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All posters

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Harmonizing taxon names in biodiversity data: a review of tools, databases, and best practices

The process of standardizing taxon names, is necessary to properly merge data indexed by taxon names. The large variety of taxonomic databases and related tools are often not well described. It is often unclear which databases are actively maintained or what is the original source of taxonomic information. In addition, software to access these databases is developed following non-compatible standards, which creates additional challenges for users. As a result, taxonomic harmonization has become a major obstacle in ecological studies that seek to combine multiple datasets.

Here, we review and categorize a set of major taxonomic databases publicly available as well as a large collection of R packages to access them and to harmonize lists of taxon names. We categorized available taxonomic databases according to their taxonomic breadth (e.g. taxon-specific vs multi-taxa) and spatial scope (e.g. regional vs global), highlighting strengths and caveats of each type of database. We divided R packages according to their function, (e.g. syntax standardization tools, access to online databases, etc.) and highlighted overlaps among them.

We present our findings (e.g. network of linkages, data and tool characteristics) in a ready-to-use Shiny web application (available at: <https://mgrenie.shinyapps.io/taxharmonizexplorer/>).

As an illustrative example, we harmonized taxon names of one of the largest databases of community time series currently available. We showed how different workflows can be used for different goals, highlighting their strengths and weaknesses and providing practical solutions to avoid common pitfalls.

Finally, we provide general guidelines and best practice principles for taxonomic name harmonization for users, database managers, and package developers.

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Justus Hennecke

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Linking the root economics space to soil-borne fungal communities in grasslands

Root traits are mainly organized along two orthogonal axes: the well-established conservation gradient from 'fast' (high nitrogen content) to 'slow' (high tissue density), and even more importantly, the recently described collaboration gradient from 'collaboration' (high diameter) to 'do-it-yourself' (high root length). This trait variation is described in the so-called Root Economics Space (RES). The collaboration gradient directly links plant functional strategies to belowground fungal communities. Overall, we expect mutualistic and pathogenic fungi to be correlated to collaboration traits and saprotrophic fungi to be more closely linked to conservation traits.

To test the predictive power of the RES framework, we sampled roots and soil in monocultures in the Jena Experiment. We measured root traits from individual plants and sequenced the fungal community in the attached rhizosphere soil. Fungal taxa were then assigned a functional guild (saprotrophs, mycorrhiza, pathogens) and we analysed their community composition of the total sequenced community.

We found that the conservation axis of root traits is indeed a main driver of the saprotrophic fungal community, even though the proportion of saprotrophs does not change along the axis. To our surprise, we found no change of arbuscular mycorrhiza proportion along the collaboration axis, while pathogen proportion increased unexpectedly towards the outsourcing/collaboration end of the axis.

Overall, we show that root traits and the root economics space can be a significant driver of soil-borne fungal community structure but effects on the abundance of fungal guilds are less clear.

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Beyond ecosystem boundaries: impact of pollen stoichiometry on phytoplankton communities

Together with temperature and light, phytoplankton growth is strongly influenced by the availabilities of nutrients in freshwater ecosystems. Pollen dispersal across boundaries of ecosystems can impact key ecological processes, particularly nutrient cycling which can strongly change the availability and stoichiometry of growth-limiting nutrients like nitrogen (N) and phosphorus (P) for phytoplankton; consequently, influencing phytoplankton growth, community composition and diversity. However, despite this apparent potential of temporal pollen amendments as a considerable nutrient-source affecting phytoplankton community dynamics in many freshwater systems, it seems like the role of pollen stoichiometry and diversity on phytoplankton growth dynamics is not well studied. In microcosm experiments, we will investigate diversity effects of pollen amendments on phytoplankton species and communities. We will assess phytoplankton nutrient uptake rates in response to pollen amendment. Imaging flow cytometry will be used as an innovative approach to analyze phytoplankton community composition, abundance and functional trait variability. Three naturally occurring phytoplankton species (each representing a different phytoplankton functional type) will be used for the experiments in a full factorial design. Further, we will experimentally investigate if differences in pollen stoichiometry between *Alnus glutinosa*, *Populus alba* and *Pinus sp.* can impact phytoplankton community dynamics. Our research will help us to assess, model and predict the role of cross-ecosystem pollen dispersal for phytoplankton competitive interactions.

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Trends of marine heatwaves in the Western Baltic Sea (1950-2020)

Marine heatwaves (MHW) are periods of high-temperature in the oceans that may have long-lasting biological and socioeconomic effects. Strong MHW events have been identified in northwestern Atlantic, in the western coast of Australia, in the Mediterranean and in many other regions. The Western Baltic Sea (WBS) is a region of ecological and socio-economic importance for northern Europe, providing many different ecosystem services. Despite its regional importance, there have been no studies into the trends and effects of MHW in the WBS. This study aims to analyze the historical trends of MHWs in the WBS from 1950 until 2020. We used a dataset of daily sea surface temperature on a 0.25x0.25° resolution for the areas 22-24 from the International Council for the Exploration of the Sea (ICES) classification. Preliminary results show frequent and stronger MHW events during summer months (May-August) with longer but milder events during October-November.

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Ronny Richter

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The hidden life in the tree canopies: Who, Where, Why and How many?

Forests are considered to be “hot spots” of biodiversity. However, the number of species, their composition and temporal community dynamics were found to vary greatly across tree species and also within a single tree. Due to the difficulties in accessing tree crowns of mature trees, the underlying mechanism and their interactions shaping the spatio-temporal patterns of biodiversity and their consequences for ecosystem functioning, remain largely unknown. The Leipzig Canopy Crane (LCC) offers full access to around 900 individual trees from 16 species and thus offers the unique opportunity to conduct observational and experimental studies to disentangle the potential drivers of biodiversity generating mechanisms and ecosystem functioning. Here we present a selection of studies, recently conducted at the LCC site, which aimed at: 1) testing biodiversity shaping mechanisms and 2) characterizing potential drivers (e.g. the local micro climate) at very high spatial and temporal resolution. Next to the tree species identity, vertical gradients of chemical and morphological tree characteristics, and phenology-driven changes of the trees, abiotic factors as well as predation pressure were identified as important drivers of biodiversity. The relative contribution of single mechanism that causes and shapes these spatio-temporal patterns of biodiversity, however, depends on the group of organisms investigated.

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Is there a difference in native and alien species success in respect to the traits, climate and soil nutrients?

