iDiv Annual Conference 2025

Monday 29 September 2025 - Wednesday 1 October 2025

Martin Luther University Halle-Wittenberg

Programme

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Workshop: Workshop 2: Metabarcoding in Biodiversity Research – Application Spectrum and New Methodological Advances **- Lecture Hall XXIII (14:00 - 15:30)**

Workshop: Workshop 3: iDiv Flexpool Project PrioDiv – A Workshop of Project Collaborators **- Lecture Hall C (14:00 - 15:30)**

Tuesday 30 September 2025

Registration - Foyer (09:00 - 10:00)

Opening - Audimax (10:00 - 10:15)

Keynote: Miguel Bastos Araújo: Modeling Biodiversity Under Climate Change: From Individual Species to Communities - Audimax (10:15 - 11:15)

iDiv Research Vision: iDiv's Topical Committees - Audimax (11:30 - 12:30)

-Conveners: Martin Quaas

[110] Complexity (11:30)

Presenters: BROSE, Ulrich (German Centre for Integrative Biodiversity Research (iDiv)), HARPOLE, W. Stanley (Helmholtz-Centre for Environmental Research (UFZ) Department of Physiological Diversity, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Martin-Luther-University Halle-Wittenberg)

[111] Functions (11:40)

Presenter: EISENHAUER, Nico (iDiv | Leipzig University)

[112] Interactions with People (11:50)

Presenter: BONN, Aletta

[113] Science for Biodiversity Governance (12:00)

Presenter: PEREIRA, Henrique (German Centre for Integrative Biodiversity Research (iDiv))

[114] Synthesis, Theory, Computational Methods (12:10)

Presenter: FRITZ, Susanne (iDiv)

Biodiversity Change - Audimax (14:00 - 15:34)

-Conveners: Hoss, Daniela (Uni Leipzig, iDiv); Georg Johannes Albert Hähn

[3] Soil biodiversity: gaps and priorities for better nature conservation in Europe (14:00)

Presenter: ZEISS, Romy (iDiv | Leipzig University)

Soil biodiversity is essential for healthy ecosystems, yet it remains largely overlooked in nature conservation efforts. Our research highlights major gaps: protected areas in Europe showed no general positive effect on soil biodiversity and functioning such as nutrient cycling and carbon storage. Soil organisms, like earthworms, springtails, and fungi, are threatened by climate change, land-use change, and global biodiversity loss. Despite their critical role in ecosystem services, we found over 80% of earthworm habitats located outside of protected areas and projected to shift under future climates. Through species distribution models, and spatial prioritization, we have been identifying areas of especially high importance for soil biodiversity conservation. Our results show an urgent need to directly include soils and soil organisms in nature conservation planning to secure ecosystem health for the future.

[23] Towards an optimal biodiversity monitoring network for Europe (14:15)

Presenter: VITI, Martina

As pressures on biodiversity intensify, a coordinated monitoring effort across Europe is urgently needed to track spatial and temporal trends and inform policy responses. Designing effective biodiversity observation networks requires capturing a broad range of species and habitats while enabling attribution of trends to underlying environmental drivers. Using Europe as a case study, we evaluated how different sampling strategies and network sizes influence the detection of biodiversity patterns and their attribution to five key anthropogenic drivers: climate change, land-use change, nitrogen deposition, biological invasions, and protection status. We tested four spatial sampling designs—random, systematic, stratified, and proportionally stratified—across network sizes ranging from 128 to 131,072 2×2 km² sites (0.01% to 13% of the study area). Networks were assessed based on their coverage of over 1,300 species and 200 habitat types, as well as their representation across gradients of driver intensity. Our findings show that network size is the dominant factor in capturing common species and habitats, while spatial design plays a greater role for rare entities. Stratified sampling, ensuring equal representation across environmental strata, outperformed other designs, particularly for rare species. This held true also for trend attribution, where the stratified sampling yielded higher representativeness across driver gradients, particularly for rare species. Habitats were generally sampled more effectively than species, regardless of strategy or scale, underscoring the challenge of capturing the full spatial heterogeneity in species distribution. These insights lay the groundwork for a scalable, adaptive monitoring framework capable of supporting robust biodiversity trend assessments and policy-relevant attribution.

[49] Monitoring wildlife comebacks with eDNA metabarcoding (14:30)

Presenter: MÉNDEZ, María (iDiv-MLU)

Wildlife is returning to human-dominated landscapes as a result of reduced direct persecution, land abandonment, and active restorations, leading to ecological benefits such as species range expansions and the trophic rewilding of ecosystems. These recolonization processes can have important ecological and conservation benefits, not only helping to improve the conservation status of particular species, but also contributing to the recovery of lost ecological functions and overall ecosystem integrity. However, human-wildlife conflicts may also increase as a result of some species' range expansions. Effective monitoring is key to evaluating rewilding progress and anticipating its ecological and societal consequences. Environmental DNA (eDNA) metabarcoding has emerged as a promising tool for biodiversity surveillance, enabling the detection of multiple taxa from environmental samples. However, its performance relative to traditional methods, and across different substrates, remains variable. Here, we present the first empirical comparison of eDNA metabarcoding and camera trapping in a rewilding site—the Oder Delta, spanning Germany and Poland. Using soil, water, and invertebrate blood meals (iDNA), we (i) develop an eDNA metabarcoding technique to complement traditional wildlife monitoring systems such as camera traps, aiming to provide information that has proven challenging to obtain in rewilding monitoring programs, and (ii) evaluate the effectiveness of eDNA versus traditional monitoring in detecting vertebrate wildlife. Preliminary analyses showed that the majority of species detected by traditional methods were also detected through eDNA metabarcoding, and additionally, ten species were identified exclusively by eDNA metabarcoding. We also assessed the comparative performance of each substrate, finding that water and, subsequently, mosquitoes were the most reliable and effective substrate for wildlife detection. Our findings contribute to optimizing biodiversity monitoring in rewilding landscapes.

[48] Rewilding trends in Europe (1992 – 2020) (14:45)

Presenter: Dr WEISSGERBER, Magali (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany Institut für Biologie, Martin-Luther-University Halle-Wittenberg, Halle, Germany)

Ecological restoration is today essential to reverse ecosystem degradation. It encompasses multiple approaches including rewilding which aims at improving the condition of ecosystems by recovering natural ecological processes. Focusing on functionality rewilding targets self-sustaining ecosystems that provide multiple ecosystem services and require little to no human management in the long term. As any restoration approach, rewilding needs to be monitored. Monitoring rewilding aims at characterizing and understanding large-scale patterns in ecosystems focusing on the components of the rewilding process. Moreover, knowing where rewilding is happening opens possibilities for science (e.g., to assess its effects on climate change through the carbon sequestration of those areas) and policy (e.g. to protect those areas). In this context, we developed a set of spatially explicit indicators for monitoring rewilding trends and outcomes between 1992 and 2020. The rewilding status of an ecosystem depends on the extent of human pressure and on its ecological integrity which has three components: connectivity, trophic complexity, and stochastic disturbance regimes. The more natural these components are, the higher the ecological integrity. We evaluate terrestrial landscape connectivity loss caused by human use (built-up areas, linear infrastructures, agriculture) with a calculation of the effective mesh size. Trophic complexity is addressed with a focus on large mammals: actual communities are compared to natural ones by a trait dissimilarity analysis. Human pressures and their restricting effects on stochastic disturbances (e.g. floods and fires) are considered through the forestry and agriculture (grazing) impacts on primary productivity. The changes of those three indicators over 30 years highlight regions of Europe becoming wilder, but also regions where some components improve while other intensify. Mapping such rewilding indicators provides insight into the potential spaces for resilient and self-sustaining ecosystems and identifies areas where restoration efforts should be focused.

[41] Genetic information for the conservation of segetal plants (15:00)

Presenter: Prof. WESCHE, Karsten

Arable land undoubtedly is the most important habitat class covering >1/3 of cultural landscapes such as in Central Europe. Segetal plants can contribute substantially to biodiversity and provide food sources e.g. for insect pollinators or herbivores. However, agricultural intensification has driven a massive decline in phytodiversity over the last decades. In contrast to for example meadows and forests, conservation efforts are still very limited for arable land. In Germany, potential restauration action is under legal control with respect to seed transfer zones (STZs) that ensure regionality of accessions. These STZs are based on general (bio)geographical parameters, and presently do not capture interspecific genetic variation. Understanding population genomic structure thus is critical for restauration efforts but such data are hardly available for segetal species. In consequence, the widely planted flower strips comprise relatively cheap crop mixtures of non-regional populations, rather than regional material from wild populations. Our project aims to investigate population genomics of seven common, nine rare and five critically endangered segetal species across Germany using the high throughput sequencing technique ddRADseq. Our analyses revealed strong genetic fragmentation and low genetic diversity within populations of critically endangered segetal species (e.g. Bupleurum rotundifolium, Euphorbia falcata and Stachys annua). In rare species (e.g. Valerianella dentata, Odontites vernus and Agrostemma githago), geographical structures were present but not captured by the current STZs. Common species (e.g. Anagallis arvensis and Thlaspi arvense) lacked any genetic structure and showed high gene flow between populations.

[1] Frost resistance - a neglected driver of plant phenology and distribution? (15:15)

Presenter: ZIEGLER, Therese

With ongoing climate change, many plants are responding to changes in CO2 levels and temperatures. It was shown that frost events may become more frequent even with a general rise in temperature. As plants shift their spring phenology to earlier dates and/or their range towards the poles and to higher elevations frost can be a potential risk for plant survival and performance and frost resistance might be an important driver of the ability of plant species to change their phenology and range. However, this has not been studied yet. To close this gap, we measured frost resistance in mainly herbaceous plant species using the electrolyte leakage method. We assume that 1) a species' ability to shift their spring phenology to earlier dates is driven by their ability to tolerate late frost events, as shifts without high frost resistance will lead to frost damage. And 2) species' ability to shift their distributional range towards the poles and higher elevational sites is driven by their ability to tolerate late-frost events, as the likelihood of late-frost events increases with these shifts. We will present our first results at the 9th iDiv Conference.

[26] A FAIR catalog for essential biodiversity variables: the EBV Data Portal (15:18)

Presenters: LANGER, Christian (Martin-Luther-University Halle-Wittenberg, Halle / Saale, Germany | German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany), OCEGUERA, Emmanuel (Martin-Luther-University Halle-Wittenberg, Halle / Saale, Germany | German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany)

Essential Biodiversity Variables (EBVs) are used to monitor the status and trends in biodiversity at multiple spatiotemporal scales. These provide an abstraction level between raw biodiversity observations and indicators, enabling better access to policy-relevant biodiversity information. Furthermore, the EBV vision aims to support detection of critical change with easy to use tools and dashboards accessible to a variety of users and stakeholders. We present the EBV Data Portal, a platform for sharing and visualizing EBV datasets. It contains a geographic cataloging system that supports a novel biodiversity-specific metadata standard called the “EBV Cube Standard”. This standard builds on metadata specifications of the Attribute Convention for Data Discovery (ACDD) and is interoperable with the Ecological Metadata Language (EML) vocabulary. The EBV Cube and Data Portal work together enabling discoverability and sharing of complex biodiversity data of different types, from remote-sensing derived ecosystems data to modelled spatiotemporal species distributions. Furthermore, the infrastructure offers a web-based interface and API resources to publish and explore data.

[62] A Novel Tool for the Extraction of Plant Phenology from Digitized Herbarium Specimens (15:22)

Presenter: KÖRSCHENS, Matthias (Friedrich Schiller University Jena)
Herbarium specimens offer valuable insights into changes of plant distribution from the past to the present, aiding in predicting future developments and responses to environmental changes. Over centuries, herbarium specimens have been collected, labeled with data like date and place of collection, collector, species name and information on habitat, and archived manually, leading to gigantic collections of important historic information. However, extracting information relevant for research from such collections manually is a considerable challenge, which is why significant digitization efforts are taking place to enable faster processing. Unfortunately, while the amount and variety of data contained in such digitized herbarium specimens is large, automated methods to extract the information are still very limited. We introduce a novel tool based on artificial neural networks to automatically extract phenological information from images of herbarium specimens. With this method, it will be possible to extract phenological information for large numbers of herbarium specimens without manual effort at high throughput and speed, which will enable further research on plant phenology from historical to present observations. Moreover, we develop the tool to be applicable to many different plant species without the need to supply own data or re-train the model on novel species. The system is developed in interdisciplinary cooperation between biologists and computer scientists.

Current Status and Challenges of Ecometabolomics in Biodiversity Research - Lecture Hall XXIII (14:00 - 15:30)

-Conveners: Uthe, Henriette (IPB Halle)

[53] Does herbicide exposure in oil palm plantations affect wild southern pig-tailed macaques? (14:00)

Presenter: WIDDIG, Anja
Agricultural expansion into natural habitats and unsustainable practices, like those caused by oil palm cultivation in Southeast Asia, harm biodiversity. Wildlife in these disturbed areas faces threats from humans, predators, and pesticides, but how these factors affect their health is less understood. We studied wild southern pig-tailed macaques (Macaca nemestrina) living at the interface between rainforest and oil palm plantation in Malaysia. They enter the plantation daily to forage for oil palm fruits and rats, resulting in regular exposure to herbicides. Long-term data suggest an extremely high infant mortality rate of 57%, potentially causing an overall decline in this population. Our previous findings indicated that the risk of infant death was significantly elevated after prolonged maternal inter-birth intervals and in first-time mothers. We suspected that herbicides may accumulate in the mothers’ bodies and pass to fetuses, thereby affecting infant survival. Here, we aim to detect herbicides in the plantation environment (i.e., water) and macaques’ food (i.e., fruits and rats), and to identify their evoked changes in macaque body odour. To do so, we collected water, macaque and rat urine, and odour/volatile samples from macaques, rats, and oil palm fruits in three conditions: before pesticide treatment at the plantation, one week after, and three weeks after treatment. Using liquid chromatography–mass spectrometry, herbicides were detected only infrequently in water and macaque urine, with a slight increase in detections in macaques following pesticide application. In contrast, rats (living permanently in the plantations) consistently showed high herbicide loads, suggesting accumulation and a possible indirect exposure pathway to macaques. Additionally, gas chromatography–mass spectrometry revealed changes in the macaques’ chemical profiles following herbicide exposure, indicating metabolomic changes caused by pesticides. Overall, our work emphasizes the importance of reducing pesticide use in agricultural landscapes to protect biodiversity against the adverse effects of chemical pollution.

