iDiv | Annual Conference 2022

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BOOK OF ABSTRACTS

Keynotes

Claire Fortunel, *Institut de Recherche pour le Développement, Monpellier*

Functional trait differences and the mechanisms structuring diverse communities

Abstract:

A long-term research goal for ecologists is to understand the mechanisms shaping local communities and the consequences for ecosystem-level processes. It also represents a major challenge as global change rapidly alters abiotic gradients and biotic interactions. In this context, there are three major questions that motivate my research: (1) what mechanisms shape communities in species-rich systems? (2) do these mechanisms act similarly across environments and regions? (3) how will diverse communities respond to global change? In order to address these mechanistic questions in highly diverse tropical forests, where we don't know much about the biology of the majority of species, I combine approaches from community ecology, functional ecology and phylogenetics. Functional traits reflect key physiological features and life history tradeoffs, while phylogenetic relationships can provide an additional estimate of overall species similarity in the absence of other information. Combining trait and phylogenetic information allows for a powerful test of the mechanistic role of species differences in shaping local communities. In this talk, I will present recent work evaluating the mechanisms shaping tropical forests and testing if these mechanisms act similarly across environments and regions. Together these studies illustrate the need to combine different approaches for improving our understanding of the mechanisms shaping communities and ecosystems. Experimental work is instrumental in providing detailed tests of how different mechanisms of community assembly shape species distribution and dynamics, but it remains difficult to conduct such detailed studies for many species at broad spatial scales. If traits can provide good proxies for species response to different mechanisms, we can leverage that information in models and simulations to better predict large scale responses of communities. To gain a stronger predictive ability of the response of these diverse communities to global change across scales, it will be critical to combine experimental and quantitative approaches.

Zeyaur Khan, *International Centre of Insect Physiology and Ecology, Kenya*

Exploiting plant and insect biodiversity for developing sustainable crop protection strategies for Africa and beyond

Abstract:

The 'push-pull' system (www.push-pull.net), developed by exploiting plant and insect biodiversity effectively controls serious biotic constraints to cereal-livestock production in Africa, stemborers, fall armyworm, and striga weed, while improving soil health. It allows income diversification with sustainable livelihood components such as livestock farming. The companion cropping system makes smallholder farms more resilient often with a tripling of yields and has now been made more climate smart. It involves attracting stemborers with trap plants (pull) whilst stemborers and fall armyworm away from the main crop using a repellent intercrop (push). Chemicals released by intercrop roots induce abortive germination of the noxious parasitic striga weed. The companion plants provide high value animal fodder year-round, facilitating milk production. Furthermore, soil fertility is improved due to improved nitrogen fixation, carbon sequestration and phosphorus availability, reduced soil erosion and degradation. The technology improves gender equity and is appropriate for smallholders, and economical as it is based on locally available plants, not expensive external inputs. It fits well with traditional mixed cropping systems in Africa. The push-pull system has been adapted to drier and hotter conditions linked to climate change by identification and incorporation of drought tolerant companion crops. This climate-smart push-pull directly responds to rising uncertainties in Africa's rain-fed agriculture due to the continent's vulnerability to climate change. The new companion crops, *Desmodium intortum* and *Brachiaria* Mulato II hybrid, can withstand extended periods of drought stress with no water. To date push-pull has been adopted by over 250,000 smallholder farmers in 18 sub-Saharan African countries whose maize yields have increased from about 1 t/ha to 3.5 t/ha. Low-input technologies that address several production constraints and deliver multiple benefits are more relevant for African smallholder farmers but also proves useful lessons for agricultural systems in the developed world.

Thematic Sessions

The Evolution of Biotic Interactions and Ecosystem Functioning

Chair: Andrea Galmán, *Martin Luther University Halle-Wittenberg*

This session includes studies exploring the ecological mechanisms underlying biotic interactions like i) plant-plant interaction, ii) plant-soil interactions, iii) plant-animal interactions, including herbivores and the third trophic level (i.e. predators and parasitoids of herbivores). In addition, the topics covered in the session include the role of functional and phylogenetic diversity shaping ecosystems, the role of abiotic factors shaping the biotic interactions and also how the creation of novel interactions, derived from global change, alter the ecosystems.

Martha Paola Barajas Barbosa

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Martin Luther University Halle-Wittenberg

Long-distance and inter-island dispersal drive functional divergence of an oceanic island flora

Oceanic island floras are well-known for their morphological peculiarities and exhibit striking examples of trait evolution. These morphological shifts have been attributed to insularity and shaped by biogeographical processes and evolutionary histories of oceanic islands. However, the mechanisms through which biogeography and evolution have shaped plant functional traits remain unclear. In this study, we describe the functional trait space of an oceanic island flora (Tenerife, Canary Islands, Spain) using extensive field and laboratory measurements, and relate it to global trade-offs in ecological strategies. We find that the island trait space is concentrated around a functional hotspot dominated by shrubs with a conservative life-history strategy. By dividing the island flora into species groups with distinct biogeographic distributions and diversification histories, our results reveal that long-distance dispersal, and particularly the interplay between inter-island dispersal and speciation at the archipelago level drive functional divergence and expand the island trait space. Conversely, speciation via cladogenesis has overall led to functional convergence, densely packing trait space around shrubbiness. Our approach combines ecology, biogeography and evolution and opens avenues for new trait based insights into how dispersal and speciation jointly shape the assembly of native island floras.

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Andressa Cabral
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The pantropical co-variation of frugivore and plant fruit trait syndromes

Mutualistic interactions between fruits and frugivores are prominent in tropical rainforests. These interactions are facilitated by the functional trait matching, and the frequency and diversity of matching traits may influence how plant and animal communities vary in space and time. Here we test the hypothesis that species and functional richness of frugivory-related plant and animal traits co-vary across major biogeographical regions, because of distinct co-evolutionary dynamics between and within these regions. To this end, we selected three vertebrate-dispersed, pantropical plant families (i.e. Annonaceae, Arecaceae, Moraceae), and two major frugivore lineages (i.e. birds and mammals), and integrated global distribution and trait data. To correct for abiotic effects on species and functional richness, we also assembled environmental variables. Preliminary analyses using multiple linear regression and Structural Equation Models indicate that regional species richness of the three plant clades was best explained by frugivore richness of both birds and mammals, but environmental variables and TDWG3 area size explained additional variation in plant richness. Additionally, we show that biogeographical realms occupy different partitions of the global functional trait space of plants and frugivores, and regional, community-level plant functional richness ('trait syndrome') variation is best explained by frugivore functional richness, species richness, climate, and TDWG3 area size. These results support the hypothesis that plant-frugivore communities are strongly shaped by co-diversification and selection on co-evolving traits, and these may thus be important mechanisms explaining species and trait diversity of plant-animal mutualisms more generally.

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Lucille Chrétien

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Geographical patterns in seedling metabolome and defence against herbivory

Plant traits mediating interactions between plants and their environment are under selection pressure by local abiotic and biotic factors. This selection process brings intraspecific variation in plant traits, and studies spanning geographical scales can help unravel the main drivers of plant trait variation. The Latitudinal Herbivore-Defence Hypothesis predicts that herbivore pressure decreases with increasing latitude, and that plant defence declines concomitantly. Empirical evidence show mixed support for this pattern, which might not be as generalizable as initially expected. This project aims at determining whether patterns of variation in seedling metabolome and defence corroborate established biogeographic theories in plant defence using a standardized approach. We compared variation in the metabolome of seven common grassland pants along a latitudinal gradient of 1,500 km (Spain to Sweden). Plants were of four families: three Asteraceae (Achillea millefolium, Leucanthemum vulgare, Jacobaea vulgaris), one Caryophyllaceae Silene latifolia, one Plantaginaceae Plantago lanceolata, and two Poaceae (Holcus lanatus, Dactylis glomerata). Plants were tested at the seedling stage, when herbivory is the main cause of mortality. We used untargeted metabolomics techniques to detect and identify patterns of variation in plant traits that might have been overlooked by previous targeted analyses. We correlated population- and regional-level variation in the plant metabolome to geography and plant defence parameters. For comparability purposes, we calculated indices measuring the probability of attack, plant palatability to herbivores, and plant tolerance to attack via bioassays with the widespread Garden Snail Cornu aspersa as a generalist herbivore.

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Andréa Davrinche

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Large within-tree leaf trait variation: responses to local species richness and soil nutrient availability.

Leaf functional traits provide important insights into plants' ecological strategies. However, while often studied at the inter-specific level and sometimes at the intra-specific level, within-individual leaf trait variation is under-researched, typically due to time and resource constraints.

In a large biodiversity-ecosystem functioning experiment in subtropical China, we used near-infrared spectroscopy to measure nine morphological and biochemical leaf traits at the intra-individual level for 420 trees of 14 species. Comparing the amount of trait variation explained

by the inter-specific, intra-specific and intra-individual levels, we found that intra-individual variation is in general as relevant as intra-specific variation, and both together account for 30-60% of total trait variation. Additionally, we show partial support for positive effects of soil nutrient availability and species richness on intra-individual trait variation, but only scattered evidence of amplifying, interacting effects.

Our work highlights the importance of integrating an intra-individual perspective to understand trait-based mechanisms in biodiversity-ecosystem functioning relationships.

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Perttu Anttonen
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Effects of tree richness, structural variation and leaf traits on herbivory and predation in different local scales in a subtropical BEF experiment

Biodiversity loss is one of the most urgent challenges in the world affecting ecosystem functions and ecosystem services (e.g.1). As part of the research consortium TreeDi "Tree Diversity Interactions: The role of tree-tree interactions in local neighborhoods in Chinese subtropical forests", we focused on how tree richness, plant nutritional quality and tree structure affect the herbivory and predation pressure in different spatial-scales in close neighborhoods, going from microhabitat scale (0.5 x 3 m), to tree with its immediate neighbors, to plot level (~21 x 21 m). Understanding how forest structure and leaf quality affect trophic interactions in relation to tree diversity in a subtropical forest is important as higher trophic level interactions can strongly affect the structuring and functioning of such species-rich forest ecosystems (e.g.2, 3). Our results showed that both, forest structure and leaf quality, affected herbivory and predation, but the effects varied between different spatial scales and tree richness levels. Scale dependence of forest structure affected especially the responses between different predator groups (arthropods, birds and mammals). Furthermore, the different predator groups responded differently to different aspects of forest structure, such as apparency and vegetation density. The results offer insight how biodiversity loss of producers affects higher trophic levels in relation to other main features of forest stands.

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Axel Touw
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Mixed responses – how microbes modulate defense responses against root-herbivores

Microorganisms form an important part of most ecosystems. They are highly abundant in soils, where they populate the rhizosphere and colonize plant roots. Although the root epidermis forms a barrier against microbes, root damage caused by herbivores can provide an entry point for pathogens. Plants respond to infections by producing chemical defenses with antimicrobial properties, such as phytoalexins. Root-herbivores like Delia radicum harbor a rich gut microbial community (GMC) as well, which performs essential digestive functions and detoxifies noxious compounds. Exposure to antimicrobial compounds could disturb the GMC and thereby affect insect performance. In that way, plant responses to microbes can form an indirect defense mechanism against root-herbivores.

To test this hypothesis, we first examined the defense response of Brassica rapa to D. radicum in terms of gene expression and the production of secondary metabolites. We identified three phytoalexins, of which cyclobrassinin (CB) was most abundant. After comparing its structure against a standard, we confirmed that CB accumulates at the site of herbivory, suggesting that D. radicum larvae are exposed to antimicrobial compounds. In the next steps, we will perform a series of bioassays to study the effects of exposure to CB on the GMC of D. radicum and on D. radicum itself.

Our results show that B. rapa responds to root-herbivory by producing a diversity of secondary metabolites, among which several with antimicrobial properties. Microbes are important mediators of plant-insect interactions, and production of antimicrobial compounds could affect the performance of D. radicum. The results of our study therefore provide insight in the co-evolution between the plant, the herbivore and its associated microbiome.

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The iDiv Barcoding Initiative – iBarc

Chair: Martin Schlegel, *Leipzig University & German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig*

Nicole van Dam, *Friedrich Schiller University Jena & German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig*

Martina Herrmann, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Friedrich Schiller University Jena*

DNA Barcoding is a molecular tool for applications in biodiversity assessment using a DNA-sequence of one or several marker-genes, so-called barcodes. We will bring together different research groups at iDiv to present and discuss their research projects, and applications in different fields (e.g. taxonomic and functional diversity, microbial communities, animal-plant interactions, quantitative approaches such as assessment of populations sizes, biomass). We intend to develop plans for further activities and to establish a competence-grid.

Luis Daniel Prada-Salcedo
Helmholtz Centre for Environmental Research – UFZ

Effects of tree composition and soil depth on structure and functionality of belowground microbial communities in temperate European forests

Depending on their tree species composition, forests recruit different soil microbial communities. Likewise, the vertical nutrient gradient along soil profiles impacts these communities and their activities. In soils of forest ecosystems, bacteria and fungi commonly compete, but they also interact between them and with their environment, therefore the mechanisms and drivers behind soil microbial structures and their functionality are complex and challenging to decipher. Using amplicon sequencing, we aimed to analyze diversity of soil bacteria and fungi in relation to forest composition and soil depth. Moreover, employing random forest (RF) models, we identified microbial indicator taxa of forest plots composed of either deciduous or evergreen trees or their mixtures, as well as three soil depths. Microbial taxa showed higher changes in relative abundance across soil depths than in relation to forest composition. The microbial Shannon diversity was especially affected by soil depth and by the proportion of evergreen trees. Our results also reflected that bacterial communities are primarily shaped by soil depth, in contrast to fungal communities, which are rather influenced by the forest composition. RF classifiers showed higher accuracy based on taxonomic composition than on bacterial metabolic pathways or fungal functional guilds. Moreover, we

identified the top ten bacterial and fungal genera associated to forest composition that differed from the microbial genera indicative for soil depths. In comparison to pure deciduous or evergreen plots, we did not find strong differences in core functions in mixed forests. However, these mixed plots had higher abundances of microbial functions linked to processes like biofilm formation, flagellar assembly and metabolism of xenobiotics, especially in top soils. This indicates an enhanced amount of soil functioning at higher levels of tree diversity, which highlights the importance of tree mixtures for forest soil functioning.

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Theresa Jörger-Hickfang
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Metabarcoding relates biodiversity and land use changes in the Peneda-Gerês National Park

Metabarcoding offers a great opportunity for monitoring biodiversity while identifying species faster and cost-effectively than current morphological identification.

We collected deadwood beetles using 70 window traps from 14 sampling locations across the northern part of the Peneda-Gerês National Park and bordering Spanish regions from May to August 2021. Matched young oak forest and old oak forest habitat patches with different sizes were collected for all sampling localities.

Here we test a methodological pipeline to estimate deadwood beetle diversity linking window trapping and DNA metabarcoding.

We aim to identify all OTUs for all specimen collected in each of the 70 samples by amplifying a short fragment of the mitochondrial COI gene. One of our main aims is to develop a cheap and fast methodological procedure to metabarcode all the samples in iDiv laboratories. Three different DNA extraction protocols are being tested to establish the cheapest, fastest and most reliable method for our metabarcoding pipeline. We aim to simplify the technique with a single PCR reaction to amplify and tagg the amplicons, instead of the more commonly used two steps PCR.

PCR products will be quantified, pooled and cleaned for library preparation. Amplicons will be then sequenced using the MinION (Nanopore Technologies) which allows for real time analysis. A reference COI library for insects in the Peneda-Gerês National Park is being created and we will compare the data obtained from the MinION with this reference dataset to create OTUs and calculate the alpha and beta diversity. We will use these estimates to compare diversity within and between habitats, patch sizes and other biotic factors.