Nutrient inputs affect the relative dominance of plant species which might cause a functional shift in grassland community composition. Traits of native and alien species are associated with ecosystem processes and thus different environmental conditions or nutrient addition might shift trait expression. Changes in nutrient availability may result in native-alien functional (dis-) similarity, as natives may have adaptations that allow them to boost nutrient extraction in the low-resource environment and consequently, have an advantage over alien species. In addition to resource availability, climatic factors, such as temperature and precipitation create an additional complexity layer of studying the trait-environment relationship and species success. The main goal of our study is to explain native and alien plant species abundance with species traits, environment (climate and nutrient treatments) and origin, using data from a worldwide grassland project NutNet. We hypothesize that there will be no difference in native and alien species success with respect to the trait-climatic relationship. However, we expect the difference in native and alien success regarding traits with nutrient additions (functional traits might respond differently according to their origin with different nutrient availability). Further, we investigate if native and alien success and traits differ between biogeographic regions. Climatic and nutrient conditions may have an antagonistic or synergistic effect on species success and their traits (e.g. nutrient availability may be significantly impacted by the change in precipitation). Therefore, studying the relationship between environment and functional traits may portray grasslands' dynamics better than focusing exclusively on species richness.

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Detection and attribution of changes in soil temperature as affected by plant diversity and climate

In a world that has to increasingly deal with extreme weather events, the question of how to mitigate the effects of such events, especially on ecosystems, becomes essential. Our research focuses on plant diversity and the impact it can have, specifically on soil-plant-climate systems. The hypothesis that we test in this context is whether plant diversity can buffer the effects of climate extremes by stabilizing the soil temperature in different depths. We analyze an unprecedented long-term climate and soil temperature dataset which was collected over almost 20 years at the "Jena Experiment" site. Our first initial results suggest a significant effect of plant diversity on the mean and the variance of the seasonal soil temperature. Furthermore, this effect seems to get stronger during extreme weather events such as extreme heat.

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Citizen science plant observations encode global trait patterns

Global patterns and diversity of functional plant traits remain difficult to quantify in detail. With the increasing popularity of species identification smartphone apps, crowd-sourced data offer large and rapidly growing collections with the potential to monitor biodiversity across the globe. These data are devoid of any scientific experimental design and with staggering over-representation of some regions. Here, the question is whether these data can be utilized to represent plant communities on a functional level and help uncover global trait patterns. We use the freely available field observations of vascular plants provided by iNaturalist, a citizen science project that has encouraged users across the globe to identify, share and jointly validate species they encounter via photo and geolocation. We test if iNaturalist observations complemented with trait measurements from the TRY database are able to represent global trait patterns. As a reference we use sPlotOpen, a global collection of vegetation plot data. Our results indicate surprisingly high correlations - considering the independent biases in both datasets - of up to 0.46 (r^2). As the sheer volume of citizen science data continues to grow exponentially, we can expect a continuous increase in reliability of the already surprisingly good representation of plant functional communities.

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Ronny Richter

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The Leipzig Canopy Crane facility: Towards a digital forest to study biodiversity and ecosystem functioning

The Leipzig Canopy Crane (LCC) is located within a species-rich floodplain forest and allows for full access to around 900 individual trees from 16 species, which enables researchers to study forest biota and forest functioning across height strata, reaching from the soil to the top of the canopy to the lower atmosphere. Within a total area of 1.6 ha, an onsite sensor network constantly provides data on a multitude of meteorological, edaphic, physiological, biological, morphological and phenological parameters at the single tree up to the stand level. This unique data is not only key to deepening our understanding of the biodiversity and functioning of temperate forest ecosystems at varying spatial and temporal scales, but furthermore allows to develop, test and calibrate innovative measurement techniques incorporating the interdisciplinary expertise from various research fields (e.g. remote sensing, data science, atmospheric research, molecular ecology) and thus will allow to address new research questions bridging the gaps between research disciplines. The newly gained information and data products will in particular foster a more detailed view on the mutual interactions between climate, forest condition and biodiversity. This will help to better understand and predict the consequences of climate change on forest health and composition and to monitor and estimate the direct and indirect effects on the vertical distribution and temporal dynamics of forest biodiversity across trophic levels. This is of striking importance as we are due to recent climate extremes currently faced with an unprecedented level of forest degradation and tree mortality.

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Solveig Franziska Bucher

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Plants as a periscope: Bringing light pollution from above to below the ground

Plants and animals use light as a source of energy and information. Artificial light at night (ALAN) is a rapidly growing and global biodiversity influence as it affects organisms in their physiology and their behaviour. However, we know very little about how these effects impact ecosystem processes and higher levels of biological organization.

We experimentally tested community-level responses to ALAN using grassland communities assembled in the iDiv Ecotron facility. We found diverse effects on animal movement, predation, and plant biomass and performance. Moreover, these effects even extended to soil organisms and soil properties. These results provide some of the first experimental evidence demonstrating that the threat of ALAN extends beyond organisms directly exposed to light.

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Species richness increases stability via asynchrony and diversity in drought-tolerance traits in a large-scale forest experiment

Extreme climate events such as droughts threaten forests and the multiple functions they provide. Understanding the drivers promoting forest stability is therefore considered crucial for forest management. Here, we examine the underlying drivers that promote stability from the tree neighbourhood to the forest community in a large-scale sub-tropical biodiversity experiment (BEF-China) with a gradient of 1 to 24 coexisting tree species. At the community level, we used Structural Equation Models to examine how tree species richness, asynchronous species dynamics, average species-level population stability and drought-tolerance traits relate to the temporal stability of productivity. We show that tree species richness increased community stability via increasing asynchrony. That is, asynchrony of inter-annual variation in productivity among tree species acted as a buffer against stress-induced reductions in productivity. This asynchrony was positively correlated with diversity in drought-tolerance, considering traits related to stomatal control and resistance-acquisition strategies, but not to the community-weighted means of these traits in the community. Observed diversity-stability relationships at the community level are likely shaped by local tree-tree interactions at the neighbourhood scale. Going the next step, we therefore explore mechanisms at the neighbourhood scale and provide insights into how tree productivity and physiological stress responses (measured as increase in wood carbon isotope composition, $\delta^{13}\text{C}$) to drought are driven by stomatal control and resistance-acquisition traits and by species richness. With these analyses across scales we hope to highlight how diversity stabilizes forest productivity.

