science and the science-policy interface.

I will give a brief introduction on the state-of-the-art in geodiversity – biodiversity interaction research, discuss the importance of incorporating the diversity of abiotic factors in biodiversity and conservation studies and indicate promising avenues for further research. This includes theoretical advancements, such as the recently introduced Essential Geodiversity Variables framework (Schrodt et al. 2019b), as well as practical matters, including remote sensing (Lausch et al. 2019) and modelling approaches suitable for expanding the geo- biodiversity interaction approach across the relevant spatial and temporal scales.

Session: Remote Sensing

Oral presentations

Exploring the limitations of machine learning inversion of PROSAIL radiative transfer modelling for biophysical trait retrieval from Sentinel-2

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In recent years, there has been an unprecedented increase in availability of Earth Observation satellites leading to unique opportunities for near real-time monitoring of spatio-temporal ecosystems processes. This steady increase of “data” offers promising opportunities for improving the monitoring of Essential Biodiversity Variables (EBV) through remote sensing which offers a great potential for increasing our ability to understand and act upon the environment.

Estimating biophysical traits of vegetation through empirical models linking remote sensing observation with field data is often challenging due to the mismatch between what is measured in the field and what RS data measures. The most common alternative is to use Radiative Transfer Models (RTM) that simulate the interaction of light with leaf and/or canopy. The most used is PROSAIL which combines two other RTM models PROSPECT with 4SAIL to generate canopy spectra response in function of the biophysical parameters, and sensor and sun positions.

While the physics behind these models is well-established retrieving biophysical traits from them is hindered by the possibility that different combinations of biophysical traits generate similar if not equal spectra (ill-posedness). The most common strategy to address this problem is to minimize the risk by reducing the potential set of possible biophysical traits values in function of some prior knowledge of a study area or system, assumptions that hinder the ability of true “global” level predictions. If we aim to monitor EBV through remote sensing to truly explore spatio-temporal ecosystem processes at a global scale it is necessary to identify the best approaches for estimating biophysical parameters of vegetation irrespective of geographic location or time. This is of importance given the recent development of cloud solutions such as the Google Earth Engine that enable the processing of large-scale global data at unprecedented temporal and spatial resolutions.

In this research we focus on ESA Sentinel-2 satellites to explore the ability of various families of machine learning algorithms to retrieve biophysical traits using a hybrid inversion scheme based on PROSAIL. The machine learning algorithms tested were Gaussian Processes, Random Forests and Artificial Neural networks which are some of the most used algorithms in the field of remote sensing and biophysical trait retrieval.

For this we first performed a sensitivity analysis to identify which biophysical traits can be recovered from Sentinel 2 data and which band are associated with each trait. To ensure that the machine learning models used are the best fit for purpose implemented hyperparameter tuning procedures before any modelling. Then we tested the ability of biophysical trait retrieved of each model for both pure and increasingly noisy data. Our results identified which biophysical traits can be retrieved from S2 and identified which models are most promising for global applications.

A first spectral library and phylogeny of Chilean native forests species: basis for biodiversity mapping using airborne hyperspectral and LiDAR imagery