Lisa Hahn
Leipzig University

Optimization of molecular methods to study beetle diversity in the Leipzig floodplain forest

With over 350,000 described species, Coleoptera represent the largest order of insects worldwide. With their great species richness and the presence of many cryptic species, many families of beetles pose a challenge for morphologically determination and require expert knowledge. Without this expertise, biodiversity is often vastly underestimated in morphological taxonomic studies. Molecular methods, such as DNA barcoding, offer a good way to avoid this problem. Here we present an optimized molecular approach for beetle determination using DNA barcoding and metabarcoding.

For DNA barcoding, the extraction and amplification method were adapted to obtain DNA from one or several legs of each beetle species. This method is used to establish a genetic reference database. This serves as a basis for a non-destructive metabarcoding approach, which does not require the destruction of the beetles. This offers advantages especially in the study of cryptic species, because after genetic examination more attention can be paid to morphological differences. This study is part of the Leipzig canopy crane (LCC) and provides, among very few projects worldwide, the possibility to explore canopy diversity. Together with the investigation of the understorey, comprehensive biodiversity studies across the whole forest ecosystem can be conducted. By optimizing previous molecular methods, our project contributes greatly to the rapid and reliable determination of the beetles and thus to answering important ecological questions. Furthermore, we contribute greatly to the compilation of reference databases, which are crucial for genetic studies, and to the further investigation of cryptic species in beetles.

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Robert Paxton
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DNA barcoding and metabarcoding bees at Martin Luther University Halle-Wittenberg

DNA barcoding of bees in Central and Northern Europe has become well-established, firstly because of the difficulties inherent in identifying species using morphological criteria; specialist knowledge is often required and, even for experienced practitioners of morphology-based determination, several European bee taxa represent morphologically cryptic species. Secondly, many Central European bee species have been barcoded, with their sequences available on NCBI and BOLD databases. We highlight our use at Martin Luther University Halle-Wittenberg of bee barcoding through two projects (i) barcoding of cryptic bumble bee species in the Bombus lucorum s.l. complex comprising Bombus cryptarum, Bombus lucorum s.s. and Bombus magnus; and (ii) barcoding pan-trap material using a metabarcoding

approach to compare insect species diversity across urban and rural habitats. Though not without its own difficulties to which we will allude, barcoding bees provides an accurate, relatively fast and cheap means to determine the species identity of bees.

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Individual vs. combined effects of novel insecticides flupyradifurone and sulfoxaflor with the fungicide azoxystrobin on the health and gut microbiota of honey bees

The western honey bee, Apis mellifera, has a relatively consistent gut microbial community that is thought to enhance host health and protect against parasites and pathogens. Several studies, however, have shown that honey bees' gut microbiome can be disrupted by some agro- and inhive chemicals, putting their health at danger. Therefore, we used a controlled and fully crossed laboratory experimental design to test the effects of chronic exposure to field-realistic sublethal concentrations of two nicotinic acetylcholine receptor agonist insecticides (nACHRs), flupyradifurone (FPF) and sulfoxaflor (SULF) and azoxystrobin (Azoxy) fungicide, individually and in combination, on the survival of individual honey bee workers and on their gut microbiota (fungal and bacterial) diversity and composition in response to the different treatments and at a time scale. The gut microbiota were assessed using a paired-end sequencing approach targeting the fungal ITS2 and the V4 region of 16S rRNA respectively.

We found more than additive interaction effects between the insecticides FPF or Sulf and the fungicide Azoxy on honey bee survival. The fungicide Azoxy substantially reduced the fungal Shannon's diversity index after chronic exposure for 10 days. The relative abundance of the top 10 genera of the bee gut microbiota was also affected differently by the fungicide, insecticides and the fungicide-insecticide combinations. The treatments significantly impacted the microbial community composition and differentially abundant microbial genera. We, therefore, present the first evidence that the insecticides FPF or Sulf, the fungicide Azoxy, and the fungicide-insecticide combinations affect the bee health and the relative abundance of beneficial and pathogenic gut microbiota.

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Birgit Gemeinholzer

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Metacoding of plants - Ingenious possibilities with pitfalls

DNA barcoding is based on the assumption that a specific genome region of an unknown organism can be compared with verified organisms in reference databases and in this way the species names can be determined.

However, plant barcoding and especially metabarcoding of plant samples from the environment has some pitfalls. Mutations in the DNA barcoding region are not always associated with morphological features that characterize a species. Species are not temporally and spatially stable entities, so evolution, speciation, hybridization, polyploidy, and introgression are common features that prevent unambiguous identification of species in mixed samples. The use of multiple DNA barcoding regions would improve species-level identification in metabarcoding analyses, but also complicates assignments at different levels that are likely to be resolved only with AI. Multicopy DNA barcoding markers with undefined copy numbers in organism genomes and PCR biases prevent abundance measurements in environmental samples. In addition, dominant species often prevent weak species signals from being identified. That being said, however, plant metabarcoding now allows for much more accurate reconstruction of ecological relationships and dependencies of and between organisms than ever before. For example, predator-prey or plant-pollinator systems can now be analyzed on temporal and spatial scales, which was not possible before.

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Frontiers in Methods in Biodiversity Research

Chairs: Juan Carvajal Quintero, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*
Daniela Hoss, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*

In recent years biodiversity research has become more and more complex, relying on methods from citizen science to remote sensing to high-end computational models, as well as the transition from established methods like genetics or chemistry to the "omics". The session features the latest work from iDiv researchers, presenting new methods and their applications in biodiversity research.

Christine Beemelmanns
Leipzig University

Chemical communication mechanisms in symbiotic interactions

The rapid development of metabolomic and genomic technologies has enabled a renaissance of natural product research. In particular, the detailed chemical analysis of complex symbiotic systems has attracted substantial attention amongst natural product and medicinal chemists as many structurally diverse microbial metabolites were found to be important regulators of these interactions, thus making them promising pharmaceutical drug candidates. Here, I will present our recent discoveries in the field of ecology-driven natural product chemistry, our analytical approaches to identify microbial signaling molecules and our molecular-biological approaches to trace back their biosynthetic origin. Here, I will first present our recent studies on microbes associated with fungus-farming termites. Macrotermitinae cultivate a symbiotic fungus (Termitomyces sp.) for nutrition. The fungus is grown on predigested plant material, which is piled up by the termites as a comb-like structure to enable optimal growth conditions. This environment is prone to exploitation by parasitic fungi (e.g. Pseudoxylaria sp.), if the colony ecosystem is out of balance. Due to the longevity and stability of a healthy termite colony, it is expected that several factors contribute to garden defense by the production of e.g. antimicrobial natural products. In the second I will discuss the identification and functional analysis of microbial signals with morphogenic activity. Here the group uses the model species Hydractinia echinata and its morphogenetic transition from the motile to the sessile phase, which is induced by the marine bacterium Pseudoalteromonas.

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Jingyi Li
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A size-constrained foraging model predicts contrasting foraging patterns in aquatic and terrestrial food webs

Understanding the emergence of food web structure is essential for disentangling the mechanisms underlying ecosystem organization, functioning and stability. Despite the high complexity, all food webs are composed of prey-predator interactions. Thus, resolving the foraging processes of predators can be the key to understanding the architecture of food webs. Body size has long been recognized as a key trait shaping the foraging patterns of predators. Although several models have incorporated size constraints into feeding interactions, a systematical evaluation on the size dependency of foraging patterns is lacking. In our study, we developed a size-constrained foraging model and parameterized it using a global dataset of 290 food webs (GATEWAy). We confirmed systematic constraints of body masses on predator foraging niches and provided novel quantitative estimates of how foraging niches vary along the prey body-mass axis, which revealed striking differences between ecosystem types. Particularly, in aquatic ecosystems, larger predators tend to feed on prey with a higher predator-prey size ratio and feeding range but lower feeding probability, whereas terrestrial predators feed on prey with nearly constant size ratio and range. According to the principle of energy flux, the foraging patterns by aquatic predators, particularly the higher consumer-resource biomass ratio, may explain the higher energy transfer rate and contributes to the stability of large predators in aquatic ecosystems compared with terrestrial ecosystems. By incorporating such size-dependent constraints, our model better explains both the feeding links and food web structure observed in natural communities, and thus provides new insights for understanding the organization of natural ecosystems.

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Intercomparing global foliar trait maps: upscaling approaches and spatial patterns

Foliar traits such as leaf nitrogen and phosphorus content (LNC, LPC) as well as specific leaf area (SLA) are key components of the leaf economic spectrum and hence important to characterize ecosystem functioning and functional diversity. However, up to now, global-scale maps of these traits have been produced using rather indirect approaches: either statistical upscaling on the basis of large plant trait databases or process-based modeling. Although there are more direct approaches to estimate such leaf traits from remote sensing, their applicability is still limited in coverage due to the sparsity of suitable ground reference data

and satellite or airborne imagery. Here, we report a comprehensive intercomparison of the currently available global maps of LNC, LPC, and SLA. Here we categorize seven different upscaling approaches and analyze the spatial patterns in the resulting trait maps at different scales.

Overall, global foliar trait maps show considerable differences in both the distribution of values and spatial patterns. Major differences in spatial patterns among products were related to differences in the use of plant functional type (PFT) categories from land cover maps in the upscaling. Similarities in spatial patterns emerged when the foliar trait maps are subset according to whether PFT information was used or not. Only the maps that used PFT information showed similarities in spatial patterns at smaller scales.

Future upscaling approaches should take into account new remote sensing data sources, such as hyperspectral reflectance from upcoming satellite missions, and provide sufficient details on the upscaling methodology as well as the intended purpose of the resulting maps.

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

Modelling species invasion using a metapopulation model with variable mortality and stochastic birth-death processes

A species entering a novel landscape has to overcome several obstacles that inhibit invasion, which often leads invaders to go extinct before they are able to form a stable local population. Estimating which species can invade new landscapes is challenging due to the complex interplay of a wide variety of ecological factors. Here, we explore the effects of individual-based influences such as individual size, growth and stochastic effects of local disturbances. To address these challenges within a single model, we extended the Levins metapopulation model by allowing mortality to vary with individual life stage, such that smaller individuals have a higher chance of dying. To incorporate individual-level variability and effects of stochastic events while maintaining continuous-time dynamics, we implement the model using Gillespie's method. Unlike the classic Levins model, for which successful invasions occur deterministically whenever colonisation exceeds mortality, we identified an Allee effect in our model, i.e. a minimum initial size below which invasions are unlikely to be successful. Moreover, we created an index that can predict the likelihood of successful invasion as a function of just two parameters – colonisation rate, and time-averaged mortality rate. Furthermore, time-averaged mortality can be expressed as an analytical function of three model parameters: an individual's growth rate, its initial size and the impact of disturbances.

Our results demonstrate that invasion success in a complex stochastic model can be predicted as a simple function of colonisation and mean mortality rates.

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Karin Mora

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Macroecological dynamics from crowd-sourced plant occurrence data via Flora Incognita

As citizen science smartphone applications are gaining in popularity, they are becoming a great source for plant species occurrence data. One such app, Flora Incognita [1] (https://floraincognita.com), identifies plant species native to Central Europe from images in real time using machine learning algorithms. Flora Incognita records the precise location as well as the time at which an image is taken. The latter is not recorded by traditional sampling programmes such as Florkart (www.floraweb.de), a mapping effort involving 5000 flora experts conducted by the German Federal Agency for Nature Conservation.

A previous study [2] on the German flora demonstrated that patterns of plant species composition over geographical space, so-called macroecological patterns, can be obtained from Flora Incognita data. These spatial patterns compare well with Florkart patterns, indicating a level of robustness to noise and biases typical for crowd-sourced data such as population density. Moreover, the authors identified which climate and soil characteristics are critical in shaping plant species distribution.

In this work we extend the previous study by exploring the temporal nature of plant occurrence data and address the following questions: Do the previously detected spatial macroecological patterns change over time and how? Can we identify seasonal phenology from these patterns and how they are affect by climate variability? This analysis gives an insight into possible approaches to understanding the dynamics of macroecological patterns. We highlight the potential of crowd-sourced time series as applications like Flora Incognita will gather more data in time.

[1] Mäder et al. (2021). Methods Ecol Evol, 12: 1335-1342
[2] Mahecha et al. (2021). Ecography, 44: 1131-1142

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Léonard El-Hokayem
Martin Luther University Halle-Wittenberg

Identifying threatened groundwater dependent ecosystems as local biodiversity hotspots in Saxony-Anhalt and globally via remote sensing

Groundwater resources are biodiversity hotspots, and provide crucial ecosystems services. Yet, groundwater dependent ecosystems (GDEs) are exposed to several anthropogenic threats, including climate change. Tackling these threats requires improving the on-the-ground identification of GDEs at the global scale. The project focus on the development of a novel combined vegetation related and hydrological ecosystem-based concept to map, analyze and evaluate GDEs at the global scale by means of mixed multiscale and multi-instrument methods. The approach combines elaboration, analysis and interpretation of existing global hydrological data sets indicating ecosystems reliant on emerging groundwater and a novel designed methodology to identify those ecosystems reliant on resident groundwater (terrestrial vegetation). For the biome-wise detection of GDEs and assessments of threats, machine learning methods integrate remote sensing and global geodata in the fields of climatology, hydrology, hydrogeology, geomorphology, vegetation geography, and land and water use. First exploration and further calibration and validation relies on the occurrence of phreatophytes available from vegetation databases (sPlot, the global vegetation database), existing local to national GDE maps, and field surveys in different biomes. After creation of a harmonized global up-to-date map for GDEs, threatened systems to model hotspots for potential changes in plant diversity will be pinpointed. As GDEs are considered biodiversity hotspots, the developed method can be understood as a further opportunity to monitor and analyze biodiversity in special environmental settings and hence will contribute to integrative biodiversity research in Saxony-Anhalt.

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Biodiversity and Ecosystem Services Scenarios in the Context of Climate and Land-use Change

Chair: Carlos Guerra, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*

This session focuses on presenting and discussing work on scenario and projections-based research covering multiple scales (from local/national to global) of multiple biodiversity (e.g., single species, groups of species, alpha diversity, beta diversity, etc.) and ecosystem services (e.g., single services, tradeoffs, multifunctionality, etc.) variables. We strive for a balance between talks and discussion and leave room for proposing new collaborative work on the topic.

Carlos A. Guerra,
Martin Luther University Halle-Wittenberg
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Global hotspots for soil nature conservation

Soils are the foundation of all terrestrial ecosystems. However, unlike for plants and animals, a global assessment of the hotspots for soil nature conservation is still lacking. This hampers our ability to establish nature conservation priorities for the multiple dimensions supporting the soil system: from soil biodiversity to ecosystem services. Here, we conducted a global field survey including >11,000 biodiversity (archaea, bacteria, fungi, protists, and invertebrates) and function (critical for six ecosystem services) observations within 615 composite topsoil samples from a standardized survey in all continents, to identify global hotspots for soil nature conservation. We found that each of the different soil ecological dimensions (i.e., soil species richness [alpha diversity], community dissimilarity, and ecosystem services) peaked in contrasting regions of the planet, and were associated with different environmental factors. Temperate ecosystems showed the highest soil species richness, while community dissimilarity peaked in the tropics, and colder high-latitudinal ecosystems were identified as hotspots of soil ecosystem services. These findings highlight the complexities of simultaneously protecting multiple soil ecological dimensions. We further show that most of these hotspots are currently not properly covered by protected areas (over 70%), and are vulnerable to all of the considered global change scenarios. Our work provides the first global estimation of soil nature conservation priorities under global environmental change, and highlights the fundamental importance of accounting for the multidimensionality of soil biodiversity and ecosystem services to conserve soils for future generations.