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Bilyana Stoykova

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Wild bee body size and wing fluctuating asymmetry as response traits to anthropogenic disturbance in agriculturally dominated landscapes in Germany

Landscape alteration, agricultural intensification and climate change are the most important global change factors driving wild bee decline, but little is known whether these drivers have resulted in changes in the life-history traits of bees. Body size is one of the most fundamental life-history traits with pervasive effects on individual fitness; it determines the biology of a species, it drives ecological network structure and dynamics and correlates with metabolic rate, life history, energetic expenditure, diet, thermoregulation and home range size. Nevertheless, despite its importance, variability in bee body size across environmental gradients has received little attention. Another component of phenotypic variation, which has also received only sporadic attention, is fluctuating asymmetry. Fluctuating asymmetry is potentially maladaptive and reflective of the level of stress organisms are enduring. It is therefore of particular interest as an indicator of population health.

Here, I use wild bee species collected yearly since 2010 across changing rural landscapes in Germany for a species comparative analysis of how bee body size, its phenotypic variation and wing fluctuating asymmetry change over time and environmental gradients of anthropogenic disturbance. Furthermore, I aim to experimentally test, using bumble bee colonies, the effects of anthropogenic disturbance on body size and its variation. Overall my project aims to characterize patterns of variability of an important quantitative trait such as body size across bee species and across environmental gradients of environmental quality and analyse and compare fluctuating asymmetry in bees, with important conservation implications for biodiversity.

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Small-ranged species lose but large-ranged gain occupancy in the Anthropocene

Humans are accelerating pressures on biodiversity during the Anthropocene. Biodiversity is changing in multiple ways, and across multiple scales, through space and time. What is less clear is exactly how biodiversity changes manifests and which characteristics of species are associated with those changes. Here, we examined the relationship between a species' range size (i.e., widespread or narrowly distributed) and changes in their proportional occupancy through time from 203 time series of metacommunities (17,213 species distributed across 715,772 samples) that were monitored for 10 or more years. We found a positive association between a species' range size and changes in occupancy across the time series. Specifically, species with larger range sizes increase their occupancy overall, whereas those with smaller range sizes decrease their occupancy. The positive effects of range size were stronger in marine than terrestrial and freshwater realms. Moreover, the effects of range size become weaker in regions that have higher levels of protection in the terrestrial realm, meaning that habitat protection might be successful in stemming biodiversity changes. Our findings provide evidence on directional biodiversity change, where small-ranged species are 'losing' but large-ranged species are 'winning' during the Anthropocene, and emphasize that habitat protection and ecological restoration can provide important mitigation against the systematic changes in biodiversity.

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Using simulated grassland communities and radiative transfer models to test the Spectral Variation Hypothesis

Earth observation may help to monitor the rapid loss of biodiversity. A frequently discussed approach is an application of the Spectral Variation Hypothesis (SVH) for assessments of plant species diversity. According to the SVH, species diversity is directly linked to spectral pixel-to-pixel variation in image data, as the spectral signal is driven by biophysical properties of plant traits.

Despite promising results in the literature, the causal links between spectral variation and trait diversity remain unclear. Further research is needed with respect to fundamental limitations of the SVH that affect its (1) universal applicability, (2) standardization, (3) transferability and (4) sensitivity.

For a systematic assessment of the relationships underlying the SVH, we developed an approach to combine trait data from field measurements with canopy reflectance simulations. We used multi-temporal in-situ trait measurements from three structurally different grassland types to simulated artificial grassland communities in different phenological stages that we can further modulate for our analyses.

Based on these simulations, we aim to test the relations between the spectral variation and trait diversity. We further investigate the effect of spatial image resolution and consider the seasonal change in leaf and canopy trait influences on the relationship between spectral variation and species diversity. First results will be discussed.

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FUNSPEC – Developing methods for spectroscopic analysis of functional traits in Herbarium specimens

Herbaria represent valuable archives for tracking the responses of plant species to global environmental changes on a timescale that few experiments reach. Studies have already made use of these archives to investigate changes of distribution and phenology on historical timescales. Research on the impact of nitrogen deposition on plant traits and communities could similarly benefit, but tends to be hampered by the necessity of destructive laboratory work to analyse leaf nitrogen contents. A useful technology in this context is Near-Infrared Reflectance Spectroscopy (NIRS), which allows for the rapid non-destructive analysis of large numbers of leaf samples. This study tested the viability of NIRS for the leaf trait analysis of Herbarium specimens, with special attention paid to the effect of different conservation treatments. Three experiments were carried out to build a calibration dataset for leaf nitrogen and study the impacts of leaf shape, conservation methods and long-term storage on the analytical method. NIRS readings were taken of leaf samples both before and after conservation treatments and compared with leaf nitrogen contents measured in the laboratory. A statistical analysis was carried out to correlate the datasets, create calibration models and compare the accuracies attained. Prediction accuracies for leaf nitrogen were good and practically identical when comparing the NIRS readings taken before and after the treatments. The calibration models created are suited for the prediction of leaf nitrogen values from NIRS readings alone. This will make possible the large-scale, non-destructive measurement of leaf nitrogen contents in historic Herbarium specimens and allow for a detailed analysis of past and present trends.

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Teja Kattenborn

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Up, down, up, down ... tracking the diurnal motion of leaves with Deep Learning as proxy for stress and productivity.

The distribution of vertical leaves angles within canopies can be an important determinant for the competitive abilities of plants, its potential light interception, productivity, current water status or its reflectance as measured by satellites. Despite the importance of leaf angles as a plant trait for various disciplines, there exist only a few methods to track leaf angle variations. These are either very laborious or expensive (e.g. leaf angles retrieved manually by inclinometers or from terrestrial laser scanning data) and hardly scalable to high temporal resolution or long time series. Here, we present an effective approach to track the leaf angle distributions of plant canopies using lowcost cameras in concert with deep learning (Convolutional Neural Networks). The method predicts the distribution of vertical leaf angles in the field of view of standard RGB photographs. The approach was tested using the Leipzig Canopy Crane Facility, where we installed 18 time-lapse cameras for several months for *Tilia cordata* and *Acer pseudoplatanus* and predicted the leaf angle distribution at minutely interval. We show how leaf angle distributions co-vary with other plant environmental variables measured on-site. The presented approach is easily transferable to a range of species, plant forms or ecosystems.

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Towards a deep learning approach to extract leaf trait variation from digital herbarium specimen images

Nowadays, data-driven approaches are prevalent in almost every discipline of natural science; however, in the field of biodiversity, a lack of data often hinders the application of such solutions. Our research aims to improve this situation for one specific type of information: we would like to take advantage of digital herbarium specimen images to explore aspects of biodiversity change. These images cover broad ranges both in terms of space (all around the world) and time (dating back from 1600 to 2022). They are available in a large number for numerous species via well-established biodiversity platforms like GBIF (<https://www.gbif.org/>) and iDigBio (<https://www.idigbio.org/>). As of 31st January 2022, 33.3 million and 24.2 million digital herbarium specimen images for Tracheophyta are publicly available from GBIF and iDigBio platforms, respectively.