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Forest biodiversity mapping, at a tree level, is currently a feasible task using remote sensing techniques and it has been successfully accomplished for relevant forest ecosystems such as tropical forests and temperate forests in Europe and North-America, but not yet in temperate forests in South America. To construct such maps, a detailed knowledge on the foliar spectral reflective properties of the forest species is needed for airborne image classification. Prior to the mapping exercise, the construction of a spectral library (i.e. a collection of the spectral signatures of all species), and a phylogeny (i.e. a tree of similitude measures between the species) is needed. Also the relationship between spectral signatures and key distinctive biophysical leaf properties is studied to understand the power of spectral data for a successful image classification. Further steps involve crown delineation using LiDAR data, extraction of the mean spectral signature per crown using hyperspectral data and finally single tree classification based on the spectral library. In this contribution, we provide the results of a first spectral library developed for the Caramávida conservation area (Southern Chile, 37°S, 73°W), which will be used for a future forest biodiversity mapping of this conservation unit. In February 2020, an intensive field campaign was carried out to measure spectral signatures of all 26 dominant trees and 4 shrub species of this area. For each species, 2 trees were climbed in order to reach the upper part of the crown (with direct sunlight) where three branches were sampled. For each sample, leaf spectral reflectance measurements were carried out using a high resolution FieldSpec Pro instrument and a leaf clip. Additionally, leaf samples were measured in situ or stored and sent for laboratory determinations of 21 leaf biophysical properties, including water content, pigments, micronutrients, carbon fraction, phenols and tannins. After a careful quality assessment a total of 3170 valid spectral signatures were measured. We present here the main features of this first spectral library of a Chilean temperate forest, together with its spectral phylogeny, comprising Chilean forest species with large latitudinal distribution such as *Nothofagus pumilio*, *Nothofagus dombeyi*, *Nothofagus alpina*, *Nothofagus obliqua*, *Laurelia sempervirens*, *Saxegothaea conspicua*, *Persea lingue*, *Embothrium coccineum*, *Weinmannia trichosperma* and also the iconic and endangered species *Araucaria araucana* and *Gomortega keule*. We discuss opportunities and limitations of this valuable database for forest biodiversity mapping, task which will be carried out in future stages of this project (LiDAR and hyperspectral data were also acquired during February 2020).

Why CEOS Is Important to GEO BON: The CEOS Biodiversity Activity

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Satellite observations play an important role in understanding and monitoring biodiversity and ecosystems. This importance was recognized by CEOS, the Committee on Earth Observation Satellites, in 2011 when the Executive Officer suggested adding the Biodiversity Activity as a formal entity. While it has taken some years to engage with CEOS, with EBVs now largely mature GEO BON is entering a new phase and that level of engagement is set to change.

This presentation will provide background on CEOS and explain why CEOS is relevant to GEO BON and the EBVs. It will then discuss the Biodiversity Activity's role in working with CEOS, why the relatively mature state of the EBVs enable more GEO BON engagement with it, and suggest an engagement approach so more of the observations and products GEO BON needs can become available.

Greater engagement starts with a stable EBV set that reflects community needs. Using that as a baseline, the observation requirements to support those EBVs and their derived products can be identified. The result is a table that associates a well-justified need with sensor and operational requirements such as type of sensor, spatial and temporal resolution, and accuracy. Such tables are best developed by each EBV working group, an activity that most groups have already started for other types of information using, for example, GEO BON-provided templates. It is hoped that these can now be extended and completed.

With direct traceability from observation and production requirements back to community-justified needs it is then possible to start exploring ideas with CEOS, a back-and-forth process that balances community needs with implementer resources and capabilities. The format for these discussions is often in the context of periodic CEOS meetings and their associated discussions and action items. For example, the Biodiversity Activity could present its traceability table and ask for thoughts and comments, which could be discussed offline as part of an action. The back-and-forth process could then begin. In part, this is just "getting a seat at the table" so the value of RS for biodiversity monitoring—and thus its value to society and to CEOS member agencies—is fully appreciated.

Background. CEOS is an organization of 34 national space agencies and 24 associate agencies whose mission is to coordinate civil space-based Earth observations for societal benefit. Focus areas include, inter alia, environmental parameters, land surface imaging, forests, agriculture, climate, capacity building, the SDGs, and data processing; it also plays a major role in GEO.

The regional SASSCAL Biodiversity Observation Network in Southern Africa

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Initiated in 2001 within the BIOTA project, the SASSCAL Observation Network today encompasses 47 fully standardized observatories of the size of one square kilometre, located in Angola, Zambia, Namibia and South Africa, accompanied by 18 Auxiliary Observatories with specialised sampling design (<http://www.sasscalobservationnet.org/>). The monitoring is focussed on higher plants, while cryptogam plants and fauna are included in selected observatories. Important drivers like land use and climate (for automatic weather stations see <http://www.sasscalweathernet.org/>) are sampled, as well.