[90] The Metabolic Inventory of Non-human Primates through Non-Invasive and Field-Friendly Fecal Analysis (14:15)

Presenter: MASCELLANI BERGO, Anna (Czech University of Life Sciences Prague)
Anthropogenic impacts such as deforestation, habitat fragmentation and hunting have a significant impact on wildlife, reducing biodiversity and affecting the physiological health of many endangered species. To monitor the welfare of wildlife, the use of non-invasively collected samples such as feces is becoming increasingly valuable for environmental and ecological research. Fecal metabolomics offers a powerful approach to investigate metabolic responses to environmental and physiological stressors. This study compared the profiles of five non-human primate species: *Pan troglodytes* (chimpanzee), *Pan paniscus* (bonobo), *Pongo abelii* (Sumatran orangutan), *Gorilla gorilla*, and *Macaca silenus* (wanderoo), all housed under similar conditions at Leipzig Zoo (Germany). Samples were collected over five consecutive days, with five biological replicates per species per day, extracted on-site and stored at −20°C until analysis. Gas chromatography and mass spectrometry were used to obtain profiles of both volatile and semi-volatile metabolites. A PLS-DA model with $R^2Y = 0.962$, $Q^2Y = 0.788$, and 66% cross-validated classification accuracy ($p = 0.05$), indicated reliable discrimination across species as a precondition to explore species-related information. Similar to human data, extracts were rich in polar organic acids, including amino acids and long-chain fatty acids, as well as sterols, bile acids, and their conjugates, while headspace analysis detected abundant short-chain fatty acids and fatty acid methyl esters. A comparison with fresh-frozen controls confirmed the suitability of the field-adapted sampling protocol for

preserving metabolic information from fecal samples. Our protocol represents an easy-to-use approach for non-invasive metabolome screening under field conditions, especially when cold chains and laboratory infrastructures are limited. Its application in remote areas could significantly improve wildlife monitoring and allow researchers to track metabolic health and environmental responses across different species and habitats. Future work will include LC-MS and 1H-NMR analysis to further assess analytical suitability and obtain information on a broader range of metabolites.

[93] Aliphatic Esters as Honest Signals in Fruit–Frugivore Interactions: An Ecometabolomic Approach in Malagasy Ficus (14:30)

Presenter: NGUYEN, Linh (iDiv, FSU Jena and MPICE)

Fruits have evolved a range of traits to attract seed dispersers, in which chemical signals, such as scent, play a key role. Among these, aliphatic esters are notable for their consistent presence in ripe fruits of species that rely on frugivores for seed dispersal, yet their ecological role and evolutionary origin remain poorly understood. Emerging evidence suggests that these compounds may function as honest signals of sugar content, linking metabolite profiles with fruit nutritional quality and potentially reflecting co-evolutionary dynamics between plants and their animal dispersers. In this study, we use an ecometabolomic framework to investigate the functional role of aliphatic esters in fruit–frugivore communication in up to 20 Ficus species in Madagascar, a biodiversity hotspot with a diverse frugivore community, including lemurs. By integrating thermal desorption gas chromatography-mass spectrometry (TD-GCMS) and high-performance liquid chromatography (HPLC), we quantify fruit volatile profiles and sugar content to test whether esters serve as reliable indicators of reward. Additionally, we sequence the alcohol acyltransferase (AAT) gene to examine whether ester production is associated with dispersal ecology. Our research sheds new light on the ecological and evolutionary roles of secondary metabolites in plant–animal interactions, revealing how these chemical traits influence biodiversity patterns across scales. By leveraging metabolomic data, we demonstrate how eco-metabolomics can address key questions in chemical ecology, offering novel insights at both the molecular and ecosystem levels.

[105] Harnessing phytochemical diversity for plant resilience breeding: an integrative omics approach to abiotic stress tolerance in Medicago sativa (14:45)

Presenter: ANAIA, Redouan Adam (University of Groningen)

Abiotic stressors such as soil salinization and drought increasingly threaten agricultural productivity, ecosystem function, and biodiversity. However, environmental pressures also shape individual plant phenotypes and populations by affecting ion homeostasis and phytochemical traits. These key axes of functional and chemical diversity, are often heritable and therefore can be selected for, to design resilient cultivars. Medicago sativa (alfalfa), a perennial legume central to forage-based agroecosystems, exhibits extensive intraspecific variation in salt and drought tolerance. While its agronomic importance is well established, the phytochemical and molecular mechanisms underlying its resilience remain poorly characterized. We hypothesize that tolerant genotypes rely on coordinated strategies involving ion homeostasis and the accumulation of specialized metabolites, such as triterpenoid saponins and flavonoids, compounds known to mediate both abiotic stress responses and ecological interactions. To investigate this, we are screening five cultivars with contrasting stress responses, including salt- and drought-tolerant lines and one non-tolerant cultivar used to generate a nested association mapping (NAM) F1 population. We apply a paired omics strategy combining untargeted LC-MS metabolomics, ion chromatography, and RNA-seq (BSR-seq or QTL-seq), to link metabolomic and ionomic profiles with gene expressed QTLs under stress across plant development. Thereby, our aim is to identify biosynthetic pathways and regulatory modules associated with functional trait variation, and ultimately, to map SNPs driving metabolomic and ionomic signatures of resilience. This will contribute to both basic understanding of chemodiversity in plant adaptation and the applied design of stress-resilient cultivars

[115] Ecometabolomics at iDiv – lessons and perspectives (15:00)

Presenter: Dr UTHE, Henriette (IPB Halle)

Ecometabolomics has long been a cornerstone of biodiversity research at iDiv. To strengthen this approach, the Ecometeor platform was established to integrate advanced metabolomics techniques and expertise into iDiv’s research, with the goal of uncovering the chemical mechanisms underlying ecological patterns and processes in plants, insects, soil, water, and even the atmosphere. Although the platform has now ceased operations at iDiv, excellent opportunities to continue and expand this research are open to iDiv at the mass spectrometry core facility MS-UL at the Faculty of Chemistry of Leipzig University and in MetaCom in the Institute of Plant Biochemistry in Halle. Here, we highlight the key achievements of Ecometeor in advancing our understanding of chemical diversity within ecosystems and show emerging directions for applying metabolomics to biodiversity research in the future.

Molecular Biodiversity and Evolution - Lecture Hall XXII (14:00 - 15:30)

-Conveners: Gerth, Michael (German Centre of Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg)

[4] Causes and consequences of recombination landscape variation in plants (14:00)

Presenter: DREISSIG, Steven (Leibniz Institute of Plant Genetics and Crop Plant Research)
The genomic landscape of meiotic recombination plays an essential role in the evolution of eukaryotes. Patterns of recombination are highly dynamic, with variation along chromosomes, between sexes, individuals, populations, and species. These quantitative variations are driven by allelic variation, environmental factors, and interactions between both. In many eukaryotes, recombination rates are elevated in sub-telomeric regions and drastically reduced near centromeres. In plant species with large genomes, this results in large low-recombining regions harbouring approximately 30 % of genes, which reduces the efficacy of natural selection on those genes. In our work, we quantify recombination landscape variation in natural and experimental populations of inbreeding and outbreeding grass species (Hordeum vulgare and Secale cereale), and explore the underlying genetic basis and environmental plasticity through genome-wide association scans. Recently, we used single-pollen nuclei (SPN) genotyping to directly measure male meiotic crossovers in 3,136 pollen nuclei from 584 individuals sampled from a large rye population grown under control and nutrient deficiency conditions. We uncovered a polygenic architecture of meiotic recombination rate variation, and strong genotype-by-environment interactions, emphasizing the environmental plasticity of meiotic recombination. Our work sheds light on factors shaping within-species genetic diversity, with implications on populations’ potential to adapt to changing environments.

[17] Bimodal centromeres in pentaploid dogroses shed light on their unique meiosis (14:15)

Presenter: Prof. RITZ, Christiane
Polyploidy and hybridisation are important driving forces for angiosperm evolution but pose a challenge for sexual reproduction, as correct meiotic chromosome pairing needs to be established. The odd-ploid widespread European dogroses (*Rosa* sect. *Caninae*, 2n = 5x = 35) overcame hybrid sterility by evolving a unique meiosis mechanism: During Canina meiosis two chromosome sets form bivalents and are transmitted to both egg and sperm cells, while the remaining three chromosome sets are transmitted as univalents only via the egg cells. Thus, dogroses combine sexual and apomictic reproduction within the very same nucleus. Chromosome-level analyses of dogrose genomes in comparison with single copy gene data from dogrose pollen and diploid species across the genus Rosa revealed that dogroses are complex hybrids. Moreover, bivalent-forming chromosome sets exhibit distinct synteny but their evolutionary origin differed between dogrose clades indicating the multiple origin of the peculiar meiosis. We found that bivalent- and univalent forming chromosomes differed by their centromere size and composition irrespective of their evolutionary origin. A rose-specific satellite repeat dominates the univalent-forming chromosomes and thus probably contributes to their meiotic drive in the female germ line.

[91] Effects of fertilization and drought stress on the diversity and composition of the phytomicrobiome in seeds and seedlings (14:30)

Presenter: Mr PELZER, Robin Jan (Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany)
Seeds harbor diverse microbial communities, both on their surfaces (epiphytes) and within their tissues (endophytes). While seed endophytes remained largely overlooked for decades, recent research highlights their critical roles in seedling development, including promoting nutrient uptake and protecting against pathogens. However, the factors shaping seed and seedling microbiomes remain poorly understood. In this study, we investigated how parental exposure to drought and fertilization, applied in a fully crossed design, affects the seed and seedling microbiome composition and diversity in *Rumex crispus*. We further examined how these microbial communities influence colonization of seedling roots and leaves under sterile conditions. Finally, we tested whether additional fertilization of seedlings modulates these microbiome assembly processes. To address these questions, we conducted next-generation sequencing of seeds and seedling tissues, using aseptic growth systems with sterilized media to isolate microbial transmission and assembly effects. Our results show that seed microbial communities differ markedly from those of seedlings, with clear distinctions between root- and leaf-associated microbiota. Preliminary findings suggest that both drought and fertilization experienced by the parent plants influence seed microbiome composition and its transmission to seedlings. Moreover, fertilization of seedlings interacts with parental treatments to further shape the microbiome structure. This study closely aligns with key research areas of iDiv combining molecular biodiversity with biodiversity change and contributes to our understanding of how climate change drivers such as drought and nutrient enrichment affect microbiome inheritance and microbiome establishment during early plant development.

[96] Field to Function: Gene Regulation and Microbial Communities Shape Phenotypic Variation in Arabidopsis thaliana Across Natural Habitats (14:45)

Presenter: LAUBINGER, Sascha (University Halle-Wittenberg)

Plant genetics has long relied on the model organism *Arabidopsis thaliana*, which has been instrumental in uncovering the molecular basis of ecologically important adaptations—such as temperature sensing, flowering time regulation, and communication with microbial and fungal pathogens. However, most gene functions have been studied under controlled laboratory conditions, often overlooking the complexity of natural environments.To bridge this gap, we conducted an extensive ecological study over five years, focusing on field phenotyping of *A. thaliana* across contrasting natural habitats. Using over 35,000 trait measurements collected from naturally occurring plants in situ, we captured intraspecific variation in growth, morphology, and developmental timing. These data enabled us to quantify phenotypic plasticity in response to seasonal and interannual variation in key abiotic factors such as temperature.Transcriptomic profiling of more than 1,500 individual plants allowed us to directly link gene functions to ecologically relevant traits, revealing novel genes and regulatory networks involved in seasonal growth regulation and stress responses. We extend this approach to leaf microbiome profiling, showing that microbial community composition (i) varies between seasons and locations and (ii) is closely associated with trait variation. This suggests microorganisms are important biotic factors, and their interactions with plants play a significant role in modulating phenotypic plasticity in natural environments. By embedding *A. thaliana* within its ecological context, we demonstrate that this model species can serve as a powerful system for dissecting the molecular basis of plant adaptation in the wild. Building on this framework, we are now extending our approach to additional plant species as a blueprint for integrating molecular resolution with ecological realism—opening new avenues for understanding plant adaptation and resilience under changing environmental conditions.

[28] Do it yourself at home, call for support abroad: Native and non-native populations differ in their belowground responses to drought (15:00)

Presenter: ROSCHE, Christoph

Understanding how plants respond to drought is crucial for predicting the impacts of global change on plant distributions. However, little is known about the eco-evolutionary drivers of intraspecific variation in belowground drought responses. Comparisons between native and non-native populations offer a promising approach to study rapid evolution in belowground traits, as introduced plants encounter novel interaction partners that may trigger alternative drought strategies. We investigated belowground drought responses in 94 native and 106 non-native populations of *Conyza canadensis*, grown under controlled dry and mesic greenhouse conditions. We recorded fine root traits, root exudation profiles, and fungal root colonization, and accounted for population co-ancestry in our models using ddRADseq-based genotype data. Native populations responded to drought with pronounced changes in fine root morphology, including increased specific root length. In contrast, non-native populations showed limited morphological plasticity but increased both the quantity and chemical diversity of root exudates. These changes were associated with shifts in the root-associated fungal community, especially an increase in the relative abundance of *Rhizophagus irregularis*. The abundance of this key arbuscular mycorrhizal fungus correlated positively with plant performance under drought. Across the investigated belowground traits, population co-ancestry explained a substantial proportion of variation, leading to more conservative assessments of rapid evolution between ranges. Our findings indicate rapid evolution in drought strategies among non-native populations. Instead of directly investing in soil exploration ("do-it-yourself strategy"), these populations increasingly rely on fungal partners. This shift appears to be mediated by root exudation ("call-for-support strategy") and may be promoted by novel biotic interactions in the non-native range. The observed flexibility in belowground responses may contribute to the invasive success of *C. canadensis* and underscores the evolutionary potential of plant–microbe interactions under drought. Our results also highlight the need to account for demographic history when assessing eco-evolutionary dynamics.

[15] Pollen and anther morphological variation was shaped by domestication in rye (Secale cereale L.). (15:15)

Presenter: WAESCH, Christina (IPK Leibniz-Institute Gatersleben)

In plants and animals, pollen and sperm morphology are incredibly diverse across species. Cross-pollination provides a mechanism to recombine genetic variants in a population which, among other evolutionary forces, may facilitate adaptation. Across plant species, pollen morphological diversity is broadly linked to different pollination systems. However, the extent of within-species diversity is less well understood. Further on, modulating pollination mechanisms in crops presents an opportunity to improve hybrid breeding programs. Our study aims to investigate quantitative variations in pollen and anther morphology in rye (*Secale cereale* L.), a wind-pollinating grass species. For this purpose, we analysed 339 rye individuals derived from a diverse set of 64 prior classified rye accessions ranging from domesticated (221), wild-like (91) and wild (4) individuals. A PCA using reduced representation sequencing data (GBS) based on 56,713 SNPs revealed a clustering based on the degree of domestication. We quantified pollen morphology in 286 individuals using multispectral imaging flow cytometry, and measured anther length via light microscopy in 314 individuals, which revealed pronounced within-species diversity. We conducted genome-wide association scans and found five and eight genomic regions associated with pollen length and anther length, respectively. A subset of these loci overlapped with previously identified domestication loci for which the underlying trait was unknown. Our *PST-FST* analysis, suggests that pollen and anther traits were under selection throughout rye domestication. A population genomic analysis revealed signatures of selection at one of five loci associated with pollen length, as well as at three out of eight loci associated with anther length. Underlining that, we found significantly higher pollen and anther length in domesticated rye. In conclusion, this suggests that selection for larger pollen grains and longer anthers occurred throughout rye domestication. Our study extends our knowledge of the genetic architecture underlying within-species pollen and anther morphological diversity and further unravels domestication traits in rye.