We are currently developing a deep learning-driven approach for the segmentation of individual leaves and the quantification of trait related information, e.g. leaf area or leaf perimeter. We will evaluate the extracted leaf trait information with leaf trait values collected via standard protocols in natural environments available in the TRY database (<https://www.try-db.org/TryWeb/Home.php>). The extracted leaf trait information will allow characterisation and understanding of leaf trait variation within and across species in both space and time based on data-driven approaches.

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Negin Katal

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Can we obtain phenology data based on plant observations collected by automated plant identification applications?

Plant phenology is the timing of seasonal events in plants, e.g., budburst, flowering, fructification, or senescence. Plant phenology is strongly linked to local climatic conditions, which are currently subject to substantial alterations due to climate change. Changes in phenology can have far-reaching consequences, from affecting species dispersal and disrupting species interactions to altering the carbon cycle and, in turn, influencing global climate itself. Therefore, great efforts are being made to observe, detect and predict changes in the timing of phenological events.

In Germany, phenological observation data are obtained by volunteers organized in a network with hundreds of stations operated by Deutscher Wetterdienst (DWD). They are broadly distributed across the country to cover the total variability, varying locally over several weeks depending on elevation and geographic position.

However, the number of observers is steadily decreasing, and alternative sources for collecting phenology data are urgently needed.

Automated plant identification apps, such as Flora Incognita, provide ten thousands of daily plant observations during the vegetation season. For many species, the observation patterns are strongly linked to the phenology of the species.

Here, we will compare the phenology data of five plant species from the DWD phenology network with Flora Incognita app users' observations data. We show that the peaking of app observations coincides with the beginning of the blooming phase obtained by the DWD observers for some of the compared species. These results imply that phenological monitoring can significantly benefit from opportunistic observations provided by plant identifications of app users.

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Jose Valdez

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Are current monitoring efforts able to detect global biodiversity trends?

Biodiversity is being lost at unprecedented rates and identifying biodiversity trends is an essential first step for effective conservation policy and management. However, quantifying biodiversity trends at the global scale remains largely unresolved and even controversial. The key question is whether monitoring sites are sufficiently representative of what is happening to biodiversity around the globe. In this study, we assess how many sites would be needed to detect global trends in local species richness and how they would be affected by time series length, site-selection biases, sampling noise, and spatial resolution or taxon group. We conclude that detecting accurate global trends using estimates from globally monitored sites is currently unreliable, and monitoring global biodiversity change requires implementing refined observation networks combined with models to account for biases, noise, and environmental drivers.

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The Global Restore Project: A metacommunity approach to ecological restoration synthesis

Ecological restoration has rapidly evolved from a local action taking place on an ad-hoc, site-by-site basis, to a major component of the United Nations Sustainable Development Goals, with the 'Decade on Ecosystem Restoration' announced to begin this year. Hundreds of millions of hectares of land are to be restored with billions of dollars spent. However, restoration outcomes are notoriously unpredictable making reliably meeting goals difficult. Setting and meeting these goals may be especially difficult when they focus on biodiversity. This difficulty may arise because compositional re-organization of ecological communities due to global change pressures interact metacommunity processes across space and time, which are also affected by anthropogenic disturbance. The paths to efficiently and effectively manage for or accelerate biodiversity recovery after anthropogenic disturbance and degradation remain unclear. We present the Global Restore Project (GRP) (globalrestoreproject.com), and point to how this project will help us to advance knowledge sharing for shared success in the United Nations Decade on Ecosystem Restoration. We highlight our metacommunity approach to synthesis and explain how this approach will help us to better understand and predict restoration outcomes and possibly plan restoration actions to better benefit biodiversity and people.

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Taking a ride on the rain - throughfall-mediated transport of bacteria within forest tree canopies

Phyllosphere microbiota play a key role in plant-microbe interactions supporting ecosystem productivity and drive biogeochemical cycles in association with forest tree canopies. Both tree species and canopy position were shown to shape phyllosphere microbial communities, however, the mechanisms underlying within-canopy spatial variation patterns have remained unclear. Here, we propose that throughfall, rainwater percolating through the tree canopy, plays a central role in the distribution of microorganisms. We leverage the infrastructure of the Leipzig Canopy Crane facility to (i) characterize the transport of microorganisms incoming from above the canopies and then via throughfall across top, mid and bottom position of the canopy of three tree species – *Quercus robur*, *Fraxinus excelsior*, and *Tilia cordata* and (ii) compare the microbial communities transported by throughfall to those attached to leaves. Throughfall samplers were deployed within the canopies at three different heights for a two-weeks period in March and May 2021. Quantitative PCR of bacterial 16S rRNA genes in throughfall revealed that abundances of transported bacteria increased from top to bottom in the leafless canopy in March. Foliage development in May led to community shifts in throughfall, along with increased numbers of transported bacteria. Moreover, 25 - 50% of the bacterial community members were shared between phyllosphere and throughfall, while throughfall shared 12 - 27% of taxa with open space precipitation. Our results suggest that transport of microorganisms by rainwater contributes substantially to spatial and temporal patterns of phyllosphere microbial communities in tree canopies and that the major source of the microbes (airborne, leaves and bark) depends on foliage development.

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Narendrakumar Chaudhari

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Accurate prediction of the metabolic potential of soil microbial communities using multiple gene annotation methods

Metagenomic surveys are instrumental in obtaining a quick overview of all the genes and genomes existing inside an environment. However, methods to detect/annotate these genes are limited by gene sequence databases and sequence similarity. Different annotation methods/parameters produce different annotation profiles for the same set of contigs/scaffolds assembled from metagenomes where the extent of false hits and incorrect metabolic reconstructions is higher.

To this end, we tried to integrate several standard methods (Kofamscan, Pfam, TigrFam, Interproscan) for annotation of contigs/scaffolds assembled from metagenomes where hits from more than one method can only be considered as correct annotation. Metabolic pathways are predicted based on only confirmed hits to assure better prediction of metabolic pathway completeness using tools like MEBS, METABOLIC, DRAM, if applied to Metagenome Assembled Genomes (MAGs). We plan to publish the code as a NextFlow pipeline compatible with HPC clusters. We also plan to use function-specific databases like dbCAN2/CAZy, MEROPS, HydDB to improve the predictions for pathways of interest.