Rémy Beugnon
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Vegetation diversity buffers macroclimate fluctuations and extremes

The frequency and intensity of extreme climatic events, such as heatwaves and droughts, are increasing with climate change, threatening humanity and other life on Earth. Especially, belowground communities and functions are known to be highly sensitive to changes in microclimatic conditions (e.g., temperature and humidity). Yet, vegetation was shown its potential to buffer macroclimatic fluctuations by providing a critical buffering layer between macro- and microclimatic conditions. Moreover, higher vegetation diversity increased primary productivity. Therefore, we would expect vegetation diversity to increase the macroclimate buffering effect, and thus protect belowground communities and functions from microclimatic extremes. Here, we tested the effect of vegetation diversity on macroclimatic buffering across ecosystems at the European scale using the SoilTemp database. Our results show that increasing vegetation diversity increases the buffering of extreme macroclimate temperature events by increasing low temperatures and reducing high temperatures. Therefore, our results suggest that the plant diversity-induced stabilization of ecosystem functions could be mediated by the stabilization of microclimatic conditions.

Authors: Rémy **Beugnon**, SoilTemp consortium, Stephan **Hättenschwiler**, Manfred **Wendisch** and Nico **Eisenhauer.**

Samuel Kwakye
Leipzig University

Analysis of insect concentrations using radars: Weather radar echoes classification

Over the past decades, insects bidiversity and abundance are decreasing. Systematically assessing the decline requires an unintrusive observation of flying insects in the atmosphere, which is also termed "aerosphere". Radar has been known to provide quantitative estimates of flying insects. A weather radar is designed to observe meteorological targets, thus the derivation of insect echoes needs special techniques. The automation of insect retrieval methods from weather radars, for this purpose artificial intelligence approaches are well suited. In this study, data from the KLOT S-band radar at Chicago, Illinois part of the radar network of the United States of America(USA) is used. Weekly aphid counts from a suction trap in Morris, Illinois is used as in-situ data. Near-surface temperature, wind speed, and cloud cover ECMWF Reanalysis v5 data are used to assess the effects of atmospheric conditions on the distribution of radar variables. Decision tree, random forest, and support vector machine models were generated to distinguish 10 combinations of scatterers. Low variability of differential reflectivity is found for precipitation scatterers and centered around zero. The differential reflectivity distributions caused by insects is broad with higher medians. Plankton and moderate insects have equivalent variability of reflectivity. Cloud cover fraction, temperature, and wind speed heavily influence the distribution of radar variables for heavy rain, snow, and plankton respectively. The random forest algorithm produces the most

accuracy to distinguish all the scatterers. Across the three algorithms, light insects' intensity and plankton are distinguished best. This study presents the initial steps of distinguishing insect echoes, and evaluation of insect concentration.

Authors: Samuel **Kwakye**; Johannes **Quaas**; Heike **Kalesse**; Patric **Seifert**; Roel **van Klink**; Christian **Wirth**.

Marie Sünnemann
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Leipzig University

Drivers of soil multifunctionality in terrestrial ecosystems

Soils provide essential ecosystem functions and services through a variety of mechanisms, making them an important resource for human well-being. However, global change factors such as climate change and modern land use threaten to alter this critical role. Here, we use four key soil enzymes, water-stable aggregates, and microbial activity and biomass as measures of soil multifunctionality in the context of land use and climate. Using structural equation modeling, we quantify the direct and indirect relationships between soil multifunctionality and abiotic factors (soil texture and moisture, pH, and climate) in different land use types. To do this, we use two different datasets: 532 soil samples from across Europe in the Land Use/Land Cover Area Frame Survey (LUCAS) and soil samples from the Global Change Experimental Facility (GCEF), a large-scale field experiment in central Germany investigating the effects of climate change and different land use types.

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Franziska Taubert
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Impact of management, environment and climate change on productivity and the proportion of herbs in grasslands: a simulation study across Germany

Temperate grasslands are important ecosystems as they provide various ecosystem services (e.g., biodiversity and biomass production). Environmental conditions and management intensity affect productivity, plant functional composition and relative abundances of plant functional types in grasslands; however, the importance of different factors and quantitative impacts are still largely unexplored. Here, we used an individual-based grassland model and created a generic regionally transferable parameterization by accounting for six different grassland observational sites along a gradient of climatic, management and soil conditions for calibration and validation. In a scenario analysis for 24 representative regions across Germany, we then analyzed how grassland productivity and the biomass proportion of herbs depend on management intensity and various environmental factors in combination with

climate change. The model-based scenario analysis revealed that intensive management generally leads to high grassland productivity and low herb proportions. Correlations with environmental factors decreased with management intensity (i.e., mowing frequency and fertilization amount). Precipitation and irradiance belonged to the most influential environmental factors. Climate change had only a minor influence on the analyzed vegetation attributes. Our study shows how process-based grassland models can be used to gain a general understanding of how environmental factors and anthropogenic interventions impact grassland dynamics – knowledge which is especially crucial with regard to climate change.

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Qicheng Bei

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
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Metagenomic analysis of soil microbiomes responses to climate and land use change during the summers 2014-2019

Research into climate and land use change has mainly focused on soil microbial community changes, rather than identifying and analyzing the functional mechanisms. Here, we investigate the soil microbiome responses to a future climate scenario at the GCEF research station (ambient climate vs. increased temperature by +0.6 °C and altered rainfall patterns) across three land use types (intensively used grassland, conventional and organic croplands). Soils were sampled for metagenomic analysis during the summers of 2014-2019. Prolonged heatwaves and drought unexpectedly occurred throughout central Europe in 2018 and 2019 summers, thus they were considered as extreme summers. In contrast to normal summers, extreme summers resulted in substantial changes in the soil microbial community composition and function. The relative abundance of Actinobacteria was markedly increased from 19.2% in normal summers to 41.4% in extreme summers. Compared to ambient climate, future climate significantly affected the abundance of Thaumarchaeota and Candidatus Eisenbacteria, although the majority of microorganisms remained largely unaffected. Results also demonstrated the significant effects of land use (cropland vs. grassland, conventional vs. organic croplands) on soil microbiomes under future climate conditions. In addition, we recovered 459 near-complete metagenome-assembled genomes (MAGs) were from 180 metagenomic datasets. Functional annotation of MAGs further supported that future climate change has affected the genes involved in nitrogen cycling, such as ammonia oxidation and denitrification. Overall, our results revealed previously unreported soil microbial genomes and extend our understanding of microbial functional traits as influenced by long-term climate and land use change.

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Complex Mechanisms in a Complex World

Chairs: Sreetama Bhadra, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*

Paola Barajas, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*

Biodiversity develops and is maintained via complex interactions of many different processes and factors. This very diverse session is a perfect example of iDiv's integration idea. It provides insights across a broad set of systems and taxa, how biodiversity interacts with each other and how outcomes of those interactions can look like. The session also offers insights into how humans perceive and communicate this complexity.

Till J. Deilmann
Friedrich Schiller University Jena

Habitat matters: Patterns in phenology and functional traits of herbaceous plant species from Botanical Gardens and natural habitats

During the last decades, many studies have shown that plant phenology has shifted related to climate change, resulting in an advance in spring phenology and an overall delayed leaf senescence. Despite the importance of different abiotic conditions, the influence of habitats on phenology and the link of plant traits to phenology is little studied.

Therefore, we studied the phenology and functional traits of 16 herbaceous species from semi-dry grasslands (SDG), mesophilic grasslands (MG), and the Botanical Garden (BG) Jena to investigate the influence of habitats on both functional traits and phenology. To achieve this, we monitored phenology on a weekly basis from April to October and measured a broad set of environmental parameters and plant and phenological traits in all three habitats.

The habitats differed mainly in terms of soil nutrients, soil moisture, relative humidity, and soil depth, with BG showing the most variation and being more similar to MG than SDG. We found a similar pattern in the distinction of plant traits which was mainly associated with leaf nutrients, specific leaf area (SLA), leaf dry matter content, plant width and flower size.

Regarding phenology, MG showed a rather consecutive flowering pattern indicating temporal niche segregation whereas SDG displayed flowering synchrony. Focussing on match species (i.e., species occurring in all habitats), we found differences across habitats in maximum flower intensity, first flowering day, and 5% leaf senescence. Furthermore, boosted regression tree analyses confirmed previous studies showing that plant traits are well-suited and robust predictors of phenology.

Our results suggest that habitat must not be neglected when studying phenology or functional traits.

Authors: Till J. **Deilmann**; Josephine **Ulrich**, Christine **Römermann**.

Taylor Dotson
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German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Biodiversity Democracy? Populism, Technocracy, and the Problem of Expertise

The political response to global challenges, such as climate change and COVID-19, is increasingly dysfunctional. Ongoing gridlock and paltry progress have led to calls to bypass popular democracy, to simply "listen to scientists." At the same time, other segments of the citizenry have been and continue to be skeptical and distrustful of "official" expertise. In other words, contemporary politics is increasingly torn between technocracy and populism, both of which have an uneasy relationship to democracy. To what extent can biodiversity politics be characterized by this same pattern, and how might stakeholders strategize to avoid falling into the same trap? The purpose of this talk is to invite conversation not only about the rightful place of science, but also ask how conflict over contentious environmental problems might be more productive.

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

Removal of a dominant C4 Genus and fire increases palatable grass in Mesic-savanna grasslands.

Grassland and savanna ecosystems harbor high plant biodiversity and provide critical ecosystem services, such as palatable biomass for grazing herbivores. Fires are natural to these ecosystems, however, positive feedbacks known as the grass-fire cycle can result in high dominance of fire-tolerant, non-palatable C4 grasses. Returning these grass-dominated systems back to a state in which they contain more even and more diverse plant communities that offer palatable biomass to grazers might not be accomplished by simply excluding fire from the system. Removal of the dominant grass species might be necessary to create open spaces that allow for the growth and recruitment of its competitors. With the help of local communities and NGOs we experimentally removed the dominant Cymbopogon grass genus (non- palatable & C4,), removed fire, and removed both the grass and fire from the Sehima-Dichanthium sp. grassland in the Peninsular India. The experiment included 53 sites that were each 25 m2. Sites in which Cymbopogon and fire were removed did not have higher herbaceous plant diversity, but removing Cymbopogon dramatically affected species composition. Sites with grass and fire removed produced lower herbaceous biomass overall, but more palatable biomass, which is important for wild and domesticated herbivores. These grasslands are home to many wildlife species, and are depended on by millions of people. Our

results have important implications for policy, as they suggest that traditional management practices can sustain biodiversity and ecosystem services.

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Pablo Castro Sánchez-Bermejo
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Martin Luther University Halle-Wittenberg

Tree phenotypic integration promotes intra-individual trait variation in a subtropical forest

As trait variation can help to reduce competition by promoting niche dimensionality, local diversity acts as an important driver of trait variation across different scales. However, traits do not vary independently, but indeed, they co-vary together in integrated phenotypes or species. Thus, there has been recent growing interest on understanding the interaction between trait variation and phenotypic integration. However, while this has been addressed at broader scales, there is scarce evidence at the individual level. We studied the interacting effect of local tree diversity and individual phenotypic integration on intra-individual foliar trait variation in ca. 500 trees of 21 species in a large tree diversity experiment in subtropical China. From every tree, we collected up to 15 leaves and measured a set of leaf functional traits to assess a set of metrics of trait variation (standard variation for every trait and distance-based functional indices) and plant trait networks properties. Strikingly, we found that intra-individual trait variation increased with increasing phenotypic integration in most of the cases. This advocates that, far from representing a constrain as it happens at larger scales, phenotypic integration might promote trait variation at the intra-individual level. Further, we found an effect of local Shannon diversity on the variation of some of the traits, suggesting that, similarly to intra-specific trait variation, intra-individual trait variation might increase with decreasing diversity in order to reduce niche overlap between individuals.

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Leonardo Bassi
Leipzig University

Increase in above- and below-ground deference traits reduces monoculture yield decline.

Plant monoculture growing on the same soil tend to reduce their productivity over time. This is known as yield decline and the accumulation of plant antagonist seems to be one of its most important driver. However, it is still unclear why some species experience stronger yield

decline than others. In this study we investigated the relationship between yield decline and twenty-four physical and chemicals above- and below-ground defense traits to elucidate the different behaviour of 27 grassland species growing in 19 years old monocultures. We hypothesize that species with higher mean defense traits or with the highest increase in defense traits after 14 years of growing in monoculture to show milder yield decline than species with lower mean defense traits or with no change in defence. In support of our hypothesis we found that the mean collaboration gradient and leaf sugar content were significantly correlated with the decline of monoculture productivity. Species on the 'outsourcing' side of the collaboration gradient had milder yield decline than species on the 'do it yourself' side of the gradient. Following the same direction, we found an even stronger significant correlation between yield decline and the change after 14 years in the collaboration gradients and leaf secondary metabolite: species that shifted their position in the collaboration gradient towards being more 'outsourcing' or that increased richness in leaf secondary metabolite showed milder yield decline than species that did not changed those traits. The link between defense traits and yield decline supports the idea that the accumulation of antagonist is an important driver of yield decline and show that functional traits can be used to predict long term monoculture productivity trends.

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Jose Valdez

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Martin Luther University Halle-Wittenberg

Spider-slugs, super-glued frogs, and vertebrate-eating insects: the overlooked world around us

As climate change and habitat loss continues to severely impact biodiversity loss, research has shifted from natural history towards laboratory experiments and complicated models. As natural history science continues to decline, we have not only lost much of the curiosity and fun of what originally made us interested in science in the first place but also our ability to relate to and communicate our science outside of academia. Natural observations can lead more young curious minds into science while also bridging the gap that has widened even further between scientists and the public. Additionally, results we get from experiments don't always translate to the natural world. Natural observations are important as it can lead to further questions down the road and a better understanding of the overlooked world around us.

Author: Jose **Valdez**

Drivers of Global Biodiversity Change
Hosted by the Macroecology & Society group

During iDiv's previous funding phase, iDiv researchers built or advanced several global biodiversity databases that enabled important new insights into different facets of global biodiversity change, from individuals and populations to (meta)communities and ecosystems. In parallel, we witnessed the emergence of many new datasets on putative drivers of biodiversity change, while modeling tools for the prediction and causal attribution of these changes matured substantially. This session aims to provide an overview of recent advances in iDiv research tackling drivers of biodiversity changes from a theoretical, data, and methodological perspective. Talks will cover:

- Empirical assessments of drivers of biodiversity change
- Advances in developing hypotheses or predictive theories related to biodiversity-change drivers
- Advances in methods to attribute biodiversity changes to specific environmental/anthropogenic causes
- New data capturing spatiotemporal dynamics in important biodiversity-change drivers
- Assessment and/or treatment of uncertainties in data or models of biodiversity change-drivers

Josiane Segar
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Martin Luther University Halle-Wittenberg

Eutrophication-dependent roles of herbivory in European forests: faunal catalyst of N time bomb or conservation actor?

Aerial nitrogen (N) deposition continues to eutrophy European forests, reducing their diversity and threatening many rare species. Concurrent widespread increases in large herbivore populations represent a separate pressure that could either dampen or exacerbate N effects on these communities, yet these interactions remain poorly understood. We used vegetation resurvey data from 52 forest sites across 13 European countries to study how herbivory and eutrophication, alone and together, drive long-term changes in forest understory cover and diversity. Increases in herbivory have accelerated species turnover and affected the understory light regime through shrub removal. Diversity effects of increasing herbivory, however, strongly depend on nutrient conditions. Under low levels of N-deposition, herbivory benefits threatened and smaller-ranged species of conservation concern while discouraging non-native and nutrient-demanding species. Yet all these trends are reversed under high levels of N-deposition. Such contrasting outcomes highlight the divergent roles that herbivory plays in different nutrient contexts and document how herbivores could either catalyze accelerating impacts from N deposition or act as a potential facilitator of threatened species.