[34] Progress and future directions of biogeographical comparisons of plant–fungal interactions in invasion contexts (15:18)

Presenter: THOMA, Arpad Erik (Martin-Luther-University Halle-Wittenberg)

Plant invasions are biogeographical phenomena that may involve shifts in belowground plant–fungal interactions, such as the release from fungal pathogens or more beneficial interactions with mutualists in nonnative ranges. However, native and nonnative ranges are not uniform but environmentally heterogeneous, and plant–fungal interactions are strongly shaped by spatio-environmental context. Intense discussion at the 45th New Phytologist Symposium revealed that we lack information on how well spatio-environmental variation within ranges has been considered in samplings and analyses of studies comparing plant–fungal interactions between ranges. Through a systematic review, we assessed the sampling quality of recent biogeographical studies. We found that the majority relied on a limited population sampling within each range, often covering only a small fraction of the species' spatial distribution and macroclimatic niche. Additionally, low similarity between the sampled climatic gradients in the native and nonnative ranges might have introduced false-positive differences across ranges. These sampling deficiencies may undermine the robustness and representativeness of range comparisons, thereby restricting our ability to accurately assess the role of plant–fungal interactions in invasion success. We recommend that future research incorporate broader and more comparable spatio-environmental variation in both ranges, and we provide practical guidelines for improving sampling designs.

[61] Combined ecological transcriptomics and phenomics uncover novel gene functions in Arabidopsis thaliana (15:19)

Presenter: MJEMA, Eneza Yoeli (Martin Luther University)

In *Arabidopsis thaliana*, the functions of only about 30% of genes have been experimentally characterized, partly because many gene functions are difficult to discern under laboratory conditions and might only be relevant under natural environments. Here, we conducted a comprehensive ecological study of Arabidopsis thaliana across natural habitats, integrating detailed phenotypic assessments with extensive transcriptomic analyses. Intensive phenotyping of over 2,500 naturally occurring plants across two distinct, environmentally contrasting habitats and multiple seasons (2021–2024) generated a dataset exceeding 35,000 data points for 9 quantitative traits. By sequencing over 1,000 transcriptomes from these plants, we linked environmental conditions directly to shifts in gene expression and regulatory networks. Leveraging advanced machine learning techniques, we integrated transcriptomic and phenotypic data to predict and experimentally validate novel gene functions. Using petiole length as a proof of concept, a trait highly sensitive to temperature and light cues, our computational predictions accurately identified both known and previously unknown genes influencing this trait, as confirmed by mutant analysis. Extending this approach to all measured traits, we validated the ecological importance of known genes under natural conditions and predicted hundreds of previously unknown gene functions. This integrative ecological genomics approach provides unprecedented insights into gene functions and regulations, offering a powerful framework for discovering critical genes involved in plant development and environmental responsiveness in natural ecosystems.

<u>Biodiversity and the functioning of Ecosystems</u> - Lecture Hall XXIII (16:00 - 17:30)

-Conveners: Robert Rauschkolb; Schwarz, Rike (University Leipzig); Christel, Henriette (iDiv)

[13] Soil food web functions in forests of different dominant mycorrhiza type (16:00)

Presenter: POTAPOV, Anton (Senckenberg Museum of Natural History Görlitz)

Forests dominated by arbuscular- (AMF) and ectomycorrhiza (EMF) differ in their carbon stocks and processes. However, differences in structure and function of higher trophic levels in these forests are largely unexplored. Here I summarise the results of our Emmy Noether project, testing hypothesis that the structure and trophic functions of soil food webs differ between AMF and EMF temperate forests. Using a combination of labelling and natural stable isotope composition analysis, we found different dynamics of particulate and mineral-associated soil organic matter but generally consistent trophic niches of soil invertebrates across the mycorrhiza types (with slightly higher importance of bacteria in EMF). Energy flux distribution varied with mycorrhiza types, suggesting that EMF isolate part of the energy from the food web. Observed functional differences between the soil food webs may explain functional differences between these forest types, which will be tested in the next project step.

[39] The use of plant, bacterial and fungal resources in soil food webs of ecto- and arbuscular mycorrhiza-dominated deciduous forests (16:15)

Presenter: HAUER, Amelie (SMNG)
Soil food webs, driven by complex interactions among plants, microbes and invertebrates, are crucial for carbon and nutrient cycling in forest ecosystems. Over the last decade it has become evident that forests dominated by arbuscular mycorrhizal fungi (AMF) or ectomycorrhizal fungi (EMF) differ in their litter chemistry and microbial community composition, leading to different carbon and nutrient cycling. Still, the role of soil invertebrates in soil food webs of AMF- and EMF-dominated forests remains undescribed. Here, we tested whether trophic positions (TP) and basal resources of nine soil invertebrate groups (Araneae, Chilopoda, Collembola, Diplopoda, Diptera, Isopoda, Lumbricina, Mesostigmata, and Oribatida) are different in AMF- and EMF-dominated deciduous forests. We addressed this question using compound-specific stable isotope analysis of carbon and nitrogen in amino acids (CSIA-AA) – a novel method that allows precise estimation of the TP and basal resource use (bacteria, fungi, plant) of consumers in field conditions. Plant- and microbial-derived resources of soil invertebrates generally varied little between AMF and EMF-dominated forests. We only found a slight tendency of soil invertebrates in AMF-dominated forests relying more on fungal- and more on bacteria-derived resources in EMF-dominated systems. Most of the variation in resource use was explained by the taxonomic identity of invertebrates, independently of the forest type. Mesofauna, particularly Collembola and Oribatida, were key consumers of fungi, while macrofauna (except earthworms) relied more on plant resources, suggesting that different size compartments of soil food webs predominantly use different basal resources. Earthworms and Myriapoda had the highest proportions of bacteria-derived essential amino acids. TPs of taxa remained largely consistent across mycorrhizal types suggesting similar vertical organisation of soil food webs across the studied forests. Overall, our study shows that TPs and basal resource use of soil fauna vary little across temperate deciduous forests, being mainly explained by the faunal taxonomic identity.

[9] Functional and taxonomic shifts in nematode diversity following enhancement of structural β-complexity in forests (16:30)

Presenter: SCHWARZ, Rike (University Leipzig)
Production forests are typically managed to optimize timber production, resulting in even-aged stands with few canopy gaps and little deadwood until the final harvest. This biotic homogenization can reduce biodiversity, with far-reaching consequences for ecosystem functioning and human well-being. To explore strategies that promote biodiversity while maintaining timber production, the BETA-FOR Research Unit investigates the effects of experimentally enhanced structural β-complexity, such as variation in canopy gaps and deadwood, on forest biodiversity. In eight forests across Germany, canopy gaps and various types of deadwood were introduced on 156 plots (each 50 × 50 m). Soils harbor a wide range of organisms, including nematodes, the most abundant metazoans on Earth. Nematodes contribute to numerous ecosystem functions and are widely used as bioindicators. We examine how increased structural β-complexity affects nematode diversity across local (alpha), site-level (gamma), and between-site (beta) scales, considering both taxonomic and functional aspects and using Hill-Chao diversity indices. Results indicate that the functional diversity of nematodes is more broadly affected than taxonomic diversity. For both taxonomic and functional diversity, beta diversity of common and frequent taxa increases in sites where structural complexity was increased. Notably, alpha and gamma diversity of functional traits decrease simultaneously among nematodes. This counterintuitive pattern suggests that, although forest patches become more functionally and taxonomically distinct from one another, they also lose widely shared functional types. This indicates a shift toward more specialized nematode communities in structurally enhanced stands.

[82] How microbial physiological traits and functions shape necromass contributions to soil organic carbon: Insights from the Biodiversity Exploratories (16:45)

Presenter: Dr BI, Qing-Fang
Microbial growth, carbon use efficiency (CUE), and functions are central to biomass accumulation and contribute to organic carbon formation through the persistent microbial residues. However, at the macroscale, mechanistic understanding remains

limited regarding how microbial community diversity, assembly, functions, and physiological traits interact to influence microbial contributions to SOC persistence. Here, within the Biodiversity Exploratories framework, we present integrated findings on how land use intensity and changes in above- and belowground biodiversity, together with associated environmental setting, affect microbial resource acquisition capacity, physiological traits, and their roles in microbial-derived C in soil organic carbon (SOC) storage in the topsoil (0-10 cm) of grassland and forest soils across three distinct regions in Germany. Our preliminary results reveal a decoupling between CUE and necromass persistence, and show distinct mechanisms underlying the general concepts of necromass contributions to SOC storage. In temperate forests, we found positive loops of microbial diversity on specific growth, CUE, and necromass-derived C in SOC, particularly for bacteria. In contrast, intensively managed grasslands exhibited higher microbial biomass, growth rate, and CUE, potentially leading to more efficient necromass recycling, which in turn results in lower microbial-derived carbon in SOC. We would like to discuss how different microbial communities within a range of physiological states, may exert profoundly different effects on soil carbon cycling, potentially mediated by community compositions and activities. Overall, we aim to disentangle the roles of environmental setting and different microbial communities as drivers of key microbial traits and functions that influence the persistence of microbial-derived SOC, which is shaped by land use intensity and biodiversity loss.

[72] Bursting with Potential: The Dual Role of Prophages in Gene Flow and Carbon Cycling (17:00)

Presenter: Dr GHANEM, Nawras (1Helmholtz Centre for Environmental Research – UFZ, Department of Applied Microbial Ecology, Permoserstrasse 15, 04318 Leipzig, Germany)

Prophages are integrated forms of phages (i.e. viruses that infect bacteria) within bacterial genomes. Beyond their role in horizontal gene transfer, prophages can carry genes that influence host metabolism and community function. They can be maintained in the host genome over generations, but they can also shift into a lytic cycle under environmental stress. This transition results in host cell lysis and the production of new viral particles, but also releases dissolved organic matter (DOM), which can be utilized by other microorganisms and influence biogeochemical cycling. This dual role in gene dissemination and carbon mobilization is particularly important in heterogenous groundwater environments, yet our understanding of prophage prevalence, activity, and function in such systems remains limited. In this study, 140 bacterial isolates from oxic and anoxic groundwater wells were evaluated for prophages, their genetic repertoire and their induction. Prophage induction resulted in host lysis and the release of viral-like particles in 37 isolates. Whole genome sequencing and analysis of these bacterial genomes revealed 118 prophage contigs, which could be grouped into 58 unique viral clusters (vOTUs). Some of these vOTUs were shared across different wells and, notably, between single isolates of the genera Pseudomonas and Azospirillum. Prophage gene analysis revealed redox-associated patterns, with lysis-related genes being enriched under anoxic conditions, and regulatory and capsid/head genes being more abundant under oxic conditions. Additionally, bacterial isolates from oxic wells harbored a higher number of auxiliary metabolic genes (AMGs) per genome. DOM released during prophage induction was analyzed via DI-MS. This approach identified 993 molecular species showing significant post-induction changes. While 39% of these molecular species were linked to host-specific traits, 3% were directly attributable to phage induction. These findings expand our understanding of how redox conditions potentially influence viral-mediated modulation of host metabolism, microbial adaptation and nutrient cycling in subsurface ecosystems.

[6] Drivers of foliar fungal endophyte communities in subtropical forests (17:15)

Presenter: DROST, Tibor

The phyllosphere comprises the tissues and the surface of plant leaves and their microbiomes. Despite its ecological significance, the factors shaping foliar endophyte communities and their interactions with trees and shrubs remain largely unexplored. Here we use the biodiversity-ecosystem functioning (BEF) research platform BEF-China, where trees were planted in a broken-stick design along a tree diversity gradient. The aim of this study is to elucidate the composition of fungal and bacterial communities in the phyllosphere of shrubs, as a function of tree diversity in the local neighbourhood, and to disentangle the underlying drivers, such as leaf traits of the host tree, direct spillover effects of microbes from heterospecific neighbours and negative density effects of conspecific neighbour species, as well as indirect effects of neighbour tree composition via microclimate. Using leaf surface sterilization followed by next generation sequencing, the Internal Transcribed Spacer 1 (ITS1) rRNA gene region and the 16S rRNA gene region were analysed for fungal and bacterial communities, respectively. We hypothesized that [H1] the removal of epiphyllous microbes through surface sterilization has a major influence on the microbial community structure of the phyllosphere, because of a prevalence of microbes on the outside of the leaves. Furthermore, we expected that [H2] the tree neighbourhood diversity has a strong effect on the foliar microbial community composition and diversity, due to spillover and dilution effects. Finally, we expect that [H3] neighbourhood tree species richness increases the stability of the microclimate for shrubs, due to a denser canopy and increased structural diversity. There was evidence in support of all our three hypotheses, which reveals the complex interplay of different drivers in phyllosphere community assembly, which directly or indirectly depend on the local diversity of host trees.

[54] MiCoDa: the Microbial Community Database (17:17)

Presenter: JURBURG, Stephanie (Helmholtz Center for Environmental Research)

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

[98] Stomatal regulation across 38 tree species as a window into water-use strategies under climate change (17:18)

Presenter: SACHSENMAIER, Lena

Climate change is increasing the frequency and severity of droughts, leading to widespread tree mortality and growth reductions in forests. Yet, it remains unclear how different tree species regulate water loss under changing environmental conditions. Stomatal conductance (gs), which quantifies the ease with which gases diffuse through stomatal pores of leaves, plays a crucial role in mediating the balance between carbon assimilation and water loss. Understanding variation in stomatal control across species and how it relates to other tree traits is essential for characterising water-use strategies and relating them to drought tolerance or avoidance strategies. In this study, we investigated stomatal regulation patterns of 38 temperate tree species at the research arboretum ARBOfun (Großpösna, Germany). We measured diurnal stomatal conductance in three tree individuals per species (27 angiosperms, 11 gymnosperms) under well-watered conditions in summer 2024. Based on these data, we modelled stomatal conductance as a function of air vapor pressure deficit (VPD) and derived physiological parameters for each species as proxies for stomatal sensitivity, including the VPD at maximum stomatal conductance and the VPD at the curve’s inflection point. We are currently analysing how these physiological traits relate to more commonly measured leaf traits, and exploring the extent to which stomatal control reflects species-specific water-use strategies and drought-related growth performances. The results of this study will help clarify how diverse tree species regulate water use under drought, supporting more accurate predictions of forest vulnerability and resilience in a changing climate.