We plan to demonstrate this on a test dataset of 314 global soil metagenomes available from iDiv Soil Taproot activities (Tea Bags Experiment) to get improved annotations using prokaryote-specific databases to look at the biodiversity and functional diversity from the perspective of a soil ecologist on a global scale. If possible, the predictions would also be applied to the MAGs recovered from these metagenomes to assess the metabolic potential and possible metabolic interactions among the most abundant microbial species. The pipeline would be implemented at iDiv server and would be directly accessible to users of iDiv HPC cluster.

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iCONNECT - integrative CONyza NETwork for Contemporary Trait evolution

Contemporary evolution of biotic interactions is a common occurrence where plant species shift their ranges and encounter novel interaction partners. However, our understanding of contemporary evolution is limited because most studies underestimate among-population variation (APV) across species ranges and do not disentangle how population histories drive APV. Furthermore, integrative frameworks of APV-focused research are lacking but could identify molecular mechanisms of contemporary evolution.

We here present the integrative network iCONNECT. iCONNECT is an open collaboration of researchers who contribute to the sampling of *Conyza canadensis* populations across the Northern hemisphere and researchers who investigate APV in their particular research field using these sampled populations.

We are performing a greenhouse experiment with 120 native and 150 non-native *Conyza* populations facing a competition × drought treatment combination. For these populations, we have field data as proxy for population history in terms of plant competitive regime, drought regime and fungal interactions in the rhizosphere. The samples will be analyzed in a coherent manner for 1) phenotypic APV (competitive ability under drought and well-watered conditions), 2) eco-metabolomic APV (mass spectrometry analyses of root exudates), APV in root-fungal interactions (amplicon sequencing), and 4) population genomics (ddRADseq).

Our experiment will shed light on how population history dictates biotic interactions across large spatio-environmental scales. Studying correlations between the investigated APVs will help unraveling how belowground mechanisms determine competitive ability and may identify metabolites and genomic regions associated with competitive ability and root-fungi interactions.

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Insights from the PanAf project: Long-term environmental stability, genomic diversity and demographic history of chimpanzee populations

Despite a wealth of work focusing on how past environmental change has affected biodiversity, we often lack insights into the mechanisms that may have driven observed patterns. These insights are highly relevant for understanding potential responses to future global change, but are particularly poorly understood in highly biodiverse tropical regions. Here, we focus on the Afrotropics, examining the genomic diversity and demographic history of chimpanzee (*Pan troglodytes*) populations across their entire range. We integrate high-throughput sequencing (whole-exome and chromosome 21) and paleoclimate data to reconstruct chimpanzee distribution and population demographic histories since the Last Interglacial (120 kya). Our results yield novel insights into population connectivity, size changes, and gene flow, which have in turn elucidated the role of landscape barriers, ecological gradients and forest refugia in shaping the contemporary diversity and distribution of chimpanzees.

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Leonie Röhler

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An online platform for robust indicators of terrestrial, freshwater, and coastal marine ecosystem extents to support Post-2020 monitoring and policies at multiple scales

Changes in the extents of different ecosystems (e.g. savannas, wetlands) are a key facet of biodiversity change. Accordingly, "Ecosystem Extent" is considered an Essential Biodiversity Variable, and the draft monitoring framework of the Post-2020 Biodiversity Framework prominently features ecosystem extent indicators. Classically, biodiversity indicators calculated directly from in-situ data are highly sensitive to unrepresentative sampling. Therefore, GEO BON promotes that indicators instead be based on contiguous 'data cubes' that integrate in-situ, remote-sensing and other data via predictive models, while explicitly controlling for biases and uncertainties.

We will present an alpha version of an online platform to annual, national- and subnational-level indicator time-series on ecosystem extents since the year of the Rio Convention (1992), embedded in a web page created using R's Shiny package. The indicators are based on the 'GlobES' data cube developed in the MAS lab. The website offers different views on ecosystem change indicators (e.g. via interactive maps and time-series charts) and allows downloading the complete indicator time-series. The indicator values will explicitly show uncertainties in the areal-change estimates, derived probabilistically from ecosystem- and region-specific classification uncertainties based on millions of global validation records. As more records become available via GBIF and other platforms, the indicators and their uncertainties will be periodically updated (e.g. half-annually). The indicators can support national reporting by countries with limited own monitoring capacities, while simultaneously providing independent, globally consistent evidence suitable for cross-national synthesis.

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Citizen Science Strategy 2030 for Germany - how to foster transformation in doing science

The current crises of climate and biodiversity change can only be met by finding joint solutions with society. Here citizen science can play a strong part, and by doing science together joint learning and development of sustainable solutions can emerge. Citizen science is now enshrined in the German government coalition contract as integral part of research. Here the Citizen Science Strategy 2030 for Germany highlights opportunities and challenges for 15 thematic areas, developed over 2 years together with over 200 participants from over 130 organisations. This talk will provide key insights into innovation potential for scientific discovery, scientific literacy and societal empowerment for collective action and illustrate this for biodiversity research in ongoing and planned iDiv citizen science projects FLOW, VielFalterGarten, MikroSafari, PflanzeKlimaKultur! and CityClim.

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SolACE - Solar Geoengineering in an Analytic Climate Economy

The paper analyzes solar geoengineering and strategic interactions in an integrated assessment model of climate change. We provide a simple formula for globally optimal sulfur deployment and analyze regional engagement in a dynamic Markov game. We derive the impact of geoengineering on the social cost of carbon (SCC). For a global social planner, solar geoengineering could cut the SCC into half if damages turn out negligible. Current damage guesstimates would reduce the globally optimal SCC by 12-22%. For non-cooperative regions, the availability of geoengineering can increase or decrease the SCC, in both active regions and the rest of the world. Our quantitative application finds that the cooling externality of the strategically acting region is negative on the margin, but positive overall, for most regions.

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People's interactions with nature and the health and wellbeing benefits that they deliver vary locally.

Greater exposure to, or contact with, natural environments, such as parks and forests have been shown to improve people's physical and mental health. The importance of nature exposure for people's health has been recognized by both global and local agencies, evident in the growing number of policies and programmes in cities that aim to increase the time people spend in nature for the health and wellbeing benefits delivered by such interactions. Yet, most of the evidence are based on studies conducted in western, non-tropical settings. Here, I will share how there is much local variation in how people interact with nature, by drawing on studies conducted in Singapore (Southeast Asia) and Brisbane (Australia). Factors that underpin our interactions with nature are culturally specific, and related to our connection to nature, inherent human values and the social groups that we refer to when making decisions. I also show how the relationships between nature exposure and people's health and wellbeing are not necessarily generalizable, and that focused studies are needed to develop effective interventions to address declines maximise the potential of nature exposure as a public health intervention tool.