Efforts to conserve and restore forest biodiversity should therefore account for the possibility of a "N time bomb" release under these twin pressures.

Authors: Josiane **Segar**, Henrique M. **Pereira**, Markus **Bernhardt-Römmermann**, Frank **Gilliam**, Jonathan **Lenoir**, Adrienne **Ortmann-ne Ajkai**, Kris **Verheyen**, Don **Waller**, (+ 21 additional forestREplot data contributors), Ingmar R. **Staude**.

Caterina Barrasso
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

A global assessment of data uncertainties in available land-use and land-cover time-series

Accurate global LULC time-series are vital to understand the factors shaping biogeographical patterns and their changes. Although the number and quality of open-access, remotely sensed LULC products is increasing, all products have uncertainties due to widespread classification errors. However, the relative magnitude of uncertainties among exiting LULC products is largely unknown, which hampers their confident selection and robust use by global change ecologists. To close this gap, we quantified region-, time-period-, and coarse-LULC class-specific data uncertainties for the 10 most widely used global LULC time-series. To this end, we developed a novel multi-scale validation framework that accounts for differences in mapping resolutions and scale mismatches between the spatial extent of map grid cells and validation samples. We aimed for a fair validation assessment by carefully evaluating the quality of our validation samples with respect to landscape heterogeneity that LULC products often fail to classify accurately. To address the issue, we supported the validation assessment with Landsat-based measures of cross-scale spectra similarity. We base our assessment on more than 1.8 million globally integrated LULC validation sites, where we mobilized around 2.8 million samples during the period 1980-2020. Here, we will present the results of the assessment, providing insights on global and regional patterns of LULC uncertainties. We found that no single product is more accurate over the others in mapping all LULC classes, regions and time-periods. We will provide recommendations on the selection of fit-for-purpose LULC time-series, and discuss strategies for addressing their uncertainties in biogeographical studies.

Authors: Caterina **Barrasso**; Ruben **Remelgado**, Carsten **Meyer**.

Steffen Ehrmann

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The LUCKINet land-use time-series (LUTS)

Land use reflects the needs and haves of societies, and land-use change (LUC) is the most apparent manifestation of human-environment interactions. It is thus not surprising that LUC is one of the main drivers of biodiversity change globally. However, detailed spatiotemporal information is needed to analyse the impact of LUC on biodiversity (change) with all its intricate socioeconomic and environmental facets.

Authors: S. **Ehrmann** (iDiv, University Leipzig); C. **Meyer** (iDiv, University Leipzig) et al. (various more collaborators of the LUCKINet).

Maximilian Lange

Helmholtz Centre for Environmental Research – UFZ

Mapping land-use intensity of grasslands in Germany with machine learning and Sentinel-2 time series

Grasslands cover about one third of the global land surface and are the most cultivated biome on Earth. They provide numerous ecosystem services and have a high importance for conservation as they are often species rich. Biodiversity, ecosystem services and functions in grasslands are strongly affected by the management regime, i.e. grazing, fertilisation, timing and frequency of mowing events, and its quantitative variation. The optimisation of farming efficiency usually leads to an increase in these treatments and thus land-use intensity (LUI), which may have numerous negative implications for the environment, such as biodiversity loss, water pollution and increased carbon emissions. Information on LUI is thus crucial for understanding trends and dynamics in biodiversity, ecosystem functioning, earth system science and environmental monitoring. However, large extent, high resolution data on LUI is rare. We developed a methodology calculating a continuous LUI index by quantifying key parameters of grassland LUI such as grazing intensity, mowing frequency and fertiliser application across Germany using Convolutional Neural Networks on Sentinel-2 satellite data with 20 m spatial resolution. Predictions of LUI and its components were validated using comprehensive in situ grassland management data. We achieved an overall classification accuracy of up to 66% for grazing intensity, 68% for mowing, 85% for fertilisation and an r^2 of 0.82 for subsequently depicting LUI. We evaluated the methodology's robustness with a spatial 3-fold cross-validation and assessed the spatial transferability by delineating the models' area of applicability. The presented methodology enables a high resolution, large extent mapping of land-use intensity of grasslands.

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German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
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Global environmental drivers of abundance-mass scaling across belowground invertebrate communities

The relationship between species body mass and density has intrigued ecologists for decades. Deviations from the general negative three-quarter power law (N $\propto$ M -0.75) were observed in several studies, with a high variation of slopes. In this study, we used data on soil invertebrate communities across different geographic locations (Canada, Germany, Indonesia, USA) to test if variation in local environmental conditions drives differences in local mass-abundance scaling relationships. A structural equation modeling (SEM) was used to disentangle the relative contribution of each variable on slopes. The data reveals a consistent negative body mass-abundance relationship for the sites analyzed. We identified that mean annual precipitation, soil pH and the body mass range analyzed have significant direct positive effects on the slope, while the carbon content in the soil has a direct negative impact. Mean annual temperature also influences, but mainly indirectly by impacting communities` body mass ranges, soil pH and carbon content. These models can be used to predict the effects of environmental changes on soil communities.

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

Deforestation dynamics in relation to socio-economic explanatory factors across the Amazon biome, 1990-2020

A necessary step towards improving the governance of tropical socio-ecological systems is to gain the best understanding possible of the effects that underlying drivers (policies, politics, power dynamics, historic inertias, etc.) have on the proximal drivers of deforestation. Changes in proximal drivers such as human population growth, agricultural and livestock production, exploitation of natural resources, among others, are known to be related to spatiotemporal patterns of deforestation. Consistent analyses of these dynamics across the entire Amazon biome are needed to understand how underlying drivers and interventions interact with proximal drivers across contexts and time, but these have not yet been produced. Aiming to fill this gap, we are developing a sub-national resolution (municipalities in Brazil, departments/states in the rest of the countries) analysis of the historic correlations between deforestation and proximal drivers of deforestation across the entire Amazon biome. We are modelling quantitative data on direct drivers of deforestation to detect correlations between drivers and deforestation, as well as interactions between the different drivers for the period 1990-2020.
In addition to analyzing drivers-deforestation dynamics, we expect to gain insights on the characteristics of the data needed for such analyses, as well as the current state and accessibility of the existent data across the Amazon. Lastly, we explore links between the effects of direct drivers and the underlying causes dictated by local, national and global governance processes at selected sites. We trace direct and underlying drivers back to political and economic levers capable of transforming current deforestation trajectories.

Authors: D. **Brizuela-Torres**, Helmholtz Centre for Environmental Research – UFZ; Y. **Zinngrebe**, Helmholtz Centre for Environmental Research – UFZ; C. **Brown**, Karlsruhe Institute of Technology (KIT); J. **Settele**, Helmholtz Centre for Environmental Research – UFZ.

Patterns & Drivers in the Anthropocene

Chairs: HyeJin Kim, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*

Alexandra Werner, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Friedrich Schiller University Jena*

The acceleration of human activity since the industrial revolution, and particularly in the 20th and 21st centuries, has challenged almost every natural habitat across the globe. Ecosystems globally face multiple and rapid challenges from changing climate, increased land use, pollution, human-mediated invasive species, and more. Speakers in this session will examine the effects of rapid change on multiple levels of different model systems.

Matthias Grenié

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

A barrier to global plant invasion ecology: gaps in trait availability for alien species

The increasing global changes affecting natural ecosystems increase the spread and impact of alien plant species. While native plant community ecology have highly benefited from the functional approach to better understand it, global alien plant functional ecology is still as its infancy. The lack of trait data for alien species in global databases prevents alien plant ecology to seek generality beyond the specificities of invaded ecosystems. In order to properly estimate the trait acquisition to be done, we are performing a thorough review of global trait resources available for alien plants. We are then providing a priority list of species, based on impact of the species and spread, for which the traits data should be first acquired. We believe syntheses efforts from the alien plant community could highly fill this gap.

Authors: Matthias **Grenié**, Marten **Winter**, Wayne **Dawson**, Helge **Bruelheide**, Franz **Essl**, Holger **Kreft**, Ingolf **Kühn**, Peter **Pyšek**, Mark **van Kleunen**, Patrick **Weigelt**.

Florian Schnabel
Leipzig University
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Impacts of the 2018–2019 drought: cumulative tree growth and stress responses around Leipzig

Climate change is increasing the frequency and intensity of extreme climate events such as droughts. In 2018–2019, Central Europe was hit by two consecutive hotter drought years. Such hotter droughts, in which drought coincides with a heat wave, may have devastating impacts on forests. Here, we examine the effect of this unprecedented event on tree growth and physiological stress responses (measured as increase in wood carbon isotope composition, $\Delta\delta13C$) in the Leipzig floodplain forest. We used tree rings to compare growth responses and $\Delta\delta13C$ during the consecutive drought years 2018–2019 with effects observed in former single drought years. In 2018, tree growth of most species was not reduced and drought responses were comparable to responses in former single drought years. Hence, the water availability in floodplain forests may partly buffer drought effects. In the second drought year 2019, we observed strong decreases in growth and increases in $\Delta\delta13C$, which were stronger than in any other drought year examined. We posit that this unprecedented response was driven by the cumulative stress both consecutive hotter droughts exerted. We discuss species-specific drought responses in light of the species' stomatal control and resistance to xylem cavitation. To broaden the perspective, we also compare these findings with preliminary results on tree growth responses of ~70 tree species to the 2018–2019 drought in the iDiv research arboretum ARBOfun. Overall, our findings highlight that consecutive hotter droughts constitute a novel threat to forests, even in floodplain forests with comparably high levels of water supply. However, a trait-based perspective may help to elucidate which species may cope relatively well with these novel climatic conditions.

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Rico Fischer
Helmholtz Centre for Environmental Research – UFZ

Accelerated forest fragmentation leads to critical increase in tropical forest edge area

Large areas of tropical forests have been lost through deforestation, resulting in fragmented forest landscapes. However, the dynamics of forest fragmentation are still unknown, especially the critical forest edge areas, which are sources of carbon emissions due to increased tree mortality. We analyzed the changes in forest fragmentation for the entire tropics using high-resolution forest cover maps. We found that forest edge area increased from 27 to 31% of the total forest area in just 10 years, with the largest increase in Africa. The number of forest fragments increased by 20 million with consequences for connectivity of tropical landscapes. Simulations suggest that on-going deforestation will further accelerate forest fragmentation. By 2100, 50% of tropical forest area will be at the forest edge, causing additional carbon emissions of up to 500 million MT carbon per year. Thus, efforts to limit fragmentation in the world's tropical forests are important for climate change mitigation.

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Guillaume Patoine
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Drivers and trends of global soil microbial carbon over two decades

Soil microorganisms play a central role in sustaining soil functions and services, including carbon and nutrient cycling. Better spatial-temporal models of soil microbial biomass are needed to evaluate the long-term effects of climate and land-cover change on soil microorganisms, as well as the sensitivity of specific regions.

I will present a recent work in which we assessed temporal trends in soil microbial biomass carbon and identified the main drivers of change globally and regionally. We used a global soil microbial biomass carbon dataset compiled from the literature, random forest modelling, and global environmental layers to predict spatial-temporal dynamics of soil microbial biomass carbon from 1992 to 2013. We assessed the environmental coverage of our predictions and identified the main areas of vulnerability and regions where microbial stocks was most affected by global changes.

We found a significant decrease in soil microbial biomass carbon stocks globally during that period. Especially northern areas were found to be vulnerable, with high soil microbial carbon stocks and strong negative effects from climate warming. In contrast, land cover change was a weaker global driver of change in soil microbial biomass carbon, but had, in some cases, important regional effects.

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Andrea Cortegoso Galmán

Martin Luther University Halle-Wittenberg

DArwin´s Naturalization Conundrum rEvisited (DANCE)

Understanding the ecological mechanisms enabling alien species to succeed in novel environments is a central goal in ecology. Phylogenetic relatedness between alien and native species has been proposed as one of the main explanatory factors. Darwin's Naturalization Conundrum (DNC) states that alien taxa more closely related to natives in the new environment are either (i) more likely to succeed because shared adaptations help them to overcome the environmental filters, (ii) less likely to establish based on higher biotic competition. There are inconsistencies between studies exploring these hypotheses that could be explain by several factors: i) The role of functional diversity remains unexplored. Taxonomic relatedness is not always a good proxy of functional similarity, biotic selection may result in phytochemical diversification among closely related taxa. To account for this source of variability we would analyse the metabolomic composition of alien and native plants in association with the EcoMetEoR platform. ii) Environmental filtering and biotic competition are not always mutually exclusive forces, they can act as complementary forces depending on the environment. Elevational gradients are perfect tools to evaluate the relative role of biotic competition and environmental filtering. With DANCE project we investigate how phylogenetic and functional relatedness affects invasivenes success along elevational gradietns. To conduct our study, we take advantage of a global Standardized vegetation survey stablished by the Mountain Invasion Research Network (MIREN, www.mountaininvasions.org) to study plant communities with native and alien species across 18 different mountain regions distributed worldwide and following a standardized data collection protocol.

Sonja Knapp

Helmholtz Centre for Environmental Research – UFZ
Technische Universität Berlin, Department of Ecology, Ecosystem Science/ Plant Ecology

What drives the establishment of plant species within urban environments? Interactions of functional traits with native status and ecosystem novelty

A key challenge in urban biodiversity conservation is to understand the drivers that govern species population establishment in different urban ecosystems. Still, many urban biodiversity

studies lack a multi-habitat or temporal perspective. We ask whether and how the ability of species to establish self-sustaining populations within a certain time span is driven by interactions of species functional traits, native status, and the type of ecosystem species occur in, with the latter distinguished by their degree of ecosystem novelty. To answer this, we use a dataset of 1178 vascular plant species occurring in Berlin, Germany that originally had been compiled to substantiate the Berlin Red List of endangered species. The dataset classifies species into casual and established species based on ≥25 years of expert observation. Whether a species is established or casual is distinguished among four broad types of ecosystems: natural remnant, hybrid, novel immature and novel mature. Further, we classify species into those native to Berlin and non-native species, and link species to selected traits and indicator values. By applying ordinal regression within a Bayesian framework, we show that the traits that drive establishment success differ across ecosystems. While overall, establishment success is highest in natural remnants, low canopy height, annual life span, and late end of flowering promote establishment in novel immature ecosystems. In hybrid ecosystems, low canopy height and reproduction by seeds are beneficial, with the latter promoting establishment in novel mature ecosystems, too. Traits were less important in discriminating establishment success in native vs. non-native species. Identifying drivers of establishment success can help to sharpen conservation measures.

Authors: Sonja **Knapp**, Matthias **Grenié**, Emilio **Berti**, Juan **Carvajal–Quintero**, Gala Mona Louise **Dädlow**, Alban **Sagouis**

Open Sessions

Biodiversity and Ecosystem Functioning

Chairs: Malte Jochum, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*
Sylvia Haider, *Martin Luther University Halle-Wittenberg*

This research area explores the context dependency of biodiversity-ecosystem functioning (BEF) relationships across spatial and temporal scales.

Verónika Ceballos Núñez

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Plant traits and Biodiversity Ecosystem Functioning

Multiple anthropogenic-derived activities have led to the dramatic loss of species around the world. This loss can alter community assembly, which in turn influences ecosystem functioning. One way that this manifests is through the Function-Dominance correlation, which is the relationship between species' biomass in monoculture and competitive strength in mixture. Ecosystems with a positive function-dominance correlation tend to be dominated by species that have high functioning, whereas ecosystems with a negative correlation tend to be dominated by species with low functioning.
Here we asked: What traits drive both dominance and function? We predicted that trait importance may vary from monoculture to mixture depending on the direction of the function-dominance correlation.