[27] Prospects for virus research in natural terrestrial ecosystems (17:19)

Presenter: Mrs ZUEVA, Anna (Senckenberg Museum of Natural History Görlitz, Soil Zoology Department)

Viruses are exceedingly numerous and diverse biological objects. Though for a long time viruses have been studied in terms of their medical and economic importance, now interest to their ecological role in terrestrial ecosystems is growing. Currently, the main areas of research on viruses in terrestrial ecosystems include - viruses of medical, veterinary, and agricultural importance causing diseases and economical loses (Andret-Link, Fuchs, 2005; Wille, Holmes, 2020); - viral agents of biological control of pests (Kalawate, 2014); - virus-induced behavioral changes in interactions of hosts with other individuals and with the environment (Hsu et al., 2019); - effects of viruses on shaping flows of matter and energy in food webs (Williamson et al., 2017). Besides being entities of medical, ecological and economic importance, viruses are also sources of molecular data clarifying processes of viral and cellular evolution and the history of virus-host interactions (Manrubia, Lázaro, 2006). In addition, merging the data on viruses’ diversity and distribution in terrestrial ecosystems and food-webs’ topography, it is potentially possible to make a new use of viral data for clarifying food-webs’ and ecosystems’ structure and functioning. Andret-Link, P., Fuchs, M. (2005). Transmission specificity of plant viruses by vectors. Journal of Plant Pathology, 153-165. Hsu, H.W. et al. (2019). The association between virus prevalence and intercolonial aggression levels in the yellow crazy ant, *Anoplolepis gracilipes* (Jerdon). Insects, 10(12), 436. Kalawate, A.S. (2014). Microbial viral insecticides. Basic and applied aspects of biopesticides, 47-68. Manrubia, S.C., Lázaro, E. (2006). Viral evolution. Physics of Life Reviews, 3(2), 65-92. Wille, M., Holmes, E.C. (2020). The ecology and evolution of influenza viruses. Cold Spring Harbor perspectives in medicine, 10(7), a038489. Williamson, K.E. et al. (2017). Viruses in soil ecosystems: an unknown quantity within an unexplored territory. Annual review of virology, 4(1), 201-219.

Biodiversity Change - Audimax (16:00 - 17:34)

-Conveners: Hoss, Daniela (Uni Leipzig, iDiv); Georg Johannes Albert Hähn

[57] Life in the City: Integrating Citizen Science and Molecular Approaches for Understanding Arthropod Responses to Anthropogenic Change (16:00)

Presenter: BOSCH, Maya

Urbanization is a major driver of biodiversity loss, with arthropods—critical to ecosystem functioning—facing significant declines in biomass and abundance as cities expand. Previous studies showed that while all insect groups are declining in abundance not all species are declining in regards to biomass. A variety of biotic and abiotic factors have a different impact on different species based on their way of life. This explains why some species are able to gain in biomass and geographic occurrence while others disappear completely. In this project we looked at urban arthropod communities and how urbanisation (measured as impervious surface), temperature and moisture impacted them while simultaneously developing new molecular methods for non-destructive DNA extraction from tapping liquid that can be easily integrated into citizen science projects. The citizen scientists (local schools and pupils) participated in sample collection, ecological data recording, and arthropod identification. Engaging local communities in conservation efforts is essential in creating urban habitats for arthropod communities. We found that that urbanization had a significant negative impact on arthropod biodiversity, while abundance showed a negative, if non-significant trend. The impact of temperature and moisture differed between the taxonomic groups suggesting different requirements of abiotic factors. Molecular analyses demonstrated successful DNA extraction from preservative liquid, though as expected, DNA concentrations were lower than destructive bulk methods. Finally, this project provided ecological insights into how urbanization negatively affects arthropod communities and the benefit that unsealed areas would provide to local biodiversity, while also motivating children to be active participants in research, engaging them in biodiversity and teaching them about the scientific process.

[70] Landscape composition and community context as drivers of wild bee body size in agriculturally dominated landscapes (16:15)

Presenter: WILD, Bilyana (Martin Luther University Halle-Wittenberg, German Centre for integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)

Understanding how global change drivers influence the functional traits of wild pollinators is critical for predicting ecological responses and guiding conservation strategies. Among these traits, body size plays a central role in bee ecology, affecting dispersal ability, foraging range, reproductive success and ecological interactions. However, the extent to which anthropogenic disturbances, such as agricultural intensification, climate variation and changes in community composition, shape body size patterns in wild bee populations remains underexplored. In this study, we investigate body size as a key response trait across more than 5,000 individuals from 10 wild bee species, sampled at multiple sites across agriculturally dominated landscapes in Saxony-Anhalt, Germany. Using a trait-based and community-ecological framework, we examine how body size variation relates to gradients in land-use intensity, temperature and community-level metrics such as species diversity, evenness and abundance. By integrating trait and community data, our work seeks to uncover how both abiotic and biotic factors jointly influence body size variation within and across species. This framework contributes to a deeper understanding of ecological filtering and competition in shaping bee trait dynamics under global change.

[35] Long-Term Plant Phenology Trends in Hustai National Park, Mongolia (16:30)

Presenter: VINCZE, Anna

Mongolia is increasingly affected by climate change, particularly through rising average temperatures and altered precipitation patterns. Plant phenology, which is highly sensitive to these climatic factors, serves as an important indicator of ecological responses to climate change. While remote sensing studies have revealed a lengthening of the growing season - marked by earlier onset and later end dates - species-specific phenological responses in Mongolia remain largely unstudied. To address this gap, we conducted a 12-year study in Hustai National Park, monitoring plant phenology of seven focus species across seven sites. In addition to analysing how changes in temperature and precipitation affect phenology, we measured plant functional traits related to competition and growth rate - canopy height, plant width, aboveground biomass, chlorophyll fluorescence, and specific leaf area - over two consecutive years to assess their influence on phenological patterns. While data analysis is still ongoing, preliminary results indicate an earlier start and a later end of growth in most species, suggesting an overall extension of the growing season. In contrast, the onset of flowering shows no significant change over time, while the end of flowering occurs earlier. At the same time, spring temperatures tend to increase while spring precipitation decreases. In contrast, summer temperatures remain stable, but summer precipitation shows an increasing trend. Although final analyses are still pending, the initial results indicate that temperature, rather than precipitation, is the primary driver of the onset of the growing season. The final results of this study will provide insights into the key climatic drivers influencing plant phenology in Mongolian steppe ecosystems and the extent of their impact. Additionally, the study will reveal the degree to which functional traits determine species-specific phenological responses to changing climatic conditions.

[101] Integrating taxonomic, phylogenetic, and functional diversity to promote the conservation of Brazilian Campos Rupestres: Velloziaceae as a model (16:45)

Presenter: CABRAL, Andressa (Leipzig University (UL) / German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)
The Brazilian *Campos Rupestres* (CR), ecosystems primarily found on mountaintops and high plateaus, harbor exceptional plant species richness, endemism, and functional diversity. Their unique combination of environmental conditions, e.g. shallow and nutrient-poor soils, high temperatures, intense solar radiation, water scarcity, and natural fire regimes, has potentially driven the evolution of multiple functional strategies in their flora. Besides the effects of climate change on mountain biodiversity, the CR already faces serious threats from human activities, such as tourism, mining, increased fire frequency, and the spread of exotic species. Given this scenario, integrative studies combining spatial, phylogenetic, and functional trait data are essential to elucidate the mechanisms behind the maintenance of diversity and to anticipate future scenarios, thus guiding more effective conservation strategies. Velloziaceae stands out as an ideal model to investigate these processes. With around 260 species concentrated mainly in the Espinhaço Range, the family shows high levels of microendemism and functional diversity. Here, we compiled spatial, morpho-functional, and phylogenetic data, evaluated species sampling trends, and estimated the effects of simulated species extinctions on patterns of taxonomic, functional, and phylogenetic diversity in the two largest genera of the family: *Barbacenia* Vand. and *Vellozia* Vand. Our analysis of potential sampling bias revealed a correlation between species occurrence and proximity to roads. Rarefaction curves indicate a continuing potential for species discovery, especially within the Cerrado and Caatinga domains, pointing to opportunities for further exploration. Comparative analyses between current and future scenarios revealed significant reductions in functional richness and originality, as well as phylogenetic diversity, with paired tests indicating negative median and mean differences across metrics. In addition, kernel density hypervolume analyses showed that nearly 50% of the current functional trait space may be lost. Our findings highlight the vulnerability of CR ecosystems to biodiversity loss and emphasize the urgency of targeted conservation actions.

[43] Managing Oak Regeneration under Canopy Decline: The Role of Understorey Competition and Drought Stress (17:00)

Presenter: LENK, Annalena (Systematic Botany and Functional Biodiversity, Leipzig University, Johannisallee 21, 04103 Leipzig, Germany)
The regeneration of pedunculate oak (*Quercus robur* L.), a light-demanding tree species crucial for Central European forest biodiversity, is hindered by homogenised, shaded conditions of dense forest stands. However, rising tree mortality caused by climate extremes and pathogens may provide a window of opportunity for oak regeneration. In the meliorated Leipzig floodplain forest, we investigated how recent canopy dieback affects understorey structure and microclimate, and whether this could facilitate oak regeneration. Over two years, we monitored planted oak saplings and recorded microclimatic air and soil conditions under varying canopy cover resulting from tree mortality. These conditions were studied with and without small-scale understorey thinning of flood-intolerant tree species (16 × 16 m), and compared to silvicultural cuttings of up to 0.7 ha. High tree mortality in the overstorey alone did not create favourable conditions for oak regeneration, as fast-growing, shade-producing maple species further limited light availability in the understorey. The combination of high mortality in the overstorey and removal of flood-intolerant maples in the understorey enhanced the growth and vitality of planted oaks. While increased light availability generally promoted oak development, this effect was weakened under increasing drought stress, as indicated by leaf carbon isotope ratios ($\delta^{13}C$). We found that soil moisture tended to be higher on silvicultural cuttings than in the forest. However, air humidity was lower, and vapour pressure deficit (VPD) emerged as the strongest microclimatic predictor of drought stress. Our results suggest that small-scale, selective interventions offer a promising strategy to support pedunculate oak regeneration under changing environmental conditions, by improving both light and microclimatic conditions compared to dense stands or larger cuttings. The study underlines the need for adaptive management as a complement to hydrological revitalisation measures in order to maintain biodiversity and ecosystem functions of floodplain forests.

[42] Comparative Analysis of Microbial Communities in the Global North and South: Exploring the Interplay between Data Availability and Mechanisms of Community Assembly Across Biomes (17:15)

Presenter: ARBOLEDA, Clara (German Centre for Integrative Biodiversity Research (iDiv))
Bacteria are the most diverse and widespread organisms on Earth, playing essential roles in the ecosystems they inhabit. Despite advances in sequencing technologies, most bacterial diversity studies have focused on the Northern Hemisphere, leaving significant data gaps in the Global South, particularly in regions that face high risks of biodiversity loss due to human activity. The sIBTEDs project aims to address these gaps by promoting equitable data reuse through Datathons and training events across the Global South. Microbiome data collected through this initiative was combined with existing datasets to create the most

comprehensive microbiome record of Latin America to date. Leveraging this dataset, we pursued two main goals. First, we assessed how data blindspots affect biodiversity estimates, comparing patterns of microbial diversity between the Global South and North using balanced sampling. Second, we analyzed how human pressures impact microbial diversity and community homogenization, comparing soil and aquatic microbiomes. This work bridges existing gaps in microbial data while providing valuable insights into the patterns and processes that govern microbial diversity, enriching our understanding of ecosystems at a global scale, contributing to global biodiversity research.

Molecular Biodiversity and Evolution - Lecture Hall XXII (16:00 - 17:30)

-Conveners: Gerth, Michael (German Centre of Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Martin Luther University Halle-Wittenberg)

[58] Tiny genomes, hidden patterns – bacterial symbionts in insects (16:00)

Presenter: MANTHEY, Christin (Max Planck Institute for Chemical Ecology)

Insects are home to a vast diversity of microbial communities, among which bacterial symbionts play a crucial role in host physiology, ecology, and evolution. They profoundly influence insect nutrition, immunity, and reproduction. Over millions of years of host association, many symbionts have undergone extensive genome reduction. This process - marked by the loss of genes unnecessary in the stable host environment - offers a powerful model for studying genome streamlining and the functional integration of microbes into host biology. A key question is: what constitutes the minimal gene set that enables symbionts to persist and function within their hosts? This study addresses that question by analyzing the genomes of 423 bacterial symbionts across a wide range of insect hosts and symbiotic relationships - spanning facultative associations, obligate mutualisms, manipulators, and pathogenic interactions. Using comparative genomic approaches, we identify core genes and pathways conserved across symbionts. We also examine how these minimal gene sets vary with factors such as symbiont localization (e.g., intracellular vs. extracellular) and the type of host interaction. These findings reveal underlying patterns in the evolution of minimal yet functional symbiont genomes and contribute to a deeper understanding of how microbial life adapts to long-term, intimate associations with animal hosts.

[79] What doesn’t kill you makes you…more diverse? The microbiome of wild, wounded Drosophila melanogaster investigated using metabarcoding and oxford nanopore sequencing. (16:15)

Presenter: PREUSS, Leopold (Martin-Luther-Universität Halle-Saale, iDiv)

Wounding occurs in all animals, including even tiny, often overlooked insects such as *Drosophila melanogaster*. Wounds can have diverse impacts on the animal’s fitness and ecology, such as the potential introduction of microbial symbionts which may act as pathogens, commensals or mutualists. Lab experiments demonstrated that the microbiome of *Drosophila melanogaster* influences their fitness and behaviour, while *Drosophila* itself possesses genes supporting the acquisition of beneficial microbes through immune response suppression. The microbiome of *Drosophila* flies under natural conditions was shown to be linked rather to its diet and the microbial community of its surrounding, rather than being associated with taxonomy. Despite the frequency of wounding of *Drosophila melanogaster* in the wild (approximately 31 %), the impact which microbes have on their hosts and the extensive research on insect-bacterial symbioses using *Drosophila melanogaster* as a model organism in the lab, it remains unclear how wounding contributes to the microbiome composition of these flies in the wild and how the native microbiome of insects responds to and is altered by introduced bacteria. Lastly, it is unknown if wounding leads to the introduction of mostly pathogenic, mutualistic or beneficial symbionts. Using over 1,000 *Drosophila melanogaster* specimen which have been meticulously scored on wounding status and type, we conducted bacterial 16S metabarcoding through affordable in-house oxford nanopore sequencing to identify differences in diversity and composition of those microbial communities with regards to their wounding status and sex and aim to taxonomically and ecologically characterize the microorganisms which are likely to be introduced through wounds. Furthermore, we tested whether COI barcoding was sufficient to detect encapsulated parasitoids in the flies bodies.