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What drives seed dispersal effectiveness? Insights from a meta analysis

Seed dispersal is a critical phase in plant reproduction and forest regeneration. In many systems, the vast majority of woody species rely on seed dispersal by fruit-eating animals. Animals differ in their size, movement patterns, seed handling, gut physiology, and many other factors which affect the number of seeds they disperse and the quality of treatment each individual seed receives, and consequently their relative contribution to plant fitness. The Seed Dispersal Effectiveness framework (SDE) was developed to allow systematic and standardized quantification of these processes, offering a potential for understanding the large-scale dynamics of animal-plant interactions and the ecological and evolutionary consequences of animal behavior for plant reproductive success. Yet, despite its wide acceptance, the SDE framework has been primarily employed descriptively, and almost always in the context of local systems. We conducted a meta-analysis of all studies that quantified SDE globally and offer an integrative examination of the factors driving variation in SDE. Specifically, we addressed four main questions: (a) is there a tradeoff between high dispersal quality and quantity?; (b) what drives more variation in SDE, seed dispersal quality or quantity?; (c) do some animal guilds systematically provide higher SDE?; (d) How does animal body mass affect SDE?

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Buffering through timing: immediate and delayed responses to climate buffers effect of environmental variability in plant populations

Changing climate variability makes it vital for population ecologists to understand its consequences for population dynamics. Four components that mediate the consequences of climate variability have been the focus of previous studies: the magnitude of climate variability, the effect size of climate on vital rates, covariance between the vital rates, and autocorrelation in the climate. Recent studies have pointed to a fifth component: the different time windows of vital rate responses to climate (e.g. two vital rates responding to current or lagged climate). We hypothesize that the combination of different time windows and autocorrelated climatic drivers might modify the effect of climatic variability on long-term population growth rates.

Here we investigate the role of all five components on stochastic population growth using simulations of a hypothetical species, and simulations on 24 plant populations (16 species) using matrix population models (MPMs).

In the simulations performed on the hypothetical species, we found that including different time windows for vital rates responses to climate reduces the negative influence of increasing climate variability. This was especially strong when climate drivers change vital rates in the same direction, and climatic autocorrelation is negative. We show in our global assessment that negative climatic autocorrelations are common, and thus the potential for a buffering effect is likely at many locations on Earth. Our analysis of 24 populations shows that the buffering effects seen in the hypothetical species can extend to other life histories.

Our results suggest that species with vital rates that respond to climate in different time windows will often be buffered from population decline in an increasingly variable world.

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Biodiversity of bacteria associated with marine hydroid Hydractinia

Bacterial communities of marine organisms are of tremendous importance for their host as they fulfill important functions within the life cycle, nutrition, and protection against pathogens and predators. Hydractinia is a colonial cnidarian and a representative for many marine invertebrates. Certain bacteria repel larvae of hydractinia, others attract them and induce settlement followed by metamorphosis to the juvenile stage. Thus, the microbial composition of marine biofilms is a major key to understand the establishment and maintenance of benthic communities.

However, we hardly know anything about the composition, importance, and functions of Hydractinia's associated bacteria and if the organism requires the constant presence of bacterial species. Here, we explored if Hydractinia colonies contain specific bacterial taxa and whether or not the mature organism maintains the bacterial strains. To address this question, we performed a metagenome study of hydractinia colonies to compare the bacterial diversity in two different hydractinia species from the North sea near the Sylt station of the Alfred-Wegener-Institute (AWI) in Sylt, Germany and the North Atlantic coast near Woods Hole Oceanographic Institution, USA. This allowed us to answer the question of whether both Hydractinia species harbors a specific microbiome and which functions they might fulfill. Our comparative analysis indicates that several bacterial lineages are specific to both Hydractinia species and fulfill important functions for the development of hydractinia colonies.

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Mammalian metabolomics: understanding chemical diversity of different scent sources in mammals

Chemical cues used for communication in many plant and animal species are ubiquitous. While plants have been studied widely, challenges remain to understand chemical signalling in animal metabolomics. A wide variety of chemical cues arises from various scent sources. In mammals, for example, secretions from specialized scent glands, excretions such as urine and faeces, or body odours convey chemical information. However, there is a gap of systematic studies investigating differences between scent sources and establishing suitable methods to detect respective chemical cues. Accordingly, this study examined chemical cues in three scent sources (urine, faeces, body odours) and compared three sampling methods (thermal desorption tubes, polydimethylsiloxane sticks, headspace analysis). Chemical samples were collected from free-ranging female (N = 8) and male (N = 6) Barbary macaques (*Macaca sylvanus*) at Affenberg Salem (Germany). After GC-MS analysis, we found differences in chemical composition of different scent sources, but also between the different sampling methods used simultaneously for each scent source. As a proof of concept, we investigated whether chemical composition was affected by sex of the individuals. Different sex-specific substances were found depending on the scent sources and used method. Our results thus show different chemical cues produced in different scent sources, which could be used for communication in Barbary macaques. Importantly, our study underlines that the choice of both, methods and scent sources, influences which part of the chemical spectrum can be studied. It thus provides a valuable contribution selecting appropriate methods for future studies in animal metabolomics such as unravelling pesticide load of wildlife in monocultures.

Authors: M. **Kücklich**, iDiv, Leipzig University, MPI-EVA Leipzig; C. **Birkemeyer**, Leipzig University; A. **Widdig**, iDiv, Leipzig University, MPI-EVA Leipzig; B. M. **Weiß**, Leipzig University, MPI-EVA Leipzig.

Francisco Javier Velásquez Puentes

Leipzig University

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

Abiotic drivers of trait evolution in the genus *Swartzia*.

The study of Morphological traits in plants is essential as traits mediate the interactions between plant species and the surrounding biotic and abiotic environment. In this study we examined traits related to leaves, fruits and flowers in the neotropical genus *Swartzia*, the most species rich papilionid legume group. The goal of the study is to determine how the abiotic environment (i.e. climatic and soil characteristics) has shaped the evolution of those traits. We hypothesize that environments with extreme conditions (i.e. those with lowest rainfall, highest temperatures and poor nutrient soil contents) have shaped trait evolution by imposing strong selective pressures. In order to test our hypotheses, we used a curated dataset of taxa for which we collected trait data from monographs and herbarium collections. We also gathered climatic and soil data from public databases. In addition, we generated a dated phylogeny with previously published plastid and nuclear markers. Phylogenetic data was integrated with climatic, soil and trait data to study the relationship between the environmental variables and the traits in an evolutionary context, in addition we applied different methods ranging from linear models and comparative phylogenetic methods to test our hypotheses. We found that different climatic variables such as seasonal environments, low rainfall and poor soil nitrogen contents are important predictors of the studied traits, and in some cases we found evidence of correlated evolution between a given trait and the environment. This study highlights the role of abiotic factors in shaping plant trait evolution in the neotropical region and contributes to the scarce literature of evolutionary studies in neotropical plants integrating traits and climate.