We expanded on an in-silico diversity experiment performed previously in six models. We compared biomass in monoculture and 32-species mixtures. The importance of the plant traits was determined using random forest models from the R package 'Party'. We observed that size related traits are the most important in four of the six models, but tradeoffs with other traits (particularly those associated with resource competition and use efficiency) can shift their effect on biomass accumulation.

For the models with positive Function-Dominance correlation the order of trait importance did not change between conditions; i.e., the traits that determine biomass in monoculture are also the same for mixtures. However, the secondary traits increased their importance in the isolation phase (when there was no seed inflow from the metacommunity). For the models with weak or negative Function-Dominance correlation we found a shift in the trait importance from monoculture to mixture.

Authors: Verónika **Ceballos Núñez**; Kathryn **Barry**, Nadja **Rüger**, Christian **Wirth**, Adam **Clark**, Björn **Reineking**, Isabelle **Maréchaux**, Jeremy **Lichstein**, Lindsay **Turnbull**, Michael **Crawford**.

Malte Jochum

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

EcoStressWeb - Investigating joint impacts of climate and biodiversity change on multitrophic interactions and ecosystem functioning

Climate and biodiversity are changing across the globe and experiments are a powerful tool to assess the consequences of these changes for multitrophic biodiversity, interactions, and ecosystem processes. In 2021, we ran EcoStressWeb, an iDiv Ecotron experiment to assess the joint impacts of soil moisture and invertebrate predation on multitrophic above-belowground communities and ecosystem functioning in a temperate forest ecosystem. We equipped 48 Ecotron subunits with soil, leaf litter, treelings, microbial communities, and two collembola species and then established three soil-moisture levels and four predation levels (spider, predatory mite, both, no predators), full-factorially crossing these two treatments. During the experiment, we continuously measured belowground organic matter decomposition and soil mesofauna activity, quantified aboveground leaf-litter decomposition, and assessed physiological parameters of the beech and oak trees. After ~4 months, we harvested the experiment and sampled invertebrate and microbial communities from the litter and several soil layers. We have measured a variety of litter- and soil related abiotic and biotic properties. The invertebrate data will be used to assess how multitrophic interactions, feeding preferences, and energy flux change with the treatments. Here, I will present the first results from this collaborative research initiative and outline how we will further synthesize across these different aspects of above-belowground multitrophic biodiversity and ecosystem functioning.

Authors: Malte **Jochum***, Merlin **Helle**, Ines **Laude**, Benjamin **Bischoff**, Helge **Bruelheide**, Julia **Tiede**, Nico **Eisenhauer**.

Nico Eisenhauer

Leipzig University
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Biotic Interactions as Mediators of Context-Dependent Biodiversity-Ecosystem Functioning Relationships

Biodiversity drives the maintenance and stability of ecosystem functioning as well as many of nature's benefits to people, yet people cause substantial biodiversity change. Despite broad consensus about a positive relationship between biodiversity and ecosystem functioning (BEF), the underlying mechanisms and their context dependencies are not well understood. This project aims at filling this knowledge gap by providing a novel conceptual framework for integrating biotic interactions across guilds of organisms, i.e. plants and mycorrhizal fungi, to explain the ecosystem consequences of biodiversity change. The overarching hypothesis is that EF increases when more tree species associate with functionally dissimilar mycorrhizal fungi. Taking a whole-ecosystem perspective, I propose to explore the role of tree-mycorrhiza interactions in driving BEF across environmental contexts, and how this relates to nutrient dynamics. Given the significant role that mycorrhizae play in soil nutrient and water uptake, BEF relationships will be investigated under normal and drought conditions. Resulting

ecosystem consequences will be explored by studying main energy channels and ecosystem multifunctionality using food web energy fluxes, and by assessing carbon storage. Synthesizing drivers of biotic interactions will allow to understand context-dependent BEF relationships. This interdisciplinary and integrative project spans the whole gradient from local-scale process assessments to global relationships by building on unique experimental infrastructures like the MyDiv Experiment, iDiv Ecotron, and the global network TreeDivNet, to link ecological mechanisms to reforestation initiatives.

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Wentao Yu

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Friedrich Schiller University Jena

The effect of pairwise tree-tree interactions on forest ecosystem functioning

The combined effect of competitive and facilitative interactions at the neighborhood scale modifies intrinsic growth of individual tree, thereby giving rise to the positive net biodiversity effects at the neighborhood scale as well as contributing to the biodiversity effects at community scale. Here, using a decade of annual growth data from a large-scale biodiversity experiment, we employ a Bayesian approach to partition growth of individual trees into intrinsic growth rate, the sum of pairwise tree-tree interactions, and the plot level diversity effect. We then (1) assess the contribution of intra- and inter-specific interactions to total tree growth, (2) test whether neighborhood diversity effect is the primary driver of overall diversity effect, (3) identify the size-related determinant for tree-tree interactions. Further, we (4) test whether the intrinsic growth rate scales with a three-quarter exponent predicted by metabolic theory. Taken together, our findings improve our understanding of how local interactions influence individual tree growth, allowing for a better prediction of forest primary productivity that is central for carbon storage in the face of climate change.

Authors: Wentao **Yu**, Georg **Albert**, Benjamin **Rosenbaum**, Helge **Bruelheide**, John **Connolly**, Werner **Härdtle**, Xiaojuan **Liu**, Keping **Ma**, Goddert **von Oheimb**, Florian **Schnabe**l, Ulrich **Brose***.

Beate Michalzik

Friedrich Schiller University Jena

Triple-funneling of trees? Intra-canopy preferential flow of water and elements induced by tree canopiesg

Trees affect the direction and distribution of crucial components of the hydrological cycle, which were mostly described by measurements on the quantity of precipitation, stemflow and throughfall (TF) collected underneath the canopy. However, due to poor accessibility of tree canopies, our knowledge on hydrological processes within canopies is limited. We propose that canopy structure shapes the spatial distribution of incoming rainfall (RF)

within the canopy as well as the intra-canopy TF composition. The Leipzig Canopy Crane facility allows to (i) determine water fluxes from above the canopies (RF) and with TF at top, mid and bottom position within the canopy of three tree species – Quercus robur, Fraxinus excelsior, and Tilia cordata, and (ii) to determine the transport of dissolved and particulate organic carbon and nitrogen with TF. In total, 81 TF collectors were set up every month for a two-weeks-period from March to October 2021. We found amplified water fluxes in TF collectors at top and mid canopy positions compared to incoming RF fluxes, while TF volumes at the bottom decreased. Dimensions of change appear related to RF amount and tree species. Moreover, stability plot analysis indicated that spatial "hot spots" of water fluxes within canopies were temporally persistent. Our results raise the question whether the "double-funneling" concept (Johnson & Lehmann, 2006) needs to be extended to a "triple-funneling" effect occurring in upper to mid canopy positions especially of ash and oak. Canopy spots with higher water and matter accumulation will alter the chemical, biological, and hydrological heterogeneity in canopy habitat structures below, with strong implications for canopy-associated microbial and epiphytic communities and ecosystem functions.

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Thomas Hornick

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

Dinner is served! - Exploring the nutritional value of diverse pollen for soil foodwebs

Pollen of especially wind-distributed species represents a temporarily limited nutrient pulse mainly during spring which may be advantageous for detrivores to be included in their diet. Pollen is produced in large quantities, is rich in nutrients, and small enough to be utilized by small organisms (e.g., microorganisms, Collembola, Insecta). However, the contributions of pollen and pollen diversity to food web functioning is largely unknown. In ´iNutriPol´ (Flexpool Support Fund) we chemically analysed and quantified the nutritional value of pollen from different tree species. Standardized lab experiments, oriented on naturally occurring pollen deposition rates, revealed strong physiological responses of microorganisms to pollen amendments in soil microcosms that was dependent on species-specific pollen chemistry. Further feeding experiments with Collembola, Earthworms and Woodlice were performed to assess accessibility and digestibility of pollen for small soil organisms. Our research will help to assess, model and predict the role of nutrient transport via pollen dispersal for soil foodwebs and thus the temporally and spatially-dependent functioning of complex ecosystems. Climate change affects pollen diversity and abundance, and our studies suggest that this may also contribute to changes underground.

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Biodiversity Change

Chairs: Roel van Klink, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*

Kimberly Thompson, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*

This research area aims at a rigorous understanding of how biodiversity is changing by combining synthesis, theory and detection. iDiv researchers study how to monitor biodiversity, assess changes in multiple dimensions of biodiversity across time and space, and uncover the mechanistic properties that underpin those changes.

Stephanie Jurburg
Helmholtz Centre for Environmental Research – UFZ

Disturbance and recovery: a synthesis of microbial community reassembly following disturbance across realms

Disturbances alter the diversity and composition of microbial communities, but whether microbiomes from different environments exhibit similar degrees of resistance or rates of recovery has not been evaluated. Here, we synthesized 86 time series of disturbed mammalian, aquatic, and soil microbiomes to examine how the recovery of microbial richness and community composition differed after disturbance. We found no general patterns in compositional variance (i.e., dispersion) in any microbiomes over time. Only mammalian microbiomes consistently exhibited decreases in richness following disturbance. Importantly, they tended to recover this richness, but not their composition, over time. In contrast, aquatic microbiomes tended to diverge from their pre-disturbance composition following disturbance. By synthesizing microbiome responses across environments, our study aids in the reconciliation of disparate microbial community assembly frameworks, and highlights the role of the environment in microbial community reassembly following disturbance.

Roel van Klink
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg

Global changes in insect biodiversity?

Insect declines remain a hot topic in the scientific literature, but, gradually, consensus is emerging that insect biomass is, on average, declining in the terrestrial realm, but mostly increasing in the freshwater realm. What remains unclear, however, is whether these changes

in biomass and abundance also apply to changes in species numbers, community structure, and community composition. We investigated global changes in insect assemblages using our global database of 176 studies of long-term insect-community monitoring. We found strong differences between the realms, where the terrestrial insects showed no change in species numbers, but strong declines in the most abundant species. Freshwater insects, by contrast, showed increases in species richness, as well as in evenness, and this could be explained by increases in the number of rare species, whereas the most dominant ones declined. In both realms there was a strong change in species composition. The loss of the most abundant species from assemblages has likely already led to a broad-scale restructuring of ecosystems, given their importance for ecosystem functioning, -services and for higher trophic levels.

Authors: Roel **van Klink**, Diana **Bowler**, Konstantin **Gongalsky**, Minghua **Shen**, Scott **Swengel**, Jonathan **Chase**

Lina Lüttgert
Martin Luther University Halle-Wittenberg

Repeated habitat mapping data reveal gains and losses of plant species

Detecting species trends across different habitat types and larger regions is required to generate a general and reliable foundation for conservation planning. While direct monitoring data covering a large spatial and temporal extent are mostly lacking, other biodiversity data sources should be considered to detect trends. We analyzed both habitat type and plant species trends over several decades (1979-2017), using repeated habitat survey data from the habitat mapping program of the city and federal state of Hamburg. Next to transitions between habitat types, we looked for differences between winner and loser species, considering also their habitat type preference, red list, and non-native status. We found declines in habitat area of semi-natural (semi-)dry grasslands and semi-ruderal vegetation and increases in habitat area of species-poor grasslands, pioneer forests, and anthropogenic habitats. More species showed positive than negative trends over time, with winners including many forest and scrub as well as non-native species, while losers were represented mostly by endangered and ruderal species.

Authors: Lina **Lüttgert**, Samuel **Heisterkamp**, Florian **Jansen**, Reinhard **Klenke**, Kerstin-Angelika **Kreft**, Gunnar **Seidler**, Helge **Bruelheide**.

Shane Blowes
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Martin Luther University Halle-Wittenberg

Integrating biodiversity change across scales reveals the prevalence of homogenisation

Earth's biodiversity is changing rapidly. Evidence for widespread reordering of species in space and time continues to accrue. Biotic homogenisation, the process of increasing similarity in species composition among sites has been proposed to be one of the most important

outcomes of the Anthropocene. Yet, a global assessment of the prevalence of homogenisation is lacking. Here, we develop a scale-explicit conceptual framework that combines smaller scale changes with those occurring at larger scales, and use it to quantify homogenisation across 254 metacommunities worldwide. We find a slight trend towards biotic homogenisation, whereby species composition among sites became more similar through time. However, almost half of the metacommunities experienced differentiation, where beta-diversity increased through time, and species richness changes were greater at larger compared to smaller scales. Among cases of biotic homogenisation, only 23% were of the type often invoked that suggest biodiversity loss increases with increasing spatial scale. Instead, the most prevalent type of homogenisation was due to increased numbers of widespread species that increase both local and regional richness (30% of cases). We find considerable variation in the direction and magnitude of scale-explicit biodiversity change, and we identified a number of sites where both local and regional diversity have substantially declined over time. Our results show that simultaneously considering biodiversity change at multiple scales provides the regional context for local scale changes. Integrating biodiversity change across scales can reveal the implications of homogenisation and differentiation, and highlight how potential local scale policy interventions combine within regions.

Authors: Shane **Blowes;** Maria **Dornelas**; Brian **McGill**; Viviana **Brambilla**; Cher **Chow**; Thore **Engel**; Ada Fontrodona **Eslava**; Nicholas **Gotelli**; Anne **Magurran**; Ines **Martins**; Daniel **McGlinn**; Faye **Moyes**; Hideyasu **Shimadzu**; Alban **Sagouis**; Roel **van Klink**; Wubing **Xu**; Jon **Chase**.

Jördis Terlau

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Friedrich Schiller University Jena

A trait-based approach to thermal niches: linking movement and metabolism to predict thermal tolerances of terrestrial invertebrates

The survival of animals under global warming strongly depends on their individual thermal niches, which result from the balance between energy loss and gain. Active movement is an important component of this energetic balance as it affects not only energy gain via food intake but also energy loss via activity metabolism.
Here, we develop a novel trait-based approach for how thermal niches arise from temperature-dependent movement. Therefore, we used image-based tracking to quantify the unimodal responses of the movement speed of carabid beetles to temperature. We used these empirical data to parameterize a mathematical model based on metabolic and predator-prey theory for net energy gain to derive a general mechanistic concept of thermal niches. This trait-based approach allows a relatively rapid and cost-effective assessment of climate change vulnerability for a wide range of animal taxa on broad geographic scales.

Authors: Jördis F. **Terlau**, Ana Carolina **Antunes**, Thomas **Boy**, Ulrich **Brose**, Benoit **Gauzens**, Samraat **Pawar**, Malin **Pinsky**, Myriam R. **Hirt**

Chris Barratt

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Life on the edge: assessing intraspecific vulnerability to global change by integrating environmental, ecological and molecular data

Global change is affecting biodiversity in unprecedented ways, with environmental changes compounded by anthropogenic activities to introduce new selection pressures. Species responses to these pressures depend not only on the magnitude of change occurring, but also on the adaptive capacity of their individuals and populations. To date, most climate change vulnerability assessments have focused on the species level, lacking insights into population vulnerability, though this is beginning to change with the growing availability of large population level datasets. Assessing the adaptive capacity of populations and quantifying their vulnerability under future global change has therefore been a neglected area of biodiversity research. These insights are essential for conservation as they provide an early warning system to detect the initial signs of population and species declines. The 'Life on the edge' project integrates environmental (climate and landscape connectivity), molecular (neutral and adaptive diversity) and ecological (species distributions and traits) data, in a novel climate change vulnerability assessment framework applicable to multiple species and geographic regions. The project leverages a large number of recently published population level datasets, addressing an important knowledge gap in biodiversity and global change for multiple threatened and non-threatened species, linking with major research themes within iDiv and general conservation goals aimed at maintaining or enhancing genetic diversity.