[63] Integrating Global Litter Decomposition Assays and Metagenomics to Map Soil Microbial Decomposition Potential Across Ecosystems (16:30)

Presenter: Dr SINGAVARAPU, Bala (iDiv, FSU)

Plant litter decomposition plays a pivotal role in nutrient recycling within soils, especially in ecosystems like grasslands and forests, which together span nearly 70% of the Earth's terrestrial surface. Despite its importance, the variation in microbial genomic capabilities for decomposing litter across these ecosystems remains insufficiently characterized. Through the

International Soil Biogeography Consortium (iSBio), we combined insights from soil microbial metagenomics with decomposition measurements across broad environmental gradients. Utilizing data from over 350 sites participating in the TeaComposition initiative and 314 soil metagenomic assemblies, we investigated European grasslands and forest systems. Our analysis revealed 96 carbohydrate-active enzyme (CAZyme) families and 2,628 subfamilies associated with the breakdown of lignin, pectin, cellulose, and hemicelluloses. Among these, 297 subfamilies from Auxiliary Activities (AA), Glycoside Hydrolases (GH), Carbohydrate Esterase (CE), and Polysaccharide Lyases (PL) groups exhibited significant differences ($p < 0.05$) in relative abundance among grasslands, broadleaf, and coniferous forests. Coniferous forests displayed the highest gene abundances for these pathways, followed by broadleaf forests and grasslands, a trend consistent with CAZyme diversity metrics and observed litter decomposition rates. Taxonomic analyses indicated dominant contributions from Acidobacteriota and Actinomycetota in early-stage degradation, whereas Pseudomonadota were more involved in downstream steps. Basidiomycota were more prominent in forested sites, especially during the initial phases of decomposition. Furthermore, protein sequence analyses revealed signatures of ecosystem-specific genomic adaptations in CAZymes. Variability in microbial functional gene profiles was strongly linked to soil characteristics such as pH and carbon-to-nitrogen ratios, as well as climatic variables like temperature and precipitation, jointly explaining 65% of the observed patterns. Our findings highlight the value of combining microbial genomic data with standardized, global-scale decomposition experiments to better model soil nutrient dynamics across ecosystems.

[14] Correcting the Molecular Bias: Optical High Throughput and Gene Copy Number Calibration for Realistic Protistan Abundance Estimates (16:45)

Presenter: Dr MÖBIUS, Nadine (FSU Jena, Institute of Biodiversity, Ecology and Evolution, German Center for Integrative Biodiversity Research (iDiv) Halle Jena Leipzig)

Protists are key players in microbial food webs, yet their role in groundwater ecosystems remains understudied—partly due to limitations in quantifying their abundances using molecular methods. A major challenge lies in the highly variable number of 18S rRNA gene copies across taxa, which can lead to a drastic overestimation of the quantitative role of specific taxa in protistan communities. We present an integrated approach that combines Multispectral Imaging Flow Cytometry, qPCR, and 18S rRNA gene amplicon sequencing to improve the quantification and characterization of protistan communities. Protistan monocultures ranging from 3 to 60 µm in size were used to build a reference image library for convolutional neural network-based classification, achieving over 85% recognition precision. This enables not only automated counting but also the potential observation of feeding events. However, image-based classification is limited to trained taxa and cannot capture the full diversity of natural groundwater communities. To identify potential key players beyond the reference set, molecular data remain essential. To account for the high variability in gene copy numbers, however, we defined taxon-specific correction factors. For instance, Ciliophora isolates harbored on average 5.4×10^3 (*Glaucoma sp.*) or 7.9×10^5 (*Colpidium sp.*) 18S rRNA gene copies per cell, while the cercozoan *Cercomonas sp.* contained only 1.5 × 10¹ copies per cell. This emphasizes the need for taxon-specific correction factors in molecular community analyses to avoid overestimations spanning several orders of magnitude. Our approach provides a framework for more realistic protistan abundance estimates in groundwater where small flagellates such as Cercozoa may dominate trophic interactions. In turn, the ecological role of ciliates may be far less prominent than suggested by uncorrected molecular data. This altogether allows for a more accurate assessment of the groundwater food web structure.

[102] Comparative landscape genetics of grassland insects reveals that ecotones, and to a lesser degree landscape-scale meadow management, support genetic diversity in agricultural landscapes (17:00)

Presenter: WILD, Christopher (Martin Luther University Halle-Wittenberg, Naturkundemuseum Erfurt)

Habitat loss and agricultural intensification are considered major drivers of insect biodiversity decline, yet their impacts on insect genetic diversity remain insufficiently understood. This study investigates how human land-use practices, particularly the role of extensively managed meadows, affect insect genetic diversity to inform conservation strategies in fragmented agricultural landscapes. Using a comparative landscape genetics approach, we evaluated how land-use composition and configuration influence genetic diversity and population structure in three grassland insect species, *Polyommatus icarus* (common blue butterfly), *Melanargia galathea* (marbled white butterfly) and *Conocephalus fuscus* (long-winged conehead grasshopper), across a heterogeneous landscape of protected areas, extensively managed meadows, intensively managed grasslands and agricultural fields in southern Germany. Genome-wide SNP data using reduced-representation sequencing (NextRAD) from 404 individuals sampled at 16 extensively managed meadow sites revealed pronounced interspecific differences. *Polyommatus icarus* exhibited the lowest genetic diversity and weakest population structure, likely reflecting its high dispersal capacity, while *M. galathea* showed intermediate levels of both and *C. fuscus* displayed the highest genetic differentiation and strongest structure. Genetic diversity in *P. icarus* and *M. galathea* showed a positive trend with the proportion of extensively managed meadows. In addition, edge density was positively correlated with genetic diversity in *M. galathea* and *C. fuscus*, indicating that fine-scale habitat configuration promotes higher population densities and gene flow for less mobile species. Additionally, isolation by distance was detected only in *M. galathea*, indicating species-specific responses to spatial patterns. Our findings emphasize that conservation strategies must go beyond preserving habitat area to focus on spatial configuration and connectivity. Promoting networks of extensively managed meadows and maintaining landscape heterogeneity are crucial for sustaining insect genetic diversity and evolutionary resilience in human-dominated landscapes.

[68] Advancing the phylogenetics on the iconic Andean tree genus Polylepis (Rosaceae) (17:16)

Presenter: OLIVAR, Jay Edneil (Leipzig University)

The culturally and economically significant Andean tree genus *Polylepis*—which forms the world's highest-elevation treelines—has long eluded a well-supported phylogenetic reconstruction, possibly due to extensive gene flow, hybridization, and polyploidization. To address this, we investigate sympatric populations of *P. neglecta* (Bolivia) and *P. incana* (Ecuador) using genomic (ddRADseq) and morphological data. Our goal is to provide empirical evidence for these evolutionary processes and to propose strategies for reconstructing the phylogeny of the genus. We hypothesize that, despite high levels of gene flow and hybridization, species boundaries remain distinct, and that ddRADseq data will provide high phylogenetic resolution.

[89] Unraveling plant-microbe interactions across space, time, and environmental contexts (17:18)

Presenter: Dr BONATELLI, Maria (Martin Luther University)

Microbes play a key role in plant health and development. They inhabit various plant tissues and are present throughout the plant's life cycle. Over this journey through space and time, the microbial composition changes and adapts—this is also true when the plant encounters challenging conditions. Plants can recruit and modulate beneficial microbes; however, we still do not fully understand the mechanisms behind this complex process. Our group has conducted an extensive ecological study in which *Arabidopsis thaliana* plants from contrasting natural environments were sampled over several years. Phenotypic and transcriptomic profiling of the plants was performed. More recently, microbiome profiling was carried out using two complementary approaches: amplicon sequencing and shotgun metagenomics. We are now analyzing this complex dataset to investigate how different plant traits and gene expression patterns impact microbial composition—and vice versa. Preliminary results show that seasonality plays a significant role in shaping the microbial composition of *A. thaliana*. The bacterial community in *A. thaliana* leaves is highly diverse, with many genera (>40%) represented at less than 5% of relative abundance. Nonetheless, *Sphingomonas* is consistently the most abundant genus in many plants across different locations and years. We are now further exploring the fungal community and attempting to recover microbial genomes from the shotgun metagenomic data. Our next step will be to integrate the phenotypic and transcriptomic profiling of the plants with the microbiome data. We hope this will help elucidate some of the mechanisms underlying the complex interactions between plants and microbes in natural environments.

Poster Session - Foyer (17:30 - 19:30)

Guided City Tour: Nachtwächtertour/ The Night Owl (19:30 - 20:30)

Wednesday 1 October 2025

Registration - Foyer (09:00 - 10:00)

Keynote: Prof. Dr. Meredith C. Schuman: Understanding biodiversity integratively across layers of biological organization, and consequences for monitoring and management - Audimax (10:00 - 11:00)

Biodiversity and Society - Lecture Hall XXII (11:30 - 13:00)

-Conveners: Meemken, Marie (Uni Jena); Rozario, Kevin (UFZ / iDiv / Uni Jena / Uni Leipzig)

[50] Pondering about the future: what is the role of science amidst a global polycrisis? (11:30)

Presenter: Dr PE'ER, Guy (UFZ / iDiv, department of Biodiversity and People)
As the globe is experiencing an increasing number of crises, the work of scientists – inter alia at iDiv – d becomes increasingly challenging. We want to understand the world: how species behave, how ecosystems work, and how we humans affect all this. We want our work to be valued and want to be approached for our knowleddge, yet we also have the urge to help address some key elements of the polycrisis. This often requires proactively approaching decision-makers or other societal actors, or jointly calling for action. It also requires addressing mis/disinformation. How can we maintain our role as scientists in delivering balanced knowledge, to serve as honest brokers? How do we address mis/disinformation, and how can we best work together to maximise our impact? Here I bring experiences from several projects (iCAP-BES, CAP4GI, Agroecology-TRANSECT, VielFalterGarten and UNP+), some focusing on European policies (especially the Common Agricultural Policy and the Nature Restoration Regulation) while others focus on people and municipalities, especially through citizen science (butterflies!). I propose that we need to work not only with facts and evidence, but also with emotions and narratives. Therefore, we have much to gain from interdisciplinarity. I conclude with some thoughts of the path we (may) take into an uncertain future, and how to work with scenarios.

[99] The political dimensions of rewilding preference (11:45)

Presenter: Dr DUNN-CAPPER, Rowan (iDiv)
Rewilding has emerged as a prominent strategy for ecological restoration in Europe, yet public support remains uneven and shaped by political values. As debates surrounding the Nature Restoration Law intensify, understanding how political identity influences support for rewilding is increasingly vital. We present findings from a discrete choice experiment (DCE) conducted in the Oder Delta, a transboundary landscape spanning Germany and Poland, to investigate how political affiliation affects willingness to pay (WTP) for rewilding interventions. Our results, based on over 2,000 representative respondents, reveal that while rewilding garners support across the political spectrum, both the probability of supporting interventions and the magnitude of WTP vary systematically with party affiliation. In both countries, supporters of left-leaning and pro-EU parties exhibit significantly higher WTP for rewilding landscapes and restoring ecological connectivity. Interestingly, support for the reintroduction of large animals—including bison and wolves—remains relatively strong across ideological divides, suggesting certain rewilding elements transcend partisan boundaries. Voting preference explains a greater share of preference heterogeneity than traditional socio-demographic variables, such as age or education. However, geographic proximity also plays a key role, especially in Germany, highlighting the importance of local context. Notably, voters of economically conservative parties in Germany and Eurosceptic parties in Poland were more likely to reject rewilding scenarios, often selecting the status quo alternative. These findings highlight the politicized nature of rewilding support and underscore the need for politically nuanced, socially inclusive policy design. As rewilding becomes more embedded in European policy, navigating ideological fault lines will be crucial to implementation success. Our study demonstrates the value of combining ecological ambition with political awareness in fostering public support for large-scale nature recovery.

[2] Seawilding: Integrating Transdisciplinary Approaches and Lessons from Terrestrial Rewilding to Restore Marine Ecosystems (12:00)

Presenter: STARK, Gavin (iDiv/MLU)
Seawilding, the large-scale restoration of marine ecosystems, presents significant potential for biodiversity enhancement and improved ecosystem services but faces unique challenges compared to land-based rewilding initiatives. Our study provides a first

comprehensive analysis of marine rewilding by integrating its ecological, socio-economic, and governance perspectives. We examine the benefits of restoring biodiversity through targeted species reintroductions and habitat restoration while critically assessing implementation complexities. These complexities include financial constraints, monitoring limitations, and the necessity for adaptive management strategies. We highlight the crucial role of transdisciplinary collaboration and community engagement in achieving successful and sustainable rewilding outcomes. We emphasize the importance of aligning marine rewilding initiatives with broader policy frameworks to facilitate large-scale restoration and achieve wider conservation goals. Our study underscores the need for a holistic approach that effectively balances ecological considerations with socio-economic factors and robust governance structures to maximize the positive impacts of marine rewilding

[29] Dasgupta meets Nordhaus: Optimal Climate and Conservation Policy under Ecosystem Capital Dynamics (12:15)

Presenter: WIESE, Malin (Leipzig University)

Interactions of human economic development with the climate system and ecosystems in the biosphere caused the twin crisis of climate change and biodiversity loss. In this paper, we contribute to addressing the challenge of quantifying socially optimal climate policy in a world with atmosphere-biosphere interactions by combining the work of two influential economists: Partha Dasgupta and Bill Nordhaus. Specifically, we include nonlinear ecosystem capital dynamics inspired by the Dasgupta Review on the Economics of Biodiversity in a recently updated DICE model to study the effects on the optimal level of ecosystem capital, economic growth, the social cost of carbon, and the social value of nature. Our results, which are robust to changes in key parameter specifications, indicate the need for more ambitious climate policy to limit damages to ecosystem capital. We also highlight the role of reducing natural resource use and waste to let ecosystems regenerate and foster the creation of co-benefits for climate mitigation through nature-based carbon removal.

[44] Social norm perceptions and support for sustainable agricultural practices and nature protection (12:30)

Presenter: MARTINI, Christina

In this paper we analyze the role of social norms regarding sustainable agricultural produce and nature protection in sustainable behavior. For this purpose, we conduct a survey and two experiments, a discrete choice experiment and a dictator game, with a representative sample of German residents. In a second data collection we test the effect of an information intervention – using information on social norms from the first wave – on the behavior in the experiments. The data collection is currently on-going, but results should be available until Mid September.

[24] Features that enable socio-ecological transformative change for biodiversity (12:45)

Presenter: KLEEMANN, Janina (Martin Luther University Halle-Wittenberg, iDiv)

Social-ecological transformation is needed to face today´s global envionmental and socio-economic changes without loosing essential parts of biodiversity. However, the initiation, promotion and support of social-ecological transformation for the conservation and restoration of biodiversity still needs to be further explored. In this study, 22 projects and processes were analysed in Germany that improve biodiversity and provide benefits for society. According to the framework on transformative change provided by Wittmer et al. (2021), the following topics were analysed: a) transformative vision, b) transformative knowledge, c) transformational dynamics, d) emancipation and agency, and e) transformative governance. In total, 16 features, enabling transformative change for biodiversity were indetified, many of which may be applicable in other countries with similar governance context. These 16 features will be shown as poster at the iDiv Conference.

[77] Taxonomic description patterns of major lineages are related to author numbers, body size, distribution, and public interest (12:47)

Presenter: SCHELLENBERGER COSTA, David (iDiv Halle-Leipzig-Jena, Leipzig University)

Taxonomic description patterns illustrate how the rate of new descriptions within taxonomic groups changes over time. This study combines description dates, phylogenetic information, and author numbers for all eukaryotic life on Earth from LifeGate, alongside occurrences from GBIF, public interest data from the Biodiversity in Literature project, and habitat preferences and body size data from Wikipedia. We fitted curves to the description patterns and estimated maximum description pace, the time to reach 10% of current diversity, expected total diversity, and variance between the empirical and fitted data. We created a structural equation model linking these variables, revealing strong support for the influence of body size and public interest, mediated by the number of authors, and to a lesser extent, other variables. Our results provide evidence for the effects of traits, distribution, and public interest on description patterns across all major lineages of eukaryotic life on Earth.