Authors: F. **Velásquez - Puentes**, iDiv, Leipzig University; T. **Pennington**, University of Exeter; A. **Zizka**, Marburg University. C. **Barratt**, iDiv, Leipzig University; R. **Onstein**, iDiv, Leipzig University.

Zhongguan Jiang

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

Multifaceted biodiversity-based conservation planning in the Yangtze river-floodplain ecosystem

Biological conservation necessitates robust understanding of multifaceted biodiversity from local to regional scales. The Yangtze River floodplain is among the most speciose whereas threatened and poorly protected ecosystems in China. Here we evaluated multifaceted (taxonomic, phylogenetic, and functional) alpha and beta fish diversity by simultaneously addressing two typical habitats (FRs, floodplain rivers and FLs, floodplain lakes) in this basin, to reliably aid conservation planning across local and regional scales. Our results

demonstrated spatially incongruent multifaceted fish diversity between FRs and FLs. Characterizing by flocks of phylogenetic close species, we detected significantly higher species richness while lower phylogenetic and functional alpha diversity in FRs. In contrast, fish assemblages in FLs exhibited significantly higher functional alpha diversity characterized by functional unique species. Consequently, conservation planning should fasten on clusters of phylogenetic close endemic species to sustain high intrinsic species richness in FRs, and sustain high functional diversity as well as protecting fish species with unique functions in FLs. Meanwhile, for all the taxonomic, phylogenetic, and functional facets, our results demonstrated significantly higher turnover components in FRs, and the dominant contribution of the nestedness components to overall beta diversity in FLs. As a result, conservation planning in FLs may just focus on several richest lakes, while multiple spatially disjunct river networks should be protected in FRs. Contradicting the anthropocentric “new conservation”, our study advocated protecting intrinsic uniqueness and peculiarity of multifaceted biodiversity as well as the ecological integrity.

Authors: Zhongguan **Jiang**; Bingguo **Dai**; Chao **Wang**; Wen **Xiong**.

Yan Li

*Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences
German Centre for Integrative Biodiversity Research (iDiv)
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Plant diversity improves resistance of plant biomass and soil microbial communities to drought

Biodiversity is known to affect ecosystem resistance and have implications for the maintenance of ecosystem functions and services under climate change. Compared to numbers of studies focusing on aboveground vegetation, the response of belowground communities to abiotic stresses along plant diversity gradients is often ignored and is considered an important knowledge gap in ecosystem ecology. Here we conducted an integrative research to evaluate the resistance of plant biomass, and soil microbial communities and associated functional profiles to drought under varying plant diversity. We carried out a three-year manipulation experiment by factorially controlling plant diversity gradient (1, 2, 4, and 8 species richness) and soil moisture treatment (drought and non-drought), and investigated the responses of plant biomass, soil bacterial and fungal diversity and community composition, soil glomalin, and five key soil enzymes. We found that plant diversity significantly improved the resistance of soil fungal communities and microbial functional profiles characterized by soil glomalin and five key enzymes, which was partly driven by the availability and accessibility of soil resources (e.g., soil moisture and organic matter) mediated by plant diversity. Further, our results indicated that the enhanced resistance of fungal communities was consistent with ecological insurance theory that diverse fungal communities at high plant diversity had a higher probability of containing taxa that adapt to drought. Our study provides novel empirical insights into the mechanism underlying the regulatory effect of plant diversity on resistance of aboveground vegetation and belowground biota to drought, with implications for understanding ecosystem response to climate change and improving biodiversity conservation practices.

Authors: Yan **Li**; Jiang **Wang**; Congcong **Shen**, Jichen **Wang**, Brajesh K. **Singh**, Yuan **Ge**.

Platforms for biodiversity science (poster session)

Jens Kattge

Max Planck Institute for Biogeochemistry (MPI BGC)

TRY Plant Trait Database

The Poster will present an update on the TRY Plant Trait Database Version 6.0: data coverage and connectivity.

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Stan Harpole

Helmholtz Centre for Environmental Research – UFZ

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

Martin Luther University Halle-Wittenberg

iCyt – integrative Cytomics-Platform (Support unit)

The iDiv support unit called “iCyt” (“integrative Cytomics”) measures cells and particles in suspension independent of their origin (water, soil or air samples of plant, animal or human origin). Our unique cutting-edge high-throughput measurement abilities of individual particles in powerful combination with deep-learning algorithms represent a transformative advance for improved air and water quality monitoring, as well as the study of plant-pollinator interactions.

Olga Ferlian

Leipzig University

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

MyDiv

The role of mycorrhiza in tree diversity effects on ecosystem functioning and trophic interactions – An experimental platform

The positive relationship between biodiversity and ecosystem functioning is often attributed to complementarity among functional traits between different species, thereby e.g., increasing nutrient uptake. Mycorrhizae play an important role in plant nutrient and water uptake from soil and, consequently, in nutrient cycling of the whole system. Ectomycorrhiza and arbuscular mycorrhiza are characterised by fundamentally different strategies. It has often been found that in plant communities with highly diverse mycorrhizae the utilisation of soil nutrients is more efficient as compared to less diverse ones. Moreover, from a trophic perspective, mycorrhizal fungi serve as food source for fungal feeding soil fauna and, therefore, contribute substantially to carbon flow between trophic levels. However, the roles of the two major mycorrhizal types within the soil food web are still poorly understood. The iDiv platform MyDiv aims to study the influence of a crucial biotic interaction – mycorrhizal association – on the relationship between tree diversity and ecosystem functioning. The experiment focuses on the following main hypotheses: (I) AM fungi and EM fungi are a source of functional complementarity between different tree species. (II) Diverse mycorrhizal associations enhance the positive relationship between tree diversity and ecosystem functioning. (III) Tree communities with diverse mycorrhizal associations foster more diverse soil animal communities compared to communities of only one mycorrhizal type.

Authors: Olga **Ferlian**, Nico **Eisenhauer**.