Authors: Christopher D. **Barratt**, iDiv, University of Leipzig; Orly **Razgour**, University of Exeter; Brenna **Forester**, US Fish and Wildlife Service; Renske E. **Onstein**, iDiv, University of Leipzig; Hjalmar **Kuehl**, iDiv, MPI-EVA; Sebastian **Steinfartz**, University of Leipzig; Malin **Pinsky**, Rutgers University.

Complexity

Chairs: Renske Onstein, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*

Saneesh Cherapurath Soman, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Helmholtz Centre for Environmental Research – UFZ*

Demetra Rakosy*, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Helmholtz Centre for Environmental Research – UFZ*

This research area aims at understanding how the complex structure of natural ecosystems begets their high biodiversity.

Ulrich Brose
Friedrich Schiller University Jena
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Biotic filtering by species' interactions constrains food-web variability across spatial and abiotic gradients

Despite intensive research on species dissimilarity patterns across communities (i.e. beta-diversity), we still know little about their implications for variation in food-web structures. Our analyses of 50 lake and 48 forest soil communities show that, while species dissimilarity depends on environmental and spatial gradients, these effects are only weakly propagated to the networks. Moreover, our results show that species and food-web dissimilarities are consistently correlated, but that much of the variation in food-web structure across spatial, environmental, and species gradients remains unexplained. Novel food-web assembly models demonstrate the importance of biotic filtering during community assembly by (1) the availability of resources, and (2) limiting similarity in species' interactions to avoid strong niche overlap and thus competitive exclusion. This reveals a strong signature of biotic filtering processes during local community assembly, which constrains the variability in structural food-web patterns across local communities despite substantial turnover in species composition.

Adriana Alzate

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Understanding the relationship between dispersal and range size

Understanding what drives the vast variability in species range sizes remains an outstanding question in ecology. The theoretical expectation of a positive dispersal-range size relationship has received mixed empirical support, despite dispersal being one of the most prominent hypothesized predictors. Here, we synthesized results from 86 studies examining the effect of dispersal on range size for plants and animals in marine, terrestrial and freshwater realms. Overall, we found that dispersal had a positive effect on range size, but its effect was highly dependent on the clade and dispersal-related traits studied. Despite potential differences in habitat connectivity, we did not find an effect of realms. Moreover, the overall strength of the dispersal-range size relationship is influenced by how range size was measured, whether phylogenetic relationships were considered, and the taxonomic breadth of the study clade. Our synthesis emphasizes the importance of considering different aspects of the dispersal process -departure, transfer, settlement- and the traits associated with them. Furthermore, ecological niche, environmental tolerance and evolutionary components, such as time for range expansion and past geological-environmental dynamics, can additionally influence current dispersal-range size patterns. We therefore call for a more integrative view of the dispersal process and its causal relationship with range size.

Alexandra Werner

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Friedrich Schiller University Jena

Multiple specialised fisheries in food web networks: how do they influence each other?

Effective ecosystem-based management of marine resources requires an improved understanding of how disturbances via fishing spread through a food web. As many fisheries exist in parallel, administrators are moving towards developing multi-species management plans, yet theoretical investigations from an ecological view are rare. Building upon previous results, I propose a bioenergetic food web model coupled with multi-species fisheries to explicitly include humans and their feedback effects on biodiversity and ecosystem functioning in marine fish communities. Testing combinations of different trophic level harvesting would allow for a greater understanding of complex feedback loops from trophic interactions driven by humans and the economy, leading to improved ecosystem-based management plans.

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Friederike Wölke

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig (Leipzig University)

Neutral and adaptive processes in the distribution and evolution of angiosperm fruit sizes

Large fruits may evolve as adaptations to facilitate long-distance dispersal by large-bodied frugivores or survival in shady habitats. However, fruit size can also evolve stochastically along the phylogeny, independent from external selective pressures. Here, we assembled fruit size data for >10000 angiosperm species to test if the global distribution and evolution of fruit size is associated with frugivore body sizes and closed forests, rather than neutral trait evolution. First, we use global distribution data to show that the distribution of large angiosperm fruits is mainly explained by climatic variables and forest structure, while body sizes of extant mammalian frugivores only explain the distribution of large fruits in certain lineages, such as tropical palms (Arecaceae). Second, we use trait and phylogenetic data for >2000 palm species to disentangle neutral and adaptive processes during fruit size evolution, using ancestral reconstructions and evolutionary model testing of simulated and empirical fruit sizes. Interestingly, our models indicate important roles for both adaptive and neutral processes in palm fruit size evolution. Specifically, we show that mainland Africa, where the largest megafauna has persisted, as well as open habitats have acted as selective regimes for large palm fruits. However, we also show that palm fruit size initially increased prior to colonization of Africa or dry habitats, suggesting that fruit size may have increased by chance, but was a prerequisite for the subsequent transition, adaptation, and radiation of palms in Africa and dry habitats. Our study emphasizes the interaction between neutral and adaptive processes during trait evolution, and how these may explain the current distribution of traits across ecological communities.

Authors: Friederike **Wölke**, iDiv; Renske **Onstein**, iDiv, Leipzig University; Andressa **Cabral**, iDiv.

Hendrik Müller

Martin Luther University Halle-Wittenberg

Reproductive diversity and the evolution of terrestrialisation in amphibians

Reproduction in amphibians commonly involves an aquatic larval stage that undergoes a dramatic transformation during its metamorphosis into the adult-like, usually terrestrial juvenile. This biphasic life cycle, with its ecological separate larval and adult stages, might have played a role especially in the diversification of frogs. However, amphibians show a great diversity of reproductive strategies that range from completely aquatic to complete terrestrial forms of reproduction. Several of these strategies have evolved several times independently within each of the three major clades of modern amphibians. A number of different factors have been proposed to drive the evolution of terrestrial reproductive strategies in amphibians, including predation, avoidance of parasites, montane slopes, and forest. While not without exceptions, montane slopes and forest environments seem to be the best predictor for the presence of terrestrial strategies in amphibians, but few empirical studies have investigated other potential drivers of terrestrialisation. Apart from the evolutionary aspects, both biphasic and terrestrial reproduction have broad and so far often only incompletely understood

implications for amphibian conservation, especially under current habitat and climate change scenarios, which I will highlight in my talk.

Author: Hendrik **Müller**, Central Natural Science Collections, Martin Luther University Halle-Wittenberg.

Samuel Fischer

Osnabrück University
Helmholtz Centre for Environmental Research – UFZ

Connecting individual-based models with empirical data to study the emergence of species-rich forests

Disentangling the role of individual traits in the emergence of diverse forest ecosystems is challenging due to the high complexity of the processes and interactions at play and the large spatial and temporal time scales that need to be considered. Here, individual-based models (IBMs) can help, as they allow researchers to account for the high mechanistic complexity of the systems as well as individual variability and interactions. However, fitting these models to empirical data can be difficult, as IBMs are often stochastic, incorporate a large number of parameters, and may be very sensitive to parameter changes. In this talk, we present a novel approach to fit stochastic IBMs to empirical data and showcase the method by fitting the forest model Formind to inventory data from a species-rich temperate forest in Changbaishan, China. We then explore the wealth of opportunities the model provides us to study the effect of individual traits on forest dynamics.

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Molecular Biodiversity and Adaptation

Chairs: Luis Daniel Prada Salcedo, *Helmholtz Centre for Environmental Research – UFZ*
Stefanie Döll, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Friedrich Schiller University Jena*

This research area aims to identify molecular and chemical mechanisms underlying organismal diversity, interaction networks and (co-)evolutionary processes that lead to local adaptation, population differentiation and speciation.

Jana Ebersbach
Leipzig University

Macroevolutionary patterns of chemodiversity across the seed plant tree of life

Besides awe inspiring levels of species diversity, plants also exhibit impressive levels of metabolomic diversity. The ability to produce such compounds, which are crucial for plant growth and plant-environment interactions, has direct implications for the short-term survival of a given plant species as well as for its long-term evolutionary success. Yet, we know relatively little about the link between the phylogenetic and chemical diversity of plants, and plant chemodiversity has not been systematically assessed across the tree of life. Here, we combine global spatial, phylogenetic, ecological and phytochemical data in order to explore large-scale spatial and evolutionary patterns of seed plants and their metabolomes. We accomplish this by integrating several well-curated datasets and databases, followed by extensive data cleaning and taxonomic harmonisation. The resulting data will provide new insights into plant evolutionary and ecological processes, and holds promise for future drug discovery.

Authors: Jana **Ebersbach**, University Leipzig; Jan **Schnitzler**, iDiv; Gælle **Bocksberger**, University of California Santa Cruz; Maria **Sorokina**, Friedrich-Schiller-University Jena; Nicole M. **van Dam**, Friedrich-Schiller-University Jena, iDiv; Christian **Wirth**, University Leipzig, iDiv; Aletta **Bonn**, Friedrich-Schiller-University Jena, iDiv, Helmholtz Centre for Environmental Research; Alexandra N. **Muellner-Riehl**, University Leipzig, iDiv.

Kaitlyn Blatt-Janmaat
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leibniz Institute of Plant Biochemistry (IPB)
University of New Brunswick (UNB)

An eco-metabolomic investigation of Radula complanata populations from Germany, Sweden, and Canada

Radula complanata (phylum Marchantiaophyta, order Jungermanniales) is an epiphytic leafy liverwort that is largely found on the bark of trees in temperate zones in the northern hemisphere. Liverworts as a whole produce unique specialized compounds not found in vascular plants, and R. complanata is no exception. Due to the large distribution of these plants some variation in metabolism is expected in isolated populations, however the ecology and evolution of R. complanata has not been explored at the molecular scale. To address this, an untargeted eco-metabolomics approach using LC/MS-MS was utilized to examine R. complanata specimens collected from three different populations found in Canada, Sweden, and Germany. In addition, targeted LC/MS-MS analysis of six prenylated bibenzyls, which belong to the most characteristic compound class in the genus Radula, was performed to identify variations within this compound class. The location and the host tree explained most of the observed variation of the metabolite profiles and metabolite compounds were also related to other evolutionary and ecological factors impacting each population. From the targeted metabolomic work, 3,5-dihydroxy-6-carbomethoxy-2-(3-methyl-2-butenyl)bibenzyl was identified as a biomarker that was only found in the Canadian samples. Taken together, eco-metabolomics analyses provide insight into the evolution of biochemistry within these populations.

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Jennifer Gabriel
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German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

The effect of intraspecific chemical diversity on plant performance and plant-herbivore-microbe interactions in White clover

Variation in plant functional traits drives processes that modify biotic interactions. This underscores the importance of intraspecific functional diversity on community dynamics. The main knowledge gap on the ecological effects of plant genetic diversity is to which extent it can modulate plant interactions and the underlying molecular mechanisms. Our study aimed to examine the impact of plant intraspecific variation in chemical traits on plant-herbivore-microbe interactions. In particular, we wanted to quantify how above- and belowground interactions are altered by the level of intraspecific diversity. Four white clover genotypes were selected according to the production of metabolites involved in herbivore defense and belowground symbioses: The production of (1) hydrogen cyanide (HCN) by hydrolysis of cyanogenic glycosides following tissue damage, and (2) flavonoids. Genotypes that either produce HCN or not and with high or low leaf flavonoid content served to establish population types that were genetically diverse or diverse on the trait level. Genotypes were grown in genotypic monocultures, trait monocultures, and trait mixtures. In two separate experiments,

each population was exposed to (1) an aboveground and/or a belowground feeding insect herbivore and (2) two root symbionts, rhizobia and arbuscular mycorrhiza. Population type affected aboveground biomass production. Populations that were diverse in their trait composition had higher total biomass on plot level in the aboveground herbivory treatment. The chemical diversity of the populations affected biomass production when plots were inoculated with rhizobium only. Our results demonstrate that intraspecific trait diversity can alter the response in plant growth according to location and type of interaction.

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Alexandra Weyrich

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leibniz Institute for Zoo and Wildlife Research

Wildlife Epigenetic

In natural environments, wild life species cope with changing environmental factors. Within a lifespan, one genotype can bring about several phenotypes. As genetics is very static and changes are rare, epigenetic mechanisms are strong candidates of molecular regulation for these rapid changes. Epigenetic modifications such as DNA methylation can change flexibly, regulate gene expression, and as such increase adaptability of (wild) mammalian species. DNA methylation is the most stable epigenetic mechanism – methylation patterns are set early in life and most remain stable throughout an individual's lifespan and across generations. Within the current presentation I will give an insight into our current and previous wildlife epigenetic studies in response to environmental changes, such as an increase in temperature, a change in diet in wild guinea pigs, and the social environment of spotted hyenas and cheetahs.

Kristian Peters

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Martin Luther University Halle-Wittenberg
Leibniz Institute of Plant Biochemistry (IPB)iESTIMATE chemical traits in plants

iESTIMATE chemical traits in plants

The iESTIMATE workflow is a general computational framework for Eco-Metabolomics data that allows to elucidate and describe molecular traits in plants. This talk will highlight the capabilities of the framework on an exemplary reference dataset containing four Riccia species R. bifurca, R. glauca, R. sorocarpa and R. warnstorfii that were collected from the same arable stubble field in Baden-Württemberg/Germany in 2021. Using methanol extracts and untargeted liquid chromatography high-resolution mass-spectrometry (UPLC/ESI-QTOF-MS) with data-dependent acquisition (DDA-MS), 130 unique compounds were identified as biomarkers to potentially discriminate the species using chromatographic separation.

Compound classes such as imidazoles, benzenesulfonamides, (neo)lignans, and organoheterocyclic and -phosphorous compounds, and molecular descriptors such as stereochemistry, number pf phosphoric acid groups, quaternary nitrogens and sulfonamide motifs were identified to further characterize the species at a meta-level.

Taken together, the iESTIMATE workflow allows to estimate molecular traits in plants at three levels: biochemical marker compounds, compound classes and molecular descriptors. In this talk, the power of the iESTIMATE pipeline is presented to elucidate and describe molecular traits in plants. By linking molecular traits to plant phenotypes, iESTIMATE has potentially also the ability to describe molecular traits functionally.

Authors: Peters, Kristian; **Neumann**, Steffen; **van Dam**, Nicole; **Bruelheide**, Helge

Laura Méndez Cuéllar
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Genetic signatures of megafauna extinctions on palms with big fruits in Madagascar

Seed dispersal is a key process in the generation and maintenance of genetic diversity and genetic structure in fruiting plant populations in the tropics. In the last 2000 years, Madagascar has suffered biased extinctions of large-bodied animals that were potentially providing long-distance dispersal events of fleshy-fruited plants. Therefore, their extinctions might have caused a dispersal limitation for bigger fruited plants, thereby lowering their genetic diversity and increasing genetic structure between populations. Additionally, humans might have taken over as "megafaunal" dispersers of some of these big-fruited plants after the extinction of the megafauna. Here, we focus on four Malagasy palm (Arecaceae) species with different fruit sizes (167 individuals from 25 populations) to investigate the role of past (extinct) and present frugivores, human-mediated dispersal and the environment in shaping their genetic diversity and genetic structure. For this, we used double-digest restriction-site-associated DNA (ddRAD) libraries to identify single nucleotide polymorphisms (SNPs) and linear mixed effect models to investigate the biotic and abiotic factors that were most important in shaping the genetic structure and diversity of these palm species. Our results indicate high genetic diversity and low genetic structure in larger-fruited palm populations, and genetic structure decreases when fewer megafaunal animals were shared between these populations in the past. Furthermore, high genetic diversity was primarily explained by abiotic factors (e.g., climate) and availability of roads, suggesting a potentially important role for human-mediated dispersal of these species and their genetic data.

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Biodiversity and Society

Chairs: Miguel Fernandez, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*
Andrea Perino, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig*

This research area aims at a systemic understanding of how society affects and benefits from biodiversity and to develop science to support target setting for policy and societal change toward a better future.