[80] Business for Biodiversity: T-Labs for social-ecological change (12:50)

Presenter: KALUSCHE, Jan Bernhard (UFZ, iDiv)
The new EU sustainability reporting requirements require companies to evaluate and reveal their impact on nature, in particular on biodiversity, as well as the associated risks and opportunities. While these regulations aim to promote accountability and environmental responsibility, they pose significant challenges for small and medium-sized enterprises (SMEs), which often lack the necessary resources and structures. Against the backdrop of ongoing political debates about the scope and feasibility of such reporting frameworks, there is an increasing demand for practical, science-based support to help SMEs navigate this evolving landscape. In the interdisciplinary Business for Biodiversity research project, we work closely with SMEs in the German food sector to help them overcome these challenges. Together with these companies, we explore how biodiversity impacts can be assessed and how practical, science-based measures can be developed and implemented to promote biodiversity-friendly business practices. A central element of this effort is the creation of Transformation Labs (T-Labs), collaborative learning spaces where researchers and employees co-develop company-specific solutions. From a natural science perspective, we plan to systematically review existing tools, data sources and indicators for assessing corporate impacts on, and dependencies on, biodiversity. This will include comparisons of major biodiversity footprint accounting approaches, as well as different methods for identifying biodiversity-related risks and opportunities. Global and regional geospatial analyses will be carried out in close collaboration with participating companies to examine which biodiversity-relevant data is already available, identify gaps and explore how this data can be used to support practical biodiversity reporting. By linking scientific knowledge with practical application, the project aims to encourage SMEs to engage more actively with biodiversity-related challenges, and to develop feasible approaches together for improved biodiversity reporting and action.

Biodiversity and the functioning of Ecosystems - Lecture Hall XXIII (11:30 - 13:00)

-Conveners: Schwarz, Rike (University Leipzig); Christel, Henriette (iDiv); Robert Rauschkolb

[16] Space-for-Time substitution to study phenological shifts in herbaceous species is most reliable for early-flowering species (11:30)

Presenter: RAUSCHKOLB, Robert
Phenological events in plants are shifting worldwide due to climate change. By studying long-term shifts of phenological events in plants using historical data records, scientists gain a deeper understanding of potential further changes. However, conducting such Time-for-Time Substitutions (TFTS) remains sparse due to limited availability of long-term data. An alternative method is the Space-for-Time substitution (SFTS), in which the temporal gradient is reflected by a spatial gradient. For this study, we used historical phenological records of 17 herbaceous species from botanical gardens in Vienna covering a period of 150 years and data from 11 botanical gardens covering a large spatial gradient to test the space-time equivalence. This is necessary to ensure that SFTS are applied reliably. We fitted a linear-mixed effect model to test for differences between the two approaches while analysing the associations between annual flowering onset dates and temperature. Additionally, we used a meta-analytical approach to examine species-specific suitability of SFTS in regard of the species' temporal niches. We showed that the space-time equivalence is fulfilled for the present species and spatial gradient and found that for both approaches, flowering was advanced by 7 days when the temperature increased by 1°C. On the species level, however, we found that the known connection that early-flowering species are more temperature-sensitive cannot be confirmed for the SFTS dataset. Furthermore, the space-time equivalence is better fulfilled for early-flowering species than for late-flowering ones. This study contributes significantly to phenological research, as it demonstrated that SFTS can be generally applied for herbaceous species monitored in botanical gardens. However, this method should always be used with caution for species-specific questions. In addition, it still remains unclear to what extent the patterns found can be confirmed in less-controlled habitats.

[55] Floral vs. vegetative structure fingerprints identified by terrestrial laser scanning intensity (11:45)

Presenter: MORA, Karin (Institute for Earth System Science and Remote Sensing, Leipzig University)
Partitioning biomass and functions such as effective separation between leaf (green part) from floral part of plant communities allows a more accurate estimation of photosynthetic vs. reproductive investment. Particularly facing the rise in global temperatures due to climate change, plant communities alter their metabolism, growth, and gas exchange, ultimately affecting functional traits. Local-scale predictions of ecosystem risks require high-resolution monitoring of these responses. However, field sampling of plant functional traits detecting early signals of climate impact remains labor-intensive, hence necessitating scalable methods that

automatize the detection of reproductive vs. vegetative structures. Proximal sensing, particularly terrestrial laser scanning (TLS), offers a promising solution by enabling non-destructive, high-resolution 3D scans of vegetation capturing plant intensities and complex architecture. A key TLS output, intensity—the strength of the backscattered laser signal—reflects surface properties and may serve as a functional and phenological trait. We tested this hypothesis by measuring TLS intensity in four plant species (Lotus corniculatus, Plantago lanceolata, Plantago media, and Trifolium pratense) under controlled greenhouse conditions (TraitComic Experiment). Each species exhibited a distinct intensity fingerprint, with further differentiation between floral and vegetative structures. Floral intensity patterns correlated with geometric shape and volume, suggesting a link to phenological traits. Our findings demonstrate that TLS-derived intensity data at 1550nm alone can discriminate species-specific and phenological features, providing a basis for upscaling to natural grasslands. By linking these signatures to ecosystem functional traits (e.g., water use efficiency, carbon dynamics), TLS intensity could enhance climate resilience assessments. This approach bridges high-resolution remote sensing with ecological trait analysis, offering a scalable tool for biodiversity monitoring under climate change.

[30] How pollen traits are shaped by aerodynamic and vegetative constraints in anemophilous plants (12:00)

Presenter: HORNICK, Thomas (Helmholtz-Centre for Environmental Research (UFZ) Department of Physiological Diversity, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)

The dispersal potential of pollen influences gene flow within and between plant populations impacting on processes such as local adaptation, speciation and long-term survival of metapopulations. However, our knowledge on physiological trade-offs (e.g. pollen size, pollen density, vegetative resources, etc.) that impact pollen dispersal are yet limited, since conventional dispersal classification systems (i.e. pollination syndromes) consider mainly combinations of floral characteristics that assign species to either being dispersed by means of a certain vector (e.g. wind) or not. We analyzed imaging flow cytometry pollen features of >500,000 single pollen grains of >100 anemophilous species in combination with literature data of vegetative plant traits and characterize trade-offs shaping pollen traits in relation to plant physiology, growth form and environmental conditions that in combination determine the pollen dispersal distance of a given species. By revealing a mechanistic understanding of these trade-offs, our framework can help to better understand pollen dispersal and consequences of global threads on biodiversity for example by habitat fragmentation.

[51] From point clouds to tree morphometrics: Assessing shape variation in forest LiDAR data (12:15)

Presenter: HODAČ, Ladislav (Max-Planck-Institut für Biogeochemie)

LiDAR-based forest monitoring provides a powerful means of capturing tree structure at high spatial resolution, yet quantitative morphometric analyses of individual tree shapes remain underexplored. Using a published LiDAR dataset covering forest plots in Southern Germany, we extracted 200 annotated point cloud renderings of individual trees from eight species, segmented with a custom-developed tool. These renderings were converted into 2D and 3D landmark-based geometric morphometric data. Our aim is to evaluate how effectively tree shapes can be captured from LiDAR point cloud renderings to quantify morphological variation within and between species, as well as across different spatial plots and tree age classes. We further compare the geometric morphometric approach to morphometric information derived directly from the point clouds using Fourier descriptors and additional shape quantification techniques. By integrating modern morphometrics with advanced point cloud processing, we assess the potential and limitations of these methods in capturing biologically meaningful variation in tree form. This work makes a contribution to the progress of shape-based analyses in forest LiDAR research, offering perspectives for future applications in forest structure monitoring and biodiversity assessment.

[95] Transformers vs. Recurrent Neural Networks for Predicting CO2 Uptake in Forest Ecosystems (12:30)

Presenter: MONTERO LOAIZA, David (Leipzig University)

Gross Primary Production (GPP), the gross uptake of CO2 by vegetation, represents the largest carbon flux in terrestrial ecosystems and is fundamental to understanding global carbon dynamics. While Eddy Covariance (EC) towers provide direct, high-frequency estimates of GPP, their global spatial coverage remains limited. When there is an absence of EC data, remote sensing (RS) techniques are typically employed, often relying on statistical models with limited capacity to capture temporal dependencies. Recent advances in Deep Learning (DL) offer new opportunities for predicting GPP from time series. However, a comparative performance analysis between Transformer-based models and Recurrent Neural Networks (RNNs) for GPP estimation remains underexplored. This study presents a comparative evaluation of two representative architectures: GPT-2, a Transformer model, and Long Short-Term Memory (LSTM), a widely used RNN variant. We assess each model’s predictive accuracy across typical and extreme conditions. Our results show that while both models achieve comparable overall performance, LSTM excels under normal conditions, whereas GPT-2 demonstrates superior accuracy during extreme events, including stress-induced downregulation and peak productivity periods. Furthermore, we examine the role of memory retention in temporal modeling, revealing that LSTM requires shorter context windows to match GPT-2’s performance.

<u>Biodiversity Change</u> - Audimax (11:30 - 13:00)

-Conveners: Georg Johannes Albert Hähn; Hoss, Daniela (Uni Leipzig, iDiv)

[74] Modelling changing animal populations in dynamic agricultural landscapes (11:30)

Presenter: VEDDER, Daniel (UFZ/FSU/iDiv)

Biodiversity losses in agricultural landscapes are a well-known problem in ecology, and widely discussed in society. They are largely caused by shifts in farming practices over the past century, including the loss of semi-natural habitat, the increased use of agrochemicals, and changes in the timing and frequency of crop management actions. However, different species are impacted in different ways, depending on their specific habitat requirements and life cycles. Ecological research over the past two decades has focussed strongly on the role of the landscape in mediating biodiversity impacts, analysing spatial patterns (e.g. habitat availability and connectivity) and their effect on species populations. Less attention has been paid to the temporal dynamics of these landscapes, despite the fact that they are continuously changing due to processes such as plant phenology, seasonal management, crop rotations, and climate change. Here, we show how a process-based model can be used to study both the spatial and the temporal dynamics of agricultural landscapes, and their influence on different animal species. Our model Persefone.jl simulates agricultural management and crop growth in different regions in Germany, thereby creating in-silico landscapes that change within the course of a year as well as between years. These landscapes form the backdrop for a suite of individual-based models of animal indicator species, which simulate these species' movement and life-history processes. This integrated modelling set-up allows us to track the effects of agricultural management on the abundance and distribution of species over both space and time. In our talk, we present the model structure of Persefone.jl and show how it emulates known ecological patterns of two animal species (Alauda arvensis and Melanargia galathea). We also present first results of a study on the likely biodiversity effects of recent changes in the Common Agricultural Policy.

[33] Seasonal Dynamics of Bird Diversity, Community Composition, and Functional Traits in Temperate Forests (11:45)

Presenter: FELGENTREFF, Esther (Friedrich Schiller University Jena)

Bird diversity, community composition and functional diversity in temperate forests are typically studied during the breeding season, yet bird communities change throughout the year. To support forest management that considers bird populations year-round, we need a better understanding of how environmental factors shape avian diversity across all seasons. In this study, we monitored bird communities at 20 forest sites around Jena, Thuringia, across all four seasons in 2024. Using passive acoustic monitoring with AudioMoths and species identification via BirdNET, we tracked seasonal shifts in species richness, community composition, and functional diversity. Our analysis includes both biotic factors, such as forest structure and vegetation variables, and high-resolution abiotic data (daily temperature, relative humidity, and light intensity) to explore how fine-scale microclimatic conditions influence bird communities. Beyond investigating species-level patterns, we also examine functional diversity to capture differences in ecological traits mirroring resource requirements. Studying functional diversity provides insights into the range of ecological functions present in bird communities, offering a more nuanced perspective than species richness alone. This is particularly relevant for understanding ecosystem resilience and function, especially under changing environmental conditions. To maintain communities that are not only diverse in species but also in ecological function, it is essential to identify the site characteristics that influence functional trait composition. By analysing how these relationships shift across seasons, we can better inform habitat management strategies that support functionally rich bird communities throughout the year. By examining how environmental influences on bird diversity vary across the annual cycle, our findings aim to provide ecologically grounded insights for forest management, supporting actions that account for the full seasonal breadth of bird community dynamics. This is especially relevant in the face of ongoing climate change, which is likely to alter both forest conditions and the seasonal behaviour of bird communities.

[5] A framework to model species responses to extreme weather events (12:00)

Presenter: KAUFFELDT, Aaron Hagen (iDiv)

Human-induced climate change threatens global biodiversity, with the impact of extreme weather events (EWEs) on species still unclear. We introduce a framework to assess the effects of EWEs on species. As a case study, we use occupancy models for 132 German bird species of conservation concern, using monthly weather and remote sensing data from 2000 to 2022. The models predict species occupancy across Germany from 1999 to 2022, allowing us to compare suitability during non-extreme months with that during extreme weather events. This approach identifies vulnerable species, communities, and regions to specific EWEs.

With this approach it is possible to identify geographic areas, species communities, taxonomic- and functional groups that may be vulnerable towards specific EWE.

[20] Utilizing mechanistic microclimate models for vegetation science (12:15)

Presenter: HÄHN, Georg Johannes Albert

To understand the impact of climate change on plant communities, ecologists often rely on historical baseline data on biodiversity across biomes and its relationship with the climatic environment. Predictions of changes in plant communities under ongoing climate change are often based on monthly bioclimatic variables, such as those provided by the WorldClim datasets, at relatively coarse spatial resolutions. However, these climate variables fail to capture the fine-scale microenvironmental variability that individual plants experience in situ. This mismatch is particularly pronounced in forest ecosystems, where canopy structure modulates the microclimate, resulting in understory conditions that can diverge substantially from regional climate averages. To address the limitations of coarse-grained climate data in explaining biodiversity patterns and community assembly we present a pipeline that leverages the mechanistic microclimate model microclimf. This model downscales hourly climate data by accounting for topography, ground conditions, and biotic factors, such as seasonal changes in leaf area index (LAI) in deciduous forests, to predict subdaily microclimate temperatures. However, because the model relies on remotely sensed vegetation data such as LAI or tree height, its application is limited when working with vegetation data collected prior to the availability of remote-sensing products. Our approach addresses this limitation by defining forest types based on tree species' functional traits to estimate their climate-buffering capacity throughout the year, and by incorporating commonly assessed vegetation sampling data such as tree height and canopy cover. This enables future research to more effectively link plant biodiversity patterns with microclimatic conditions across broad spatial and temporal scales, thereby improving our understanding of baseline diversity and enhancing predictions of biodiversity change under future climate scenarios.