With two decades of observation the network is now able to identify drivers and processes of change, even in arid ecosystems. The presentation reports on the status and achievements of the network which also integrates remote sensing tools, hydroecological monitoring and soil fertility data.

Using the GEDI satellite lidar mission with nationwide airborne laser scanning surveys in fast changing forest ecosystems

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1: University of Lisbon, Portugal; 2: 3edata. Centro de iniciativas empresariais

Background: The Global Ecosystem Dynamics Investigation (GEDI) satellite mission aims at scanning forest ecosystems on a multi-temporal short-rotation basis. The GEDI data can be used to validate and update nationwide airborne laser scanning (ALS). The GEDI laser shots can fairly describe the structural complexity of fast-growing plantation accounting for growth and forest dynamics. We present a case in the Northwest of Spain comparing forest statistics derived from GEDI and from nationwide ALS in four forest ecosystems across 1 million hectares of fast- and slow-growing species. The contribution aims at reinforcing the change of paradigm when it comes to describe forest productivity using wall-to-wall data and avoiding the restrictions in traditional growth and yield modeling when using site index and age to express forest production.

Methods: Descriptive statistics on forest structure were derived from the ALS surveys collected between 2017-2018. The raster maps were used to evaluate the statistics computed from GEDI laser shots. The spatial scale of both data sources matched. The harvesting activities across the landscape were detected from changes between ALS time acquisition and GEDI scanning in the 2019. The study shows how to further integrate the 25-m beam full waveform laser statistics by improving existing forest management planning information such as the Forest Map of Spain. We assessed four forest ecosystems ranging from commercial Eucalyptus plantations to slow-growth oak forests.

Results: The fast-changing forest dynamics were accurately detected from 2017 (ALS) to 2019 (using GEDI laser). The integration of GEDI data into the fragmented forest landscapes was challenging and several steps were recognized to influence the results. Co-registration, steepness of the terrain and proximity to forest edges were important. The capture height growth dynamics were useful to monitor forest properties while identifying areas prone to be harvested or affected by natural disturbances.

Conclusions: The GEDI laser data has the capability to fill the need of operational forest planning in fast-growing plantations when it comes to detect growth dynamics and update ALS-based statistics computed for forest management units. The combination of satellite and airborne laser technology precisely describe remote forest areas converting global wall-to-wall mapping into a reality in the short-term when the GEDI orbits are completed within the lifespan of the mission. The presentation aims at highlighting the benefit of GEDI to monitor small-scale forest areas indeed with the perspective of relying more and more on laser data to conduct forest management planning.

rasterdiv - an Information Theory tailored R package for measuring diversity from space

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The variation of species diversity over space and time has been widely recognised as a key challenge in ecology. However, measuring species diversity over large areas might be difficult for logistic reasons related to both time and cost savings for sampling, as well as accessibility of remote ecosystems.

In this talk, I will present a new R package - rasterdiv - to calculate diversity indices based on remotely sensed data, by discussing the theory beyond the developed algorithms. Obviously, measures of diversity from space should not be viewed as a replacement of in-situ data on biological diversity, but they are rather complementary to existing data and approaches. In practice, they integrate available information of Earth surface properties, including aspects of functional (structural, biophysical and biochemical), taxonomic, phylogenetic and genetic diversity.

Making use of the rasterdiv package can result useful in making multiple calculations based on reproducible open source algorithms, robustly rooted in Information Theory.

RS-enabled EBV Road Map

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The ESA funded GlobDiversity project was the first large-scale project explicitly designed to develop and engineer Remote Sensing enabled Essential Biodiversity Variables (RS-enabled EBVs) and ended in June 2020. The project also aimed to contribute with the documents and procedures generated to the development of a workflow starting from user requirements to final products that can be used for policy relevant global biodiversity monitoring and assessments.

As a final step, the project developed a road map discussing the project's outputs, e.g., strategic documents, processing chain and data products derived when focusing on particular RS-enabled EBVs, in the context of the overall EBV framework with and in context of relevant players such as the Group on Earth Observations Biodiversity Observation Network (GEO BON), CBD, IPBES, CEOS, the EBV user community and decision makers, Copernicus Services and the space agencies.