Victor Cazalis

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Using models to prioritise reassessment of Data Deficient species

The IUCN Red List of Threatened Species is a central tool in biodiversity conservation; it is therefore crucial that the information it includes is accurate and complete. Unfortunately, 14% of assessments are made with insufficient data to assign a threat category to species, which are then classified as "Data Deficient" species, bringing high uncertainty to the Red List. Statistical approaches can be very useful to identify which Data Deficient species could probably be reassessed in a data sufficient category (e.g., because new data has been gathered since their last assessment), in order to help expert prioritising reassessments. I will present a model that estimates the probability of being Data Deficient for >60,000 species (all vertebrates and odonata) depending on the amount of existing data, ecological traits, human pressure in species range, or taxonomy. We find for instance that the number of GBIF data available, or the GDP of countries of occurrence, are strong correlates of the species probability to be Data Deficient. This model will enable to predict which Data Deficient species could probably be reclassified in a data sufficient category nowadays. We expect this model, that will be run before each Red List assessor workshops, to help assessors to prioritise reassessments of relevant species.

Authors: Victor **Cazalis**, Luca **Santini**, Resit **Akcakaya**, Ana **Benitez-Lopez**, Monika **Böhm**, Stuart **Butchart**, Pedro **Cardoso**, Viola **Clausnitzer**, Manuela **Gonzalez-Suarez**, Michael **Hoffmann**, Martin **Jung**, Pablo **Lucas**, Giordano **Mancini**, Carsten **Meyer**, Michela **Pacifici**, Guillaume **Patoine**, Alexander **Zizka**, Moreno **Di Marco**

Kevin Rozario

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Helmholtz Centre for Environmental Research – UFZ
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The more the merrier?! The role of forest biodiversity on mental health and well-being. An experimental, multicentric field study.

A growing body of evidence highlights the potential of forests for fostering human mental health and well-being, yet research on the contribution of specific forest properties regarding mental health promotion is scarce. In recent years, more and more studies suggest that biodiversity, by its intriguing stimuli, positively influences mental health and well-being. Whether this also applies for forest biodiversity, however, is less well investigated. By conducting an experimental, multicentric field study in three peri-urban forests in Europe, we aimed to shed light on the particular role of forest biodiversity on mental health and well-being by emphasizing stress mitigation and attention restoration as potential mediating pathways. In a 4x2 between-within subject design, we randomly assigned 223 participants to 20-minute stays in either a low, medium or high forest biodiversity condition or an urban control. Forest patches were selected according to visual tree species richness as biodiversity proxy (monoculture vs. 2-species vs. 4-5 species). We found that actual forest biodiversity indirectly influences mental health and well-being via perceived biodiversity and the restoring capacities pathways of attention restoration and stress recovery. However, results for attention restoration were less univocal. Whereas increases in perceived forest biodiversity were associated with higher ratings of perceived restorativeness that in turn aligned with better mental health and well-being, no significant effects were found for focused attention. Besides its importance for resilient forests in the face of climate change, forest biodiversity further contributes to the mental health promotion which seeks for transfer into forest management practices.

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Veronik Liebelt

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-
Leipzig Leipzig University

Hedonic analysis of biodiverse urban green: a survey-based cased study of 22 German cities

Natural amenities contribute to human well-being by providing various benefits that are particularly valuable for urban citizens those city-life often associated with hecticness and stress. Urban green spaces serve citizens with recreational opportunities, aesthetic enjoyment, contribute to public health, climate regulations, cooling effect, and have an impact on the attractiveness of neighborhoods and housing prices. Thus, in view of global

urbanization and biodiversity loss, the valuation of urban green spaces becomes increasingly essential.

We analyzed the impact of biodiverse urban green spaces on rental prices across 22 German cities by applying a hedonic pricing analysis. This analysis complements the existing literature by including the diverse measurements of urban green spaces and their biodiversity that we innovatively cluster as 'objective' -variables, i.e. spatial data computed from satellite images and 'perceived' -variables retrieved from an online survey. Furthermore, we analyzed rental prices in contrast to most studies that consider selling property prices. Finally, we incorporated an online survey as a source of perception data with a monetary valuation method. The key preliminary results at the aggregated level suggest that: (i) rental prices are positively correlated with the distance to the next urban green space. This outcome poses a puzzle since it implies a negative willingness to pay for access to urban green space. (ii) Biodiversity of the urban green spaces as well as around the flat have a positive, albeit not significant, effect on rental prices. Ongoing research based on the second round of online surveys enables to investigate further the obtained counterintuitive results by performing the analysis at the level of individual cities.

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Anna Holzner

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University
Max Planck Institute for Evolutionary Anthropology (MPI EVA)

Wildlife on the edge: Effects of oil palm agriculture on forest-dependent primates in Malaysia

Worldwide, wildlife is critically affected by the conversion of natural habitats into agricultural land. Partially diverting their foraging activities from forest into oil palm plantations, southern pig-tailed macaques (Macaca nemestrina) may benefit farmers as they actively hunt for plantation rats that cause substantial yield loss. Significantly reducing rat numbers, this primate can act as a biological pest control, as we previously showed. However, when ranging in plantations, macaques face multiple threats, such as an increased predation risk, exposure to pesticides or conflicts with humans. To date, detailed knowledge on these impacts and potential behavioural adaptations is still lacking. Data on two groups of macaques inhabiting a forest-oil palm matrix in Peninsular Malaysia showed that, despite its strong dependency on the presence of nearby forest, M. nemestrina can partially adapt to anthropogenic habitats. However, this comes at cost of their social behaviour, the reduction of which is critical given that sociality significantly affects fitness. Likewise, mother-infant relationships were found to be disrupted by increased maternal protectiveness when ranging in plantations, potentially hampering population growth in this threatened species. Beside these behavioural changes, we expect direct implications for the macaques' health. In a current Flexpool-project, we will investigate the link between the intake of pesticide-contaminated plantation foods and the pesticide load of macaques by collecting chemical samples of macaques and the environment. Overall, our work stresses the importance to establish primate-friendly, pesticide-free

plantations, taking into account the economic value of a sustainable plantation management, including biocontrol by macaques.

Authors: Anna **Holzner**, Anja **Widdig,** Nadine **Ruppert**

Isha Dube
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
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Love of Variety and the Long-Term Welfare Effects of Trade in Open-access Renewable Resources

We analyze welfare effects of trade in open-access renewable resources, which is induced by consumer love of variety in resource consumption. We consider two countries that are heterogeneous in incomes – high and low income – and symmetric in all other respects. We show that increasing trade freeness benefits the high-income country, as it improves access to a larger variety of resources and also increases the high-income country's resource stock. Welfare in the low-income country may depend on trade freeness in a non-monotonic fashion. We derive conditions such that welfare first decreases and then increases when trade freeness varies from autarky to costless trade. In direct comparison, autarky may generate higher welfare than costless trade only if the love of variety effect is sufficiently weak.

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Hanna Schenk
Leipzig University
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

The economics of evolutionary overexploitation

Fisheries typically target large fish, putting strong selection pressure on fish to mature at smaller sizes. Due to life-history trade-offs, fish grow more slowly after maturation, reducing maximum size. Because large fish contribute more to reproduction and are economically more valuable than small fish, fisheries-induced evolution can reduce sustainability and economic benefits of fisheries. We include these processes in an economic-ecological-evolutionary fishery model to study economic implications of fisheries-induced evolution and to derive optimal management strategies. Revenues of fishing depend on the size structure of catches, as prices depend on the size of the fish caught. Costs of fishing depend on the size of the fish population and the gear. We apply the model to the North Sea cod fishery and find that the socially optimal fishing strategy is sensitive to discounting. It is known that under high discount rates it can be optimal to exploit a natural population until extinction. We find that whereas for a low discount rate the optimal strategy is to rebuild the population and reverse evolution, the optimal strategy for an intermediate discount rate is to rebuild the stock but to overexploit the beneficial genes and continue to fish on the evolved population. Our results highlight the importance of including evolutionary and economic dynamics in fisheries management.

Authors: H. **Schenk**, iDiv, Leipzig University; F. **Zimmermann**, IMR, Tromsø, Norway;
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Interactive Sessions

RGame

Chairs: Diana Bowler, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Helmholtz Centre for Environmental Research - UFZ*

Corey Callagham, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*

The R statistical software is ever-expanding. But how do you keep up with all the latest and greatest? Is there a package that has been a 'game-changer' for you? Think it might be helpful to others? In this workshop, we invite people across all research areas to share their latest R package finds. Each contributor presents a 3-5 min talk that showcases their favorite package, with a particular focus on the latest and greatest. The goal for a presenter is to really show off why that particular R package is cool and convince the audience that they need to download that package for themselves. At the end of the workshop we hope to provide new tools for our next data analysis project.

This session is open to different types of packages — but there is a preference for non-mainstream packages (e.g., can probably avoid tidyverse packages given their overwhelming popularity). We ask people to send in proposals beforehand, so presentations can be organized into thematic sessions (e.g., data retrieving, data processing, data visualization, analyses, spatial).

Each session comprises several 3-5 min talks depending on participation, with a short Q&A at the end. In total, we expect the talks, Q&As, and any potential discussions, to take about 1.5 h.

To add a little spice, we will finish with a voting session to award The Winner.

Jens Kattge
Max Planck Institute for Biogeochemistry (MPI BGC)

The 'rtry' R package

The 'rtry' package is an R package that provides a set of easily applicable functions for the basic steps of data preprocessing and is designed in particular to support the data exploration and removal of the plant trait data, taking advantage of the features of trait data released from the TRY database. This package is supposed to be applicable without advanced knowledge of the data structure released from TRY or the R software.

Authors: J. **Kattge**, Max Planck Institute for Biogeochemistry, iDiv; G. **Boenisch**, Max Planck Institute for Biogeochemistry; C. **Wirth**, University of Leipzig, Max Planck Institute for Biogeochemistry, iDiv; S. **Díaz**, Instituto Multidisciplinario de Biología Vegetal, Universidad Nacionalde Córdoba, Córdoba, Argentina; S. **Lavorel**, Laboratoire d'Ecologie Alpine (LECA), CNRS, Grenoble, France; P. **Leadley**, Ecology, Systematics and Evolution, Laboratory (ESE), University of Paris-Sud, Orsay, France; I.C. **Prentice**, Faculty of Natural Sciences, Department of Life Sciences, Imperial College London, London, United Kingdom; and the TRY consortium.

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

R package gen3sis

I present a modular spatially explicit model of diversification: gen3sis | general engine for eco-evolutionary simulations. Mechanistic modeling approaches enable bringing disciplines back together using virtual eco-evolutionary experiments. For example experimenting on the deep-time Earth history dynamics effects on the emergence of biodiversity patterns.

Author: O. **Hagen**, iDiv, University Leipzig.

Corey Callaghan
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Martin Luther University Halle-Wittenberg

Creating html plots in R

How to use plotly and/or leaflet to make simple html interactive plots in R.

Author: C. **Callaghan**, iDiv, Martin Luther University.

Matthias Grenié

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

{targets} the R workflow engine to help your analyses be reproducible

{targets} is an R package that offer a pipeline toolkit to make your analyses reproducible. It allows you to tweak your pipeline to only run the necessary computations, by avoiding rerunning unaffected parts. {targets} also offers native parallel computing, branching - to avoid repeating the code for similar targets - and many more.

Steffen Ehrmann

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Leipzig University

Using checkmate to set bugs checkmate

Checkmate package (https://github.com/mllg/checkmate), bec allows package developers to define expectations for input and output data that can then be tested in unit-test, or it can simply be used to assert that or test whether certain requirements are fulfilled.

Author: S. **Ehrmann** (iDiv, University Leipzig).

Guillaume Patoine

Leipzig University
German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

R package purrr

set of tools to work with functions and vectors, without using for loops

Author: G. **Patoine**, iDiv, University Leipzig.

Minghua Shen

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig &
Martin Luther University Halle-Wittenberg

Litsearchr

facilitates quick, objective, and reproducible search strategy for systematic reviews

Author: M. **Shen**, iDiv, Martin Luther University.

Alban Sagouis

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Martin Luther University Halle-Wittenberg

Renv

dependency management tool for reproducible workflow

Author: A. **Sagouis**, iDiv, Martin Luther University.

Diana Bowler

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

Inlabru

point-pattern analysis of species occurrence records

Author: D. **Bowler**, iDiv, UFZ.

The iDiv Barcoding Initiative – iBarc

Chair: Martin Schlegel, *Leipzig University & German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig*

DNA Barcoding is a molecular tool for applications in biodiversity assessment using a DNA-sequence of one or several marker-genes, so-called barcodes. We bring together different research groups at iDiv to present and discuss their research projects, and applications in different fields (e.g. taxonomic and functional diversity, microbial communities, animal-plant interactions, quantitative approaches such as assessment of populations sizes, biomass). We intend to develop plans for further activities and to establish a competence-grid.

Jule Freudenthal
University of Cologne

Deep molecular characterization of eukaryotic microorganisms´ diversity and community composition in the canopy region using a metatranscriptomics approach (micDiv II)

Tree canopies form an important interface between the Earth's terrestrial biomass and the atmosphere. Interspecific differences in bark and leaf surface texture, further structured by e.g. epiphytes (lichens, mosses), provide a variety of diverse microhabitats. From a microbial perspective, these microhabitats resemble island-like isolated biogeographic entities, making tree canopies ideal model systems to study the neutral and selective processes shaping evolution, community composition and biodiversity of microbial communities.

A metabarcoding approach revealed highly diverse communities of microbial eukaryotes (protists) in tree canopies. Here, we aim to disentangle the mechanisms leading to the high diversity of protists in tree canopies such as neutral community assembly from passive dispersal and deterministic, niche-based processes. We use a metatranscriptomics approach to gain an exhaustive assessment of the whole protist diversity. To this end, we sampled tree canopies of the Leipzig floodplain forest with the Leipzig Canopy Crane facility (LCC). Currently, we are working on the extraction of RNA from leaves, bark and epiphytic mosses as well as on the comprehensive bioinformatic pipeline for data analysis.

Authors: J. **Freudenthal**, Terrestrial Ecology, University of Cologne; K. **Dumack**, Terrestrial Ecology, University of Cologne; S. **Schaffer**, Molecular Evolution and Systematics of Animals, University of Leipzig; A.M. **Fiore-Donno**, Terrestrial Ecology, University of Cologne; M. **Schlegel**, iDiv, University of Leipzig; M. **Bonkowski**, Terrestrial Ecology, University of Cologne.

Kenneth Dumack
University of Cologne

From the taxonomic assignment via metabarcoding to the exploration of functioning

With the rise of metabarcoding, increasing knowledge was acquired about the distribution of (microbial) taxa. This explorative phase in ecology lasts now more than a decade. Recently there is a shift from the mere description of the distribution of taxa to a meaningful interpretation of the functioning of taxa in their environment. In bacteriology, and to a certain degree also in mycology, functions are inferred from the presence and/or transcription of functional genes. In many other groups, whether animals, plants, or protists, this approach is not yet feasible. These fields of research must rely on trait databases that connect historical and experimental knowledge with taxonomic data. I will present how the automated assignment of traits to environmental sequencing helps in untangling functioning in ecology.

Stephanie Jurburg,
Helmholtz Centre for Environmental Research – UFZ

CoMiDa: a community microbiome database

Ever-improving sequencing technologies have revolutionized biology and altered our relationship to microbes, highlighting their diversity and their crucial ecological roles in virtually all environments. These works have created massive amounts of microbiome data, which can now be used to fill major gaps in the field, including the scale-dependence of sequence-based biodiversity assessments, the lack of integration of research findings across microbial realms (e.g. marine, animal associated, soil) and into macroecology through synthesis. Here, I present a database of curated and processed microbial community data (CoMiDa) that is designed to facilitate synthesis research in microbial ecology. The data base was created by applying text parsing algorithms to microbial ecology articles to select datasets with comparable sequence data. These sequences have been reprocessed together with the Earth Microbiome Project data. CoMiDa currently hosts nearly 30,000 comparable samples and manually curated metadata, making it one of the largest microbiome databases out there.