[103] BiodivBank: a streamlined solution facilitating FAIR and open sharing of structured species abundance and assemblage data (12:30)

Presenter: KAZEM, Anahita (iDiv & Friedrich Schiller University Jena)

Understanding biodiversity and applying this knowledge for positive impact relies on access to reliable data with broad geographic and taxonomic coverage. Data on species abundances are particularly valuable for documenting trends over time or community effects, and whilst a wealth of such information exists, much is neither interoperable nor readily usable. We have recently implemented a prototype for a dedicated global and openly accessible data repository and web portal, with the goal of gathering and harmonizing the heterogeneous datasets currently scattered across generalist repositories, smaller subject-specific databases and the academic literature, together with incoming new datasets. The platform features a dynamic metadata entry form, to facilitate more rapid, intuitive and accurate entry of the extensive contextual information required to underpin advanced search functionality for portal users as well as to make data genuinely reusable. Data upload options are flexible, and when structured data is imported following pre-defined templates, Darwin Core Archives can also be generated and registered with the Global Biodiversity Information Facility (GBIF) at the press of a button. Variables can additionally be mapped to alternative community-accepted data standards, ontologies or external services. Our product therefore combines the advantages of a fully-fledged data repository with the additional visibility and harmonization possibilities offered by mobilization to GBIF. The repository was designed with newer standards such as the Humboldt Extension to Darwin Core in mind, and we are conducting user tests to understand how we can best support data providers in representing their event-based field data using this extension. We welcome comment on the web platform currently under construction, with the aim of ensuring the portal meets the needs of a diverse range of potential stakeholders.

Biodiversity and Society - Lecture Hall XXII (14:00 - 15:30)

-Conveners: Rozario, Kevin (UFZ / iDiv / Uni Jena / Uni Leipzig); Meemken, Marie (Uni Jena)

[100] How tree species contribute to cultural ecosystem services: An indicator-based approach (14:00)

Presenter: TÖLLE, Max

Cultural ecosystem services (CES) – one of the key categories of ecosystem services – are often overlooked in research and management. Trees contribute to the provisioning of a wide range of CES, e.g. by enhancing the aesthetic value of landscapes or supporting the cultural identity of people to nature. Despite the clear contribution of trees to CES, research on how individual tree species contribute to these services remains limited. One major challenge in assessing cultural ecosystem services (CES) lies in the difficulty of obtaining objective and comprehensive data. Therefore, we constructed an indicator-based approach which comprises different methods of collecting tree species related data: 1.) We used text analyses of school books, hiking tour descriptions, newspapers and literature, 2.) we scraped social media platforms like reddit, flickr and youtube or knowledge databases like Wikipedia or WebOfScience 3.) we compiled data of natural monuments including trees, 4.) we carried out two surveys asking people about their favorite tree species or the aesthetic value of trees and 5.) We compiled data from tree nurseries about the price and cultivars of different tree species. Focusing on native and selected “promising” introduced tree species in Germany, we analyze the dimensionality of these indicators and investigate the presence of trade-offs and synergies. First preliminary results show that the indicators span a multidimensional space which might be categorized in different groups or services. Some tree species have an overall high score in each service compared to other tree species. However, most species vary in their amplitude of contributing to different services. In general, native and broadleaved species contribute more to the provisioning of CES than non-native and needle-leaved species. Further results will be evaluated by the time of presentation. With our research, we contribute to a better understanding of CES at the tree species level, which need to be considered in forest and urban management.

[106] Is palm oil a threat or opportunity for Peru's forests? (14:15)

Presenter: BRIZUELA-TORRES, Diego (Helmholtz Centre for Environmental Research)

Oil palm is the world’s main source of edible oil, supporting rural incomes but also driving deforestation and other impacts. As new production regions emerge, understanding the links between sustainability and governance— ranging from government regulations to market demands —is essential. We examined Peru’s oil palm sector, focusing on the main producing Regions, San Martin and Ucayali. We quantified palm expansion, associated deforestation, and the role of a key land-use policy tool. Then, through 30 stakeholder interviews, we identified factors driving palm expansion and its impacts, highlighting pathways for a deforestation-free sector. We found that Peru’s oil palm sector is largely supplied by smallholders, but becoming profit-oriented and industrializing quickly. Excepting isolated past large deforestation events, palm has not yet been a major deforestation driver, but risks persist that it could become one. These risks include low yields, weak land-use governance, and land tenure issues that promote expansion over productivity gains. Furthermore, the land-use, tenure and forestry policies that could address these risks suffer from incoherencies and weak implementation and enforcement, particularly in Ucayali. Global sustainability standards are the main sustainability lever at present, but many others require stronger public-private collaboration. Lastly, we propose a public-private pre-competitive agenda to align stakeholders towards sustainable oil palm. Two years after fieldwork, we co-hosted a participatory workshop in Pucallpa with the Peruvian Coalition for Sustainable Production. Key stakeholders from the palm oil value chain discussed and prioritized elements of a proposed pre-competitive agenda, aiming to develop an applied research workplan addressing the sector’s main sustainability challenges. As global markets increasingly value sustainability, Peru has a chance to integrate its palm sector into responsible supply chains—but urgent action is needed to strengthen multi-stakeholder platforms and implement locally tailored deforestation control strategies before this opportunity closes.

[25] Experiences with classic psychedelics are associated with greater spiritual wellbeing and nature connectedness (14:30)

Presenter: ROZARIO, Kevin (UFZ / iDiv / Uni Jena / Uni Leipzig)

In many cultures worldwide, the use of psychedelics is an integral part of spiritual practices. Psychedelics are suggested to increase mental wellbeing, while their potential for improving nature and social connectedness as part of spiritual wellbeing is an emerging research area. With this cross-sectional survey based on 212 participants, we assessed whether experiences with natural and synthetic classic psychedelics were associated with spiritual wellbeing in general, and its four subdomains, i.e. nature, transcendental, personal and communal connectedness. Participants who consumed classic psychedelics before (n=108) were further asked whether their experiences were enriching or harmful. We also assessed the effect of frequency of experiences with classic psychedelics and specifics for each drug. Participants who had consumed classic psychedelics compared to those who had not showed greater nature and transcendental connectedness. The frequency of psychedelic drug experiences in general was positively associated with spiritual wellbeing, as well as nature and transcendental connectedness. Regarding specific drug effects, the more psilocybin experiences people reported, the greater their spiritual wellbeing, while also increases for nature, transcendental and communal connectedness were found. Of participants with psychedelic drug experiences, 67% stated that the experiences made were enriching for their lives, while 7% reported harmful effects. Enriching experiences were specifically found for psilocybin, while doing psychedelics in nature opposed to a party setting probably buffers adverse effects. We could show that the consumption of psychedelics - in particular of psilocybin - is associated with nature and transcendental connectedness, while less associations were found for the social connectedness domains of spiritual wellbeing. In view of the relevance of spiritual wellbeing for mental health, psychedelics may offer innovative revenues for complementing established therapeutic approaches. At the same time, psychedelics probably reconnect people with nature, thereby fostering environmental stewardship.

[71] Modeling the Impact of Urban Stressors and Nature Use on Health: A Structural Equation Approach in Leipzig (14:45)

Presenter: MEEMKEN, Marie (Uni Jena)
Urban environments influence human health, both through negative and positive effects. This study investigates the associations between urban environmental conditions and psychological as well as physical health outcomes in a large, population-based sample from Leipzig, Germany (N ≈ 5000, age 19-87 years, 52% women). Drawing on a comprehensive dataset, we examine associations between sociodemographic characteristics (e.g., age, gender), personality (e.g. social connectedness, optimistic or pessimistic attribution style), urban stressors (air pollution levels, environmental noise exposure), and exposure to natural environments (both passive exposure to nature spaces and active nature use) and self-reported and/or clinically assessed health indicators (e.g. heart rate, depression). Structural equation modelling will be employed to disentangle the relative contributions of each variable and uncover both direct and indirect pathways linking the aforementioned variable classes to psychological and physical health outcomes. The dataset has been fully curated and model specification is currently in progress; results will be finalized in time for presentation at the conference. The study will contribute to growing evidence on the pathways linking urban living with health, with implications for public health policy and city design.

[81] PollenNet - Harnessing opportunistic observations to predict local pollen loads of allergenic plants (15:00)

Presenter: RZANNY, Michael (Max-Planck-Institute for Biogeochemistry, Jena)
One third of the world's population suffers from pollen-induced respiratory allergies. For those affected, knowing the local pollen loads and thus the local risk of allergy symptoms is of the utmost importance for their daily life and medication. However, real data on pollen abundance needs to combine knowledge of flowering times, pollen release and ultimately local pollen occurrence, and this kind of information is not widely available. The currently available pollen forecasting models, although undoubtedly helpful, are based on very limited data in terms of adequate real-time flowering information, pollen abundance, resolution, and considered species. The PollenNet project aims to provide accurate predictions of local pollen loads for specific species and even the local risk of allergy symptoms. In order to address the lack of local data on the flowering of allergenic plants, we will use the real-time data that is provided by users of the Flora Incognita plant identification app. Thousands of geolocalised observations of allergenic plants per day enable both the estimation of their fine-grained local distribution and the recognition of their current flowering stages at a given location. A citizen science project within the app, which is updated regularly with pollen-related information, has already proven highly effective in motivating people to provide observations and images of the full range of flowering stages of plants, such as hazel (*Corylus avellana*) and birch (*Betula pendula*). These images allow the development of a species-specific flowering stage classifier. Next, the observed flowering stages will be coupled with data from pollen traps and local weather forecast models to provide precise and fine-grained predictions of local pollen loads.

[86] BioImpact: Visualizing and Quantifying Corporate Impacts on Biodiversity via Trade, Land Use, and Emissions (15:01)

Presenter: VOSKAMP, Alke (FSU)
Human consumption and international trade are key drivers of global biodiversity loss. Major pressures such as land-use change, overexploitation, climate change, invasive species, and pollution are often rooted in unsustainable business practices. In response, global and European policy frameworks have introduced ambitious targets to protect nature, climate, and human well-being. As a result, companies face increasing expectations to assess not only their climate footprint but also their biodiversity impacts. To address this emerging need, our research bridges biodiversity science with private sector decision-making. In collaboration with a German climate tech company specialized in science-based impact assessments, we develop methods to quantify corporate impacts on biodiversity. We focus on three of the five key drivers of biodiversity loss: land-use change, climate change, and biological invasions. Using globally available datasets and corporate case studies, we explore how these pressures can be measured and visualized across supply chains. The result is a practical, scalable approach to support companies in understanding and reducing their biodiversity impacts.

[94] The World's First Fully Interactive Physical Data Cube for Exploring Spatiotemporal Data in Earth and Biodiversity Research (15:02)

Presenter: Mr SÖCHTING, Maximilian (Universität Leipzig)
Essential Biodiversity Variables (EBVs) and Essential Climate Variables (ECVs) are best provided as spatiotemporal data. When these data are structured on regular spatial and temporal grids, they are known as Analysis Ready Data Cubes (ARDCs). Recent developments in the Earth observation community have led to broad adoption of ARDCs, facilitated by cloud-native data formats

that support efficient hosting and querying of very large datasets. However, a major challenge remains: how can we build intuition for such high-dimensional data? To address this, novel visualization and data exploration tools are needed. Over the past years, we have developed Lexcube.org – an interactive web-based platform that allows users to explore large ARDCs interactively without coding or technical barriers, as well as an open-source Python package aimed at scientists with the same capabilities. However, limited to regular computer displays, both applications offer only a two-dimensional interface for what is fundamentally three-dimensional data. Here, we present the first interactive touch-enabled physical data cube, enabling users to explore spatiotemporal datasets through multiple touchscreen interfaces. We hope this new approach inspires the iDiv community to engage more deeply with large spatiotemporal data cubes to enhance ecosystem assessments and analysis capabilities. The cube will be physically available during the meeting and can be explored by the visitors.

Biodiversity and the functioning of Ecosystems - Lecture Hall XXIII (14:00 - 15:30)

-Conveners: Schwarz, Rike (University Leipzig); Christel, Henriette (iDiv); Robert Rauschkolb

[18] Functional Diversity Buffers Insect Disturbance Impacts in Forest Ecosystems: A Process-Based Modelling Study Using QUINCY (14:00)

Presenter: MA, Yimian (Lepizig University)

Insect outbreaks significantly affect forest composition, carbon and nutrient cycling, and water and energy fluxes. Functional diversity within forest communities may mitigate insect disturbance impacts by reducing host tree dominance and constraining insect population growth. To investigate biodiversity-ecosystem functioning (BEF) relationships under insect pressure, we conducted a series of site-level simulations using the terrestrial biosphere model QUINCY (QUantifying Interactions between terrestrial Nutrient CYcles and the climate system), enhanced with a new insect impact module. This module explicitly represents defoliator feeding on broadleaf trees and bark beetle-induced mortality in needleleaf trees, while accounting for disturbance-driven changes in carbon pools (e.g., snags, frass), nutrient leaching, and compensatory regrowth. We introduced a simplified insect severity model based on cold survival, temperature-driven phenology, host availability, and predator suppression. Forest diversity was represented by combining pure and mixed PFT (plant functional type) simulations with controlled dispersal capacity. Our results show that increased tree functional diversity buffers forest ecosystems against insect outbreaks by reducing host accessibility and slowing carbon loss. This framework provides a tractable process-based approach to explore how biotic interactions, especially those between insect and forest diversity, shape forest resilience and long-term carbon dynamics.

[84] Effects of tree diversity and facilitation on microclimate in the Brazilian Caatinga (14:15)

Presenter: KÖHLER, Michael (German Centre for Integrative Biodiversity Research (iDiv))

The Caatinga, a seasonally dry tropical forest in northeastern Brazil, remains one of the most understudied biomes in terms of biodiversity and ecosystem functioning. To address this gap, the BrazilDry Experiment was established to explore how tree species richness, functional composition, and facilitation influence microclimate and contribute to ecosystem restoration and resilience against desertification. We recorded canopy-level temperature and humidity using automated loggers across experimental plots varying in species richness and facilitation, covering a full seasonal cycle to capture diel and seasonal dynamics. Preliminary results indicate that higher tree species richness and facilitative interactions contribute to buffering microclimatic extremes, particularly by reducing daytime temperatures and stabilizing humidity levels. These effects were most pronounced during the dry season, suggesting that facilitative species can help maintain favorable microhabitats under climatic stress. Importantly, species-specific effects were highly variable, revealing that individual species modulate microclimate differently—likely due to differences in canopy architecture, phenology, and functional traits. This highlights the importance of species identity in shaping biodiversity–climate feedbacks. These early findings provide new insights into the role of biodiversity and facilitation in enhancing microclimatic stability in dry tropical forests. As climate extremes intensify, understanding species-specific contributions to local microclimate regulation will be essential for designing effective restoration strategies and increasing ecosystem resilience in the Caatinga.