We will thus present this RS-enabled EBV road map strategic document with the aim to put in place the project's output into the EBV frame work. The proposed workflow includes discussions about the involvement of different users from the very beginning, to the development of any EBV data set, as well as to the implementation and use in the framework of the indicators. In addition, we will discuss the project's experiences gained while developing biodiversity products based on remote sensing. In particular, we will present knowledge gaps and recommendations when evaluating the proposed road map. Thus, we will present this strategic document, so that the biodiversity community can most benefit from GlobDiversity's outcome.

CEOS Ocean Variable Enabling Research & Applications for GEO (COVERAGE): A Prototype Big Data Platform for Integrated Access to Interagency Environmental and Biological Data in Support of MBON

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The CEOS Ocean Variables Enabling Research and Applications for GEO (COVERAGE) initiative seeks to provide improved access to multi-agency ocean remote sensing that are better integrated with in-situ and biological observations in support of oceanographic and decision support applications for societal benefit. COVERAGE is an international initiative and 3 year pilot project within the Committee on Earth Observation Satellites (CEOS) involving interagency participation. It aligns with programmatic objectives of CEOS and the missions of GEO-MBON (Marine Biodiversity Observation Network) and GEO-Blue Planet, which are to advance and exploit synergies amongst marine observational programs. COVERAGE focuses on implementing technologies, including cloud-based solutions, to provide a data rich, web-based platform for integrated ocean data delivery and access: multi-parameter/platform observations, easily discoverable and usable, organized thematically, available in near real-time where possible. These will be complemented by a set of value-added data services available via the COVERAGE portal including an advanced Web-based visualization interface, subsetting/extraction and other relevant on demand processing capabilities. COVERAGE development is organized around priority use cases and applications identified by partnering stakeholders. The initial phase has focused on system architecture aspects and developing inventory of global interagency products from the four CEOS Ocean Virtual Constellations (VCs) that would serve as a baseline dataset for COVERAGE and integrating these with select in-situ biological datasets of different kinds. Here we provide an overview of the initiative and the status of the technical implementation work that is under-way. Emphasis is also placed on describing the thematic demonstration application of relevance to MBON that the COVERAGE prototype will be supporting relating to pelagic fish community dynamics in relation to the environment. Stakeholder involvement and International collaborative aspects of the project are also discussed with the intent of soliciting community feedback.

Spatial-temporal dynamics of alpine treeline ecotones in the western United States under climate change

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In global mountain ecosystems, the transition zone from closed-canopy montane forests to treeless alpine tundra areas is often referred to as “alpine treeline ecotone” (ATE). It is an essential habitat for numerous species, such as diverse trees, understory plants, mammals, and breeding birds. Under the human-mediated climate change, global ATEs are expected to be driven upslope, which could lead to a variety of cascading ecological consequences, including changes in carbon sequestration, alpine biodiversity, nutrient and water cycling, snow retention, albedo, and surface roughness. Consequently, the dynamics of ATEs has the potential to serve as a powerful indicator of the changing climate. However, as field data collection is often labor-intensive and time-consuming in mountainous regions, it is very difficult to monitor ATE changes through time consistently. Therefore, most existing studies on the ATE dynamics were limited to a single study site or a set of single locations with relatively small geographic ranges.

Accordingly, the objectives of this study are: 1) to define an automated ATE detection metric using easily accessible remote sensing datasets, and 2) to apply the developed metric to monitor the spatio-temporal dynamics of ATEs during the past decades in the western United States. We first determined “climatic ATEs” (CATEs) in the study domain. Then, we defined three characteristics of ATEs, which included: a) sharp spatial gradient in normalized difference vegetation index (NDVI), b) intermediary values of NDVI, and c) spatial co-variation of elevation and NDVI. According to these characteristics, we developed an ATE-detection Index (ATEI) ranging from 0 to 1 at 141 sampled LANDSAT pixels in the CATEs. The average identification accuracy of ATEI was around 0.713 (standard deviation = 0.111) based on a 100-time repeated 10-fold cross-validation. Then, we calculated the annual ATEIs from 1984 to 2018. Additionally, we randomly generated 32,186 transects across the region and estimated the yearly ATE elevations within each transect.