Priority Biodiversity Change Drivers for iDiv - World Café

Hosted by the Macroecology and Society Group, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Leipzig University*

This World Café session aims to develop a common understanding of major interests, opportunities, and remaining challenges for integrative research of biodiversity change drivers at iDiv. To this end, it will identify critical (or underexplored) linkages between biodiversity change drivers and outcomes, and explore how we can leverage iDiv's expertise on both needs (question-driven perspective) and potentials (data-oriented perspective) during the new funding phase.

The World Café will be organized around 3 main questions, each of which will be addressed in four parallel break-out groups (each facilitated by a session co-chair), interchanging with three short plenary sessions.

Q1) What are the presumed/expected most critical (or most exciting/underexplored) linkages between different biodiversity-change drivers and outcomes (e.g., potentially including interactions between drivers, effects on different facets of BD change, etc.)?

Each group will synthesize and present their questions in the first plenary, and we will vote on the top 2 or 3 questions to take into the second round (meanwhile, some of the session chairs will start collating data options for these variables).

Q2) For the prioritized driver-outcome relationships, what are the specific needs in terms of spatial, temporal, and thematic scope and detail (e.g. extent and grain), and how would the ideal driver variable(s) be defined? What type of applications would breakout groups prioritize over the near-term (e.g. big-picture, pattern-descriptive assessment vs. causal hypothesis tests vs. continuous monitoring of driver-response relationships vs. scenario modelling vs. concrete support for local conservation interventions, etc.)?

The second plenary will synthesize these requirements and summarize available options of existing driver data.

The third break-out session will turn perspectives from needs to opportunities, by asking

Q3) How well do the attributes of existing (or near-term conceivable) driver products approximate the prioritized ideal driver variable? What implications

do any deviations between ideal and feasible driver definitions/scales of representation have for our biodiversity outcome variables/processes of interest?

During the second plenary, break-out groups will briefly report on their assessments and session chairs will present a brief overview of available (and/or near-term conceivable) driver data options.

The final plenary will be used to further discuss and synthesize the emerging perspectives. Depending on how the discussion goes, possible outcomes might range from a wishlist of driver variables that may inspire future product-development work at iDiv, to ad-hoc match-making between outcome- and driver-oriented iDiv experts, to continued discussions in smaller teams or join work towards a perspectives paper.

Interactive lecture for diversity and inclusion
Chair: Judith Rakowski, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Helmholtz Centre for Environmental Research - UFZ*

This session includes:

1) lecture about D&I, including clarification of language and "ABC of anti-discrimination" with (social) identity, privilege, power, discrimination and its different levels (internalized, interpersonal, institutional, ideological), internal bias, intersectionality

2) exercises for e.g. personal reflection about identity, privilege, interdependencies, power, communication

3) benefits of D&I, relating it to iDiv/academia, brainstorming about needs, visions, roadmapping, collection of problems, etc.

Crash Course High-level policy - How to navigate the world of "distinguished delegates"
Chair: Andrea Perino, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig*

In this interactive session we will give a crash course to high-level policy such as CBD meetings, IPBES plenaries or policy work on the EU level.

Where do you find the important information, how do the processes work and how can you as a scientist get engaged? The session will consist of short input talks and a longer, interactive part.

The Future of Biodiversity Monitoring in Europe
Chair: Jessi Junker, *German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg*

The EU Biodiversity Strategy for 2030, a core part of the European Green Deal, is a major attempt to fight the current biodiversity crisis. In order to track progress towards achieving its goals and to enhance evidence-based decision-making in policy and practice, biodiversity monitoring is of utmost importance. Effective biodiversity policy and impactful conservation and restoration action in Europe are currently hampered by spatially and temporally fragmented, taxonomically biased monitoring efforts that lack integration. Effective improvements of data collection, data flows and reporting need to be tailored to the needs of policymakers and other data users at sub-national, national, and European levels.

In this session, we present potential avenues to enhance and harmonize biodiversity monitoring across Europe: assessing user and policy needs; mapping current monitoring initiatives; identifying essential monitoring variables; enhancing monitoring to support the Nature Directives, Climate and Soil Policies, and Bioeconomy Strategy. Ultimately, we propose to create a Europa Biodiversity Observation Network (EuropaBON) to deliver an integrated, co-designed monitoring framework. We close the session with a presentation of a related project in the Tropical Andes (TAO) and provide a hands-on session on the GEO BON EBV Data Portal.

Henrique M. Pereira, Jessi Junker

General introduction to the project

Putting biodiversity on a fast track of recovery; making sure that ecosystems deliver ecosystem services in the long-term; and restoring degraded ecosystems by 2050, represent the three major biodiversity goals of the EU's biodiversity strategy for 2030. While these goals may seem relatively straight-forward, the implementation of policies enabling biodiversity and ecosystem conservation in Europe is hampered by the limited availability of harmonized, long-term, spatially explicit and regularly updated biodiversity data at the EU-scale. To bridge this gap, EuropaBON (Europa Biodiversity Observation Network) will design an EU-wide monitoring framework for biodiversity and ecosystem services. Together with 15 partners from nine European Union countries and the UK, this 3-year project builds on stakeholder engagement and knowledge exchange during all stages of the design process: 1) identify user and policy needs for biodiversity monitoring; 2) capture and assess current workflows of monitoring efforts delivering biodiversity information in Europe to identify gaps, data and workflow bottlenecks; 3) identify essential biodiversity variables (EBVs) and ecosystem services variables (EESVs) to be monitored by the system to track and assess biodiversity

change; and demonstrate the operationalization of EBVs and EESVs for policy through showcases in support of the various EU Directives. The EBV integrated datasets produced by each of EuropaBON's showcases will feed directly into the GEO BON EBV Data portal, which is a platform for distributing and visualizing EBV/EESV datasets. Finally, we will conclude this session by presenting the Tropical Andes Observatory (TAO) project, which serves as a case in point for designing a user-driven biodiversity observation network following the GEO BON recipe and framing the process within the framework concept of the Essential Biodiversity Variables.

Hannah Moersberger, Juliette Martin, Ian McCallum, Aletta Bonn

Presentation 1: User and policy needs assessment of biodiversity monitoring in Europe

EuropaBON aims to design an EU-wide monitoring framework for biodiversity and ecosystem services. This requires engaging stakeholders at all stages of the design process. To define the various user needs, we engaged stakeholders in four key steps: a stakeholder conference, a survey, an expert meeting and semi-structured interviews. The results of this assessment show a fragmented biodiversity data landscape that cannot easily answer all relevant policy questions. With exceptions such as some bird species and some priority habitat types, monitoring schemes do not cover the full range of genetic, taxonomic and ecosystem diversity within the respective countries. The coverage of different species and ecosystems is biased, as many of the national monitoring activities are mainly influenced by the reporting obligations of the Birds and Habitats Directives. Countries across European regions face different biodiversity monitoring challenges. Roadblocks to monitoring by national agencies include lack of support to establish coordinated monitoring programs and insufficient technical capacity. A lack of detailed geo-referenced information is severely hampering assessments of biodiversity and ecosystem trends, as well as infrastructure planning. Although most countries responded that they use biodiversity monitoring data for some modelling, its full potential is currently not exploited due to lack of capacity and funding. The following solutions are proposed as potential avenues to address the challenges and to build a European Biodiversity Observation Network.

- Enhanced overall coordination, cooperation and synchronisation
- Enhanced data standardisation, coupled with increased data gathering and mobilisation, and dedicated data sharing mechanisms
- Increased modelling efforts and the use of new technologies
- Adequate substantial financial resources
- Capacity building to harness and develop a network of skills and knowledge.

Alejandra Morán-Ordóñez, David Martí Pino, Lluís Brotons

Presentation 2: European biodiversity monitoring workflows

In this talk, we present the EuropaBON biodiversity database (monitoring.europabon.org), a web-based platform explicitly describing current workflows of monitoring efforts delivering biodiversity information in Europe. The website serves the dual purpose of being a platform

for data entry, as well as to allow the visualization and quick consultation of the collected data. This database is a key tool to understand how biodiversity data collected in monitoring schemes across Europe flows through different institutions and programs and gets processed to produce Essential Biodiversity Variables (EBVs), Ecosystem Services Variables (EESVs) and /or other European policy-relevant indicators. It serves as a basis to evaluate the current gaps and bottlenecks that biodiversity monitoring in Europe faces to deliver cost-effective EBV-based products that can effectively inform policy at the European scale.

For a given monitoring network, the database collects information about three distinctive elements: 1) the biodiversity data collected in monitoring programs (e.g. taxa, spatio-temporal resolution); 2) the "integration nodes": platforms/projects/institutions processing the biodiversity data to generate EBVs, EESVs or any other indicators (e.g. funding available, type and spatial level of data processing) and 3) data flows.

Preliminary analyses of the database suggest that most integration of biodiversity data at the European level is carried out by non-governmental bodies and that there is a geographic and taxonomic bias in monitoring efforts across Europe, with data on plants and birds dominating over other taxonomic groups. Data from systematic monitoring programs are most commonly integrated to generate EBVs, ESSVs and indicators at the European level; however, only a small fraction of these data is currently open access.

Henrique M. Pereira, Néstor Fernández, Miguel Fernandez, Jessi Junker, Jose W. Valdez

Presentation 3: Essential Biodiversity Variables for EuropaBON

Identifying which variables need to be monitored to track and assess biodiversity change is a key design question for EuropaBON. We are tackling this issue in two steps: (1) user driven selection and (2) expert driven selection. We started the user driven selection by compiling a list of candidate essential biodiversity and ecosystem service variables across a range of EU policies and also cross-sectorally. Next we conducted a survey to ask from the point of view of users and policymakers, how do they rank in importance the different variables and to identify what policy questions they hope to address with them. This has resulted in a set of 45 ranked variables, specifying the class of variables (e.g. species populations or ecosystem function), the name of the variables, the biological or taxonomic scope, the spatial and the temporal resolution. In the expert driven selection we are building on this list and relative importance ranks to produce a balance set of essential variables, that ensure cross-realm coverage (e.g. marine, freshwater and terrestrial), taxonomic coverage, policy questions, but also feasibility from a point of view of observation and modelling.

Néstor Fernández

Presentation 4: Showcasing EuropaBON's contribution to environmental EU policies

Current European biodiversity policy reporting streams use highly heterogeneous data and methods for assessing biodiversity change. This represents a major limitation for assessing progress in the implementation of the European Nature directives. Furthermore, restoration

planning and implementation required under the Biodiversity Strategy for 2030 and the European Restoration Law require spatially explicit information of biodiversity patterns and trends that are currently sparse. Enhanced data workflows and models, when adequately connected to regulatory monitoring and reporting streams, can leverage monitoring data on biodiversity and potential drivers to assess the status of selected terrestrial and aquatic habitats and species. Furthermore, the WFD regulatory monitoring can serve as the backbone for better integrated aquatic biodiversity monitoring in Europe. By integrating multiple data sources including remote sensing, coordinated monitoring programs, and citizen science, we propose ways in which data workflows under the European Nature Directives can be effectively implemented. Ensuring production and distribution of such datasets, including with the EBV Data Portal developed and hosted at iDiv, is key for supporting comprehensive and coherent monitoring within the EU Member States.

Christian Langer, Henrique M. Pereira, Néstor Fernández

Presentation 5: Cataloging Essential Biodiversity Variables with the EBV Data Portal

Essential Biodiversity Variables (EBVs) are used to monitor the status and trends in biodiversity at multiple spatiotemporal scales. These provide an abstraction level between raw biodiversity observations and indicators, enabling better access to policy-relevant biodiversity information. Furthermore, the EBV vision aims to support detection of critical change, among other things, with easy to use tools and dashboards accessible to a variety of users and stakeholders.

We present the EBV Data Portal, a platform for distributing and visualizing EBV datasets. It contains a geographic cataloging system that supports a large number of spatiotemporal description features and enables their discoverability. To facilitate user interaction, it offers a web-based interface where users can (1) share and/or (2) find essential biodiversity spatiotemporal data through intuitive interaction with cataloging and visualization tools. Using the EBV Catalog module, the user can explore the characteristics of the data based on the definition of an EBV Minimum Information metadata standard. The Catalog also allows you to browse the description of the metadata as both the ACDD standard (JSON) and the EML standard (XML). This enables easy interoperability with other metadata catalogs.

An example application is the calculation of EBV summary statistics for selected countries and areas. Using the EBV Data Portal, users can select EBVs and calculate basic biodiversity change metrics from spatiotemporal subsets and visualize conveniently complex, multidimensional biodiversity datasets. These visualization and analysis tools of the EBV Data Portal are a first step towards an EBV-based dashboard for biodiversity analyses.

Luise Quoss, Néstor Fernández, Christian Langer, Jose W. Valdez, Henrique M. Pereira

Presentation 6: ebvcube: An R package for netCDF of Essential Biodiversity Variables

Multidimensional geospatial data is increasingly used in biodiversity research. This data can cover spatiotemporal estimates of biodiversity metrics using models and projection scenarios, and biodiversity products derived from remote sensing. However, the disparity of formats and criteria used to arrange the data severely limits their interoperability. The Essential Biodiversity Variables (EBV) datasets are defined as measurements providing essential information for analysing, tracking and reporting the state of biodiversity. A data and metadata standard has recently been developed to consistently organize and document the EBV cubes. The EBV data cubes are defined along the three dimensions of space, time and biological entities (e.g. species or types of ecosystems). These cubes are organized in hierarchical groups to allow for multiple biodiversity metrics and scenario projections per cube. However, tools that facilitate the production of these EBV cubes have been missing. In this talk, we present the ebvcube R package, a tool tailored to produce EBV cubes using a specification of the netCDF format and compliant metadata with the ACDD and CF conventions. The package functionality covers access to existing EBV netCDF datasets as well as the creation of new ones. The user can retrieve the metadata, which is distributed across the different netCDF components. Different visualization functions are available for fast data exploration, covering the temporal and spatial scope of the data. Specific functions have been implemented to access data subsets and to perform spatial resampling of the data in order to spatially align multiple EBV cubes. The creation of the EBV datasets can be accomplished in interaction with the EBV Portal and the R package. Finally, the created EBV datasets can be uploaded and shared through the EBV Portal. Together with the EBV Data Portal, ebvcube facilitates the exchange of interoperable scientific biodiversity data.

Jose Valdez, Miguel Fernandez, & Henrique M. Pereira

Presentation 7: TAO from data to decision in the Tropical Andes

The Tropical Andes is a region that includes a great diversity of ecosystems, climates, and altitudinal gradients in South America. Covering approximately an area equal to France, Germany and Spain combined, the Tropical Andes is recognized as a global biodiversity hotspot due to its high levels of endemism, disproportionate number of species, and high rates of habitat loss. It is in this highly diverse area that the TAO Project team: from data to decisions, has been working for the last two years on the process. We are designing a user-driven biodiversity observation network following the GEO BON recipe and framing the process within the framework concept of the Essential Biodiversity Variables. At the core of this process a wide consultation with more than 400 experts and stakeholders at the regional level has prioritized six key topics that the system should address: 1) land-use planning and risk management, 2) development and infrastructure projects, 3) tourism and gastronomy, 4) international agreements and commitments, 5) use of natural resources by local communities, 6) education and capacity building. These findings provide the basis for building a system tailored to the needs of users in the region, ensuring the sustainability of this initial multi-country biodiversity observation effort in the region.