[45] Traits in the light of diversity: Exploring intra-individual leaf trait responses to local light availability and biodiversity in a subtropical forest experiment (14:30)

Presenter: PROSS, Tobias (Martin Luther University Halle-Wittenberg)

Leaf traits are key indicators of ecosystem functioning and vary not only between species but also within species and within individuals. However, within-individual variation is often neglected due to measurement limitations. Light availability, influenced by surrounding vegetation, is a major driver of leaf trait variability, especially across the strong vertical light gradients found in forest canopies. In the BEF-China subtropical forest experiment, we investigated how within-individual leaf traits respond to local light availability and tree species richness. We sampled leaves across vertical light gradients in monocultures and mixtures of up to 24 species. Light availability was measured with sensors placed adjacent to each sampled leaf. Using visible and near-infrared spectroscopy, we predicted 14 leaf traits from 4,981 leaves across 15 native tree species. We assessed whether neighboring species identity or overall species richness had a stronger influence on the leaf trait–light relationship. Most trait values responded to light availability, though this response differed between deciduous and evergreen species. We found that tree species richness and a tree's direct neighbour could modify the light–trait relationship at the individual level. In some instances, a focal tree's direct neighbour influenced its leaf trait values more than the tree species richness in its local neighbourhood. Specifically, in conspecific tree pairs of evergreens, specific leaf area and leaf nitrogen displayed a stronger response to changing light conditions. This response to light availability suggests a mechanism for avoiding within-species competition that is observable at the within-individual level. Our results show that biodiversity influences ecosystem functions through its effects on within-individual leaf trait variation. The fact that the interplay between light availability, biodiversity and leaf traits can be observed within individual trees highlights the importance of within-individual leaf trait variation in biodiversity research.

[11] Functional traits explain growth response to successive hotter droughts across a wide set of common and future tree species in Europe (14:45)

Presenter: KRETZ, Lena

In many regions worldwide, forests suffer from climate change-induced droughts. The 'hotter drought' in Europe in 2018 with the consecutive drought years 2019 and 2020 caused large-scale growth declines and forest dieback. We investigated if tree growth responses to the 2018–2020 drought can be explained by functional traits related to drought tolerance, growth, and resource acquisition. We assessed growth response during the drought compared to pre-drought-conditions, using branch shoot increments of 71 planted tree species in the research Arboretum ARBOfun. We leveraged gap-filled trait data (BHPMF approach) related to drought tolerance (P50, stomatal density and conductance), growth and resource acquisition (SLA, LNC, C:N, Amax) and wood density from the TRY database to explain growth resistance, while accounting for different growth programs (spring vs. full-season growing species). We found significantly reduced growth during drought across all species. Legacy effects further decreased growth resistance in 2019 and 2020. Gymnosperms showed decreasing growth resistance with increasing P50 and acquisitiveness, such as high SLA, LNC, and Amax. Similar results were found for angiosperms, however, with less clear pattern. Four distinct response types emerged: 'Sufferer', 'Late sufferer', 'Recoverer' and 'Resisters', with gymnosperms predominately falling into the 'Sufferer' and 'Late sufferer' categories. Our study provides evidence for significant growth reductions and legacy effects in response to consecutive hotter droughts, which can be explained by functional traits across a wide set of tree species. The a posteriori classification into response types revealed the diversity of temporal responses to a prolonged drought. We expect our findings to facilitate the development of management strategies for forests under a future climate regime characterized by more frequent, severe and prolonged droughts through supporting tree species choice and the improvement of forest models. We conclude that high drought tolerance bolsters growth, while acquisitive species suffer stronger under drought.

[19] Fine root traits mediate drought resistance in a rhizo-tube experiment (15:00)

Presenter: SAXENA, Srijna (Leipzig University)

As climate change progresses, drought events are becoming more frequent, and water scarcity is increasingly affecting plant productivity and survival. Plants access water through their root systems, which involve various root economic traits related to belowground resource acquisition. Therefore, it is critical to study the role of key root traits involved in water uptake—such as root system architecture, specific root length (SRL), mean rooting depth (MRD), and root tissue density (RTD)—in conferring drought resistance. Moreover, water transport is regulated by hydraulic traits such as turgor loss point and root shrinkage. However, it remains unclear (1) how fine root traits mediate drought resistance, and (2) how they are linked to hydraulic traits. We expect that traits associated with the fast end of the conservation gradient in root economic space support drought recovery, while slow traits relate to drought resistance. As for hydraulic traits, we speculate that they do not align with either axis within the root economic space, representing an independent strategy. To test this hypothesis, we conducted a PVC-tube-based greenhouse experiment with control and drought treatments, carried out in three phases: establishment, drought, and re-watering to measure drought resistance and resilience. The experiment included 20 selected grassland species representing four functional groups (tall herbs, short herbs, grasses, and legumes). We measured classical root economic traits ex situ and assessed biomass allocation and above-ground response traits, such as leaf fluorescence and leaf production rate, in situ. Our results show that total root length significantly decreased under drought conditions and later overcompensated during the re-watering phase. A similar trend was observed in above-ground traits: both fluorescence and leaf production rate declined during drought, indicating stress, but overcompensated after re-watering. Additionally, we found that hydraulic traits do not align with the root economic space, highlighting their independent role.

[47] Utilizing belowground traits to predict ecosystem productivity across different environments (15:15)

Presenter: ANDRACZEK, Karl (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)
Herbaceous dominated ecosystems – including grasslands, savannas, and shrublands — cover almost half of earth’s terrestrial land surface and play a key role in carbon sequestration. Understanding how they maintain productivity under environmental stress is crucial for climate mitigation. Recent evidence from forests suggests that conservative species outperform fast-growing ones under stressful, resource-limited conditions. Yet it remains unclear if these patterns hold in herbaceous ecosystems, or which traits best predict productivity under environmental constraints. Plant trait-based frameworks often have low predictive power, likely due to the neglect of belowground traits that underpin plant persistence (long-term survival) and resource uptake strategies, and limited insights into how the strength and direction of trait-functioning relationships vary with environmental constraints. Here we show, using global research networks and a novel belowground trait database, that fine root traits, root system extent, and resprouting & clonality strongly predict aboveground biomass production. Specifically, conservative traits and belowground resprouting sustain biomass production in hot and arid environments. These findings challenge assumptions that fast-growing traits universally enhance productivity and highlight that incorporating a broader suite of belowground traits significantly improves predictions of ecosystem functioning especially in stressful environments. We conclude that conservation and restoration efforts should prioritize belowground functional traits to enhance resilience, particularly as droughts intensify in a warming world.

Biodiversity Dynamics and Complexity - Audimax (14:00 - 15:30)

-Conveners: Gauzens, Benoit (German Centre for Integrative Biodiversity Research (iDiv)); Berti, Emilio (iDiv)

[104] Multi-taxa Pan-European Connectivity: Prioritization of Continental Connections (14:00)

Presenter: DERTIEN, Jeremy (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany)
Fragmentation of terrestrial and freshwater habitats produces negative impacts to wildlife populations, plant community persistence and overall ecosystem function. Preserving connectivity between crucial habitat areas and across large landscapes is vital to sustain biodiversity during ongoing anthropogenic global change. Identifying key ecological corridors at spatial extents large enough to capture current and future ecological dynamics and at resolutions fine enough to be useful for practitioners is a vital step in prioritizing areas for connectivity conservation. We used a novel multi-method connectivity framework to model the continental connectivity of 30 terrestrial vertebrate archetypes using over 900 individual species distribution models. We identified key ecological corridors across the continent, prioritizing each corridor by archetype and cumulatively across all terrestrial vertebrate species. The cumulative corridor prioritization identified many of the highest priority corridors for protection as being within the Mediterranean bioregion and corridors with mountainous regions that connected the continent’s largest most intact protected areas. There was consistent spatial overlap of corridors selected within archetypes of the same taxonomic class but substantial differences between archetypes of different classes. In addition, our results failed to identify corridors in some of the most developed and heavily fragmented portions of Western Europe, highlighting the scale of conservation efforts needed to restore adequate species habitat to allow for increased connectivity potential. This work represents the most comprehensive multi-taxa connectivity analysis completed at a multinational scale and provides guidance for EU member states as they attempt to meet the goals of the EU Biodiversity Strategy and Nature Restoration Regulation.

[37] Combining GBIF data with national atlases reduces spatial bias in climate niche modeling (14:15)

Presenter: COQUERY, Thibault (German Centre for Integrative Biodiversity Research (iDiv), Helmholtz Centre for Environmental Research (UFZ, Halle), Martin-Luther-University Halle-Wittenberg)
Investigating climate niche properties of plant species is, in face of climate change, of great interest, especially to predict their future distribution or their response to future conditions. The fitting of climate niche requires both reliable climatic variables and distribution data. Most of the studies use distribution data from the well-known open access Global Biodiversity Information Facility (GBIF). However, the data coverage in this database is uneven between countries, with a good coverage in Western Europe and often a lack of data in Central and Eastern European countries. This bias in distribution data may lead to truncated modeled climate niche or inaccurate niche properties. In this study we aim to quantify the potential impact of this bias on the accuracy of fitted climate niches of a large number a grassland species that all occur in Central Europe but exhibit different distribution patterns. For this, we compare climate niches, fitted for each of these species based on three different datasets, i) raw GBIF data, ii) digitalized expert range maps covering the whole distribution of the species, and iii) GBIF data enriched with data from digitalized national atlases of several Central European countries. We expect for the latter dataset values of niche size and optimum position intermediate between those based on the raw GBIF data and expert range maps. Moreover, we expect the change in niche properties between the raw GBIF dataset and the enriched one to be stronger for rather continental species than for rather oceanic or widely distributed ones. With this study, we call for a careful use of GBIF data in climate niche modeling. The targeted integration of other data sources helps tackling the geographical bias in data availability and leads to more accurate

modeled niche properties.

[46] In-depth analysis of the origin of Primary Biological Aerosol Particles (PBAPs) in a temperate forest of Leipzig (14:30)

Presenter: Ms VALATH BHUAN DAS, Bhavana (University of Leipzig)
Primary Biological Aerosol Particles (PBAPs) are airborne materials of biological origin, comprising viable and non-viable entities such as bacteria, archaea, fungi, viruses, spores, pollen, subcellular fragments, and plant/animal detritus (Després et al., 2012). Emitted directly from the biosphere into the atmosphere, PBAPs can undergo short- or long-range atmospheric transport. Their dispersal is influenced by atmospheric turbulence, meteorological conditions, and landscape structure (Fröhlich-Nowoisky et al., 2016; Duan et al., 2023). The mix of local emissions and long-range transport complicates source attribution and accurate assessments of ecological and climatic impacts. PBAPs are increasingly recognized for their diverse roles in atmospheric processes, including ice nucleation and cloud condensation, and their broader environmental significance. They function as vectors of allergens, toxins, and pathogens, affecting human, animal, and plant health, as well as agricultural productivity and ecosystem stability. To better understand PBAPs' origins and distribution, an integrative biodiversity study was conducted in the spring and autumn seasons using air and soil litter samples across spatially defined tree sites at the Leipzig Canopy Crane facility (Leipzig Auwald). High-throughput sequencing enabled taxonomic profiling of airborne microbes and their possible terrestrial sources. Findings reveal strong environmental filtering, with only a selective subset of soil microbes appearing in the air. Compositional differences between soil and airborne communities among dominant and rare taxa suggest selective atmospheric pressures on microbial dispersal. While soil serves as a rich microbial reservoir, airborne PBAPs likely originate from multiple sources, including soil, phyllosphere, and nearby ecosystems. Phylogenetic clustering among soil samples and seasonal convergence in airborne communities highlight the greater influence of temporal rather than spatial drivers in structuring atmospheric microbial assemblages.

[56] Phyllosphere bacterial dynamics and throughfall-mediated bacterial transport in a temperate hardwood floodplain forest (14:45)

Presenter: SANKA LOGANATHA CHETTI, Dinesh (Friedrich Schiller University of Jena and German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)
The phyllosphere of temperate trees is a dynamic environment and undergoes phenological changes throughout the growing season. However, the key drivers of phyllosphere microbiome dynamics are still poorly understood. Following bacterial community composition and throughfall-mediated bacterial transport for oak (*Quercus robur* L.), ash (*Fraxinus excelsior* L.) and linden (*Tilia cordata* MILL) across early (May), mid (July) and late (October) phenological stages, we hypothesized that phenology-driven changes will have a stronger effect on phyllosphere bacterial communities than tree species identity, and that throughfall-mediated transport of bacteria will shape distribution patterns within the canopy. We collected leaves and throughfall samples at the top, middle, and bottom canopy positions at the Leipzig canopy crane facility (Germany). Phyllosphere bacterial community assembly was mostly driven by dispersal limitation at the early phenological stage while communities became more homogeneous and functionally redundant during mid–late phenological stages. During the early phenological stage, early-colonisers such as *Erwiniaceae* possibly occupied niches through priority effects, while later new bacterial taxa got introduced at mid–phenological stages and shared the niches with successional bacteria. The strong decline of potential plant pathogens towards the late phenological stage may be attributed to plant defense or microbially mediated biocontrol mechanisms, evident from a higher enrichment of steroid and polyketide synthase pathways in the communities' functional potential. Throughfall-mediated transport of bacteria increased substantially from March to May, indicating the strong influence of wash-off effects from the emerging foliage on the transported communities. Patterns of preferential attachment to leaves and mobilization by throughfall appeared to be taxon-specific across different canopy positions. Our findings demonstrate that in temperate forests, phenology-driven effects on the phyllosphere microbiome are far more important than tree species' specific effects. Selectivity of throughfall-mediated mobilization and detachment may play an important role for the spatial heterogeneity of microbial communities in tree crowns. Key words: Phyllosphere; throughfall; temperate forest; drift and dispersal limitation

[66] Dynamics of pairwise tree interactions during increasing diversity effects over time (15:00)

Presenter: MADER, Sebastian (iDiv / Friedrich-Schiller-University Jena)
During times of unprecedented biodiversity loss, understanding biodiversity ecosystem-functioning (BEF) relationships is essential to mitigate the consequences. One well-established observation is that the effect of biodiversity on ecosystem functions strengthens over time. A proposed explanation for this pattern is the increase of trait dissimilarity between co-occuring species, which results in more complementary utilisation of resources and thus, less competition. Another process that can determine species growth and coexistence, and hence ecosystem functioning, is facilitation. Increasing facilitation between species over time

is another potential reason for strengthening BEF relationships. To test their relative importance, we zoom in on individual tree pairs in the large-scale tree diversity experiment “BEF-China” and assess how facilitative and competitive inter-specific as well as intra-specific pairwise interactions change over time. We applied Bayesian statistical modelling on tree growth data spanning seven years and partitioned individual tree growth into intrinsic growth and its pairwise interactions with neighbouring trees. Our results reveal that, over time, intra-specific interactions (predominant in low diversity plots) become more negative, while facilitative and competitive inter-specific interactions (predominant in high biodiversity plots) become marginally more positive or more negative, respectively. This result hints at a strengthening diversity effect on biomass growth as the difference between inter- and intra-specific interactions increases. However, when simulating biomass growth, we find that the temporal pattern of these interaction strengths is not the driving force behind the steepening of the diversity effect, as perturbing it produces similar results. Instead, the overall more positive inter-specific interactions yield more biomass in plots with species mixtures, which in return produce more biomass in a positive feedback loop. With this study, we provide insights into the temporal dynamics of tree-tree interactions and elucidate the mechanisms underlying the steepening of diversity effects on productivity over time.

Closing - Audimax (16:00 - 17:00)