We found that, since the 1980s, the ATE elevation had a median increase of 6.25 m/decade in 50.9% of the transects, a median decrease of 5.66 m/decade in 22.9%, and was relatively stable in the remaining 26.2%. This study generates a regional consistent ATE detection metric. It allows us to assess the ATE change over the full time-series of available data, which improves our understanding of the mechanisms of geographic range dynamics of plant species in mountainous areas under the changing climate.

Session: Remote Sensing

Poster presentations

UAV and satellite data synergies for biodiversity monitoring: a review

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Unmanned aerial vehicles (UAV) and satellites are both essential Earth observation systems for monitoring land surface dynamics. UAVs are frequently used for their capability to acquire spontaneous images (even under clouds); conversely, satellites are interesting for the supply of times series data on wide areas. However, satellite spatial and temporal resolutions are often insufficient or too expensive to provide appropriate data in heterogeneous and dynamic landscapes, or at key periods. The combination of UAV and satellite data, defined here as 'synergy', makes it possible to overcome these problems by refining or combining information at different spatial or temporal resolutions. Various synergies are possible and not widely known. This study aims at reviewing and characterizing these synergies observed in the literature. Three main categories can be distinguished: Multiscale Analysis, Model Calibration and Data Fusion. Multiscale Analysis refers to exploitation of the satellite wide swath to conduct analysis on a regional scale in combination with a detail-scale analysis produced by very high spatial resolution imagery from UAVs. The Model Calibration synergy is defined through the use of UAVs data to provide qualitative (labelling) or quantitative (biophysical parameters) information that satellite cannot provide alone, to calibrate satellite-based models. Data Fusion consists of creating a new data cube enriched by the respective resolutions from each data source. A focus on ecological applications is made in order to highlight the potential of these synergies to the production of Remote Sensing Essential Biodiversity Variables.

First results show that ecological applications only use the Model Calibration synergy (60% qualitative; 40% quantitative). This synergy is used to derive key factors driving the distribution of species (e.g. land use/cover type or hydrological dynamics), functional traits (e.g. fraction vegetation cover, biomass, chlorophyll content) and to detect directly biological organisms as invasive vegetal species to prevent ecosystem degradation. Meanwhile, the two other synergies are not used yet for ecological studies unlike in geosciences and precision agriculture applications. To highlight the potential of each of these synergies for ecological applications, the monitoring of a Natura2000 wetland is given as a case study throughout three examples: (1) a multiscale analysis of spectral diversity metrics, (2) a unmixing model calibration for habitat mapping and (3) a data fusion for the characterization of subtle temporal and spatial patterns.

This study illustrates that UAVs can play an interesting role to fill the gap between field surveys and satellites. Finally, the strength of these synergies lies in the complementary but also in the compatibility of UAV and satellite data. Thus, it depends on the capacity that the remote sensing community has to open data and facilitate their accessibility, to establish facilities for reproducible science via data and methods sharing, and to apply effective data intercalibrations.

The combined effect of global climate and land use change on biodiversity under Shared Socioeconomic Pathways

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Global biodiversity plays a key role in ecosystem functions and services. However, biodiversity on earth has been witnessed to be and will keep declining since the beginning of the Anthropocene epoch, and the World Economic Forum (WEF) has reported in 2020 that the biodiversity loss ranks the third of highest risk in the next decades. Global climate change and land-use change are considered to be the two most significant factors for biodiversity loss. Although there are piles of studies on the impact of climate change or land-use change on biodiversity, most of them are limited to small-scale investigations. The combined impacts of climate change and land-use change on biodiversity on a global scale remains unclear. Therefore, in order to investigate how climate change and land-use change affect global biodiversity. Here, we first calculated the land-use naturalness and intensity for different land-use types. Then, a spatial distribution model of global biodiversity was established by using random forest regression. Based on the Shared Socioeconomic Pathways (SSPs), we projected the spatial distribution of global biodiversity for 2050, and further analyzed the trend of biodiversity change. The results show that climate and land-use factors both have impacts on global biodiversity. In which near-surface temperature is the most important factor to biodiversity, followed by land-use naturalness. The importance of precipitation varies from species to species. In addition, we also find that, induced by the combined effect of climate change and land-use change, about 20% of the world's land will suffer biodiversity loss in 2050. Europe will suffer the heaviest biodiversity loss, accounting for about 70% of its terrestrial area. Furthermore, the migration of future biodiversity will be inclined to high latitudes and high elevations. A slightly increasing biodiversity is projected the area above 30°N or 4,500 meters above sea level, while the biodiversity loss will mainly locate at the 20°S~20°N. Additionally, the expansion of amphibian species and bird species in 2050 will range to high latitudes in the North hemisphere.

Mapping change in grasslands biodiversity using Sentinel 2 data in the Gorce Mts.

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Grasslands cover 51% of the land surface. Part of grasslands is the alpine pastures which are marked areas of high-altitude ecosystems. Nutrient-rich mountainous grasslands and herbaceous vegetation play an important role in determining the grazing patterns of livestock, distribution of herbivore population, and overall ecosystem health and stability. Currently, remote sensing data and methods start to be a powerful tool for grasslands monitoring in varying spatial and temporal scales and helping us a better understanding of grassland productivity, and in response to the changing climate system and land use, among other biophysical attributes. A lot of approaches where satellite data have been used have been developed so far but we still need more advanced methodologies which allow us to assess grassland ecosystems changes.

Therefore, the main aim of this study is to develop a new approach which allows to estimate changes in the condition of grassland. Additionally, we attempt to assess the influence of the EU agricultural policy in the resumption of mowing or grazing in previously abandoned grasslands. We located our test study area in a part of the Carpathians, the Gorce range. Grasslands in the Carpathian Mountains are primarily the result of human agriculture activities. The Gorce Mountains were taken as the study area due to the occurrence unique grasslands habitats on the European scale.

We used here the satellite images from Copernicus Mission, optical sensor Sentinel 2-MSI level-2. The data came from the growing season (April-October) in the years 2017-2019. The period between April and October is suitable to investigate if the grasslands were mowed. The analysis was made in Google Earth Engine with supervise methods. Seasonal spatially and spectrally linked, free-clouds composites were created from Sentinel 2 data. Based on these composites, using SVM classification algorithms, we assess grasslands condition changes including mowed in each year.

The preliminary results showed that the abandoned grassland area is still growing, therefore the degradation of grassland ecosystems is proceeding in this area. Notwithstanding, in the Gorce National Park is observed rising grasslands area mowed.

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Session: Soil BON

Poster presentations

Land-use changes negatively affect soil fauna communities: preliminary results of a meta-analysis

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Soil fauna plays an important role for delivering ecosystem services, such as food production, climate mitigation and soil erosion. However, land-use changes can alter the characteristics of soil fauna communities which could affect the functioning of the ecosystems. Research into anthropogenic effects on soil has grown in recent decades. After this data generation, there is a need to synthesize land-use effect on soil biodiversity in order to identify general patterns. We conducted a meta-analysis to assess the effect of land-use changes on the abundance, richness and diversity of soil invertebrates. We performed a search in online databases to find studies comparing soil invertebrate communities in reference/natural sites (primary and secondary forests and grasslands) with communities in sites under different uses: agriculture, plantations, logging and pastures. We identified 146 suitable studies evaluating land-use change effects. The overall effects of land-use changes across all studies were negative and significant for three community characteristics although the effects were more pronounced for abundance and species richness of invertebrates. It remains to be examined if these effects vary according to type of land use, time since land change, taxonomic group of invertebrates among other moderator variables. Our results indicate a strong reduction of soil fauna communities in anthropogenic landscapes, which may severely compromise ecosystem services essential for human wellbeing.