Abigail Moreno-Pedraza

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

Using mass spectrometry to elucidate the spatial distribution of metabolites during plant-herbivore interactions

Mass spectrometric imaging (MSI) has become a very popular and powerful technique to study the localization of molecules directly from tissues, mainly used in mammals and more recently implemented in plant sciences. MSI can be carried out using traditional techniques operating in a vacuum, but also under ambient conditions. The latter offers the possibility of studying biological systems in their native state, analyzing tissues with minimal manipulation and even without sample preparation, which allows a much more realistic result to be obtained. Among the ambient techniques, a combination of a laser desorption and a low-temperature plasma ionization source (LD-LTP) has recently been developed and tested for the analysis of undisturbed plant material with a lateral resolution of 50 μm . Thanks to the Alexander von Humboldt postdoctoral fellowship, I will be able to set up an ambient imaging system in the Molecular Interaction Ecology laboratory to study the metabolic status during plant-herbivore interactions in order to have better insights into the metabolic state in Brassica plants, however, the imaging platform will be available for studying the metabolic state of diverse samples ranging from a few millimeters to centimeters.

Authors: Abigail **Moreno-Pedraza**; Nicole M. **van Dam**.

Alexandra Weigelt

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

The iDiv Greenhouse: an innovative facility accommodating a wide variety of demands for experimental biodiversity research

The iDiv research greenhouse offers 700 m² of effective area for high-end experimental biodiversity research. This includes 400 m² innovative greenhouse space subdivided in 10 regular cabins and 2 cabins for S1 use. All cabins are equipped with tables adaptable to differing pot sizes. Cabins provide different water types using an automated dripping system. Optimized artificial lights complement the natural sunlight, and air humidity is regulated with a high-pressure fog system. Cabin temperatures are regulated actively via modern and energy-effective heating and cooling systems and passively via energy screens on the out- and inside of the greenhouse roof. Experimental microcosms need proper preparation; experiments often need to be set up in short time spans with many helpers to maximize comparability of plants and treatments – this needs working space inside and outside. At final harvest, samples need to be stored cool before being processed, frozen, dried or freeze-dried, shredded, milled, weighed or counted. Often also roots need washing and scanning before further processing. To accommodate all these demands, the greenhouse is supplemented with a 300 m² building part which offers an open working space with a root washing table, two fully equipped labs, freezers, drying ovens and a cooling room. The iDiv greenhouse is equipped to accommodate a wide range of approaches aiming to support the wide variety of excellent biodiversity research at iDiv. Last and certainly not least, users will benefit from the expertise of Alvin Barth (gardener), and Robert Altmann (greenhouse technician). The iDiv greenhouse can be used for research projects of all iDiv members and their groups. Application forms are available online.

Nico Eisenhauer

Leipzig University

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

The Jena Experiment

The last three decades of biodiversity–ecosystem functioning (BEF) research have provided compelling evidence for the significant positive role of biodiversity in the functioning of many ecosystems. Despite broad consensus of this relationship, the underlying ecological and evolutionary mechanisms have not been well understood. The current Research Unit of the Jena Experiment aims at filling this gap of knowledge by applying novel experimental and analytical

approaches in one of the longest-running biodiversity experiments in the world. The central aim of the Research Unit is to uncover the mechanisms that determine BEF relationships in the short- and in the long-term. Increasing BEF relationships with time in long-term experiments do not only call for a paradigm shift in the appreciation of the relevance of biodiversity change, they likely are key to understanding the mechanisms of BEF relationships in general. The subprojects of the this Research Unit fall into two tightly linked main categories with two research areas each that aim at exploring variation in community assembly processes and resulting differences in biotic interactions as determinants of the long-term BEF relationship. The unification of evolutionary and ecosystem processes requires collaboration across the proposed subprojects in targeted plant and soil history experiments using cutting-edge technology and will produce significant synergies and novel mechanistic insights into BEF relationships. The Research Unit of the Jena Experiment is uniquely positioned in this context by taking an interdisciplinary and integrative approach to capture whole-ecosystem responses to changes in biodiversity and to advance a vibrant research field.

Yvonne Poeschl-Grau

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

EcoMetabolomics Platform for Ecology & Biodiversity Research (EcoMetEoR)

Metabolomics is an untargeted biochemical approach to measure many thousands of metabolites, small metabolic molecules, in different species. Eco-Metabolomics is the application of metabolomics techniques to ecology with the aim to characterize biochemical interactions of organisms across different spatial and temporal scales. [1]

We will present our platform EcoMetEoR that aims to provide full access to a team of biodiversity researchers and ecologists with instrumental infrastructure and personal expertise to implement targeted or untargeted (eco-)metabolomics.

One of the greatest advantages of metabolomics is that it can be applied to any species. In order to understand the relevance of the myriad of still largely undiscovered compounds produced by these organisms, untargeted metabolomics is most suitable. It provides a snapshot of the physiology of the organism and helps to identify patterns of metabolites that have biological relevance for the specific ecological question. In addition, we routinely do targeted analyses e.g. for phytohormones or volatile organic compounds. [2]

Usually, researchers having a project idea, where metabolomics data can help to answer the research questions approach us for support. Together we set up a pre-experiment to evaluate the feasibility of the project. Based on that, we give guidance on sampling and sample preparation, whereas we perform the sample measuring on our instruments. Finally, we support data processing, data analyses and compound annotation and give guidance on data sharing in open access data bases.

Please meet us at the iDiv conference to discuss opportunities for doing metabolomics in your project.

1 Peters, K., et al. (2018). doi:10.3390/ijms19051385

2 Uthe, H., et al. (2020). doi:10.1016/bs.abr.2020.09.019

Authors: Yvonne **Poeschl**; Nicole **van Dam**; Henriette **Uthe**.

Jes Hines

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

iDiv Ecotron: What would you do if you could rebuild the world?

Assemble. Disassemble. Reassemble. The iDiv Ecotron is a mesocosm facility that provides infrastructure for experimental manipulation of biotic communities (aboveground and belowground) and abiotic environment (e.g. precipitation, nutrients) in terrestrial ecosystems. Established in 2017, based on a collaboration between UFZ and iDiv, the iDiv Ecotron has hosted eight unique experiments and is now a key feature of many current project proposals by iDiv members and beyond. Each of 24 EcoUnits can be divided into 4 subunits allowing for 96 experimental units with either intact soil monolith cores or a filled soil profile. We welcome proposals from scientists who wish to test hypotheses in a wide variety of plant and animal systems. What would you do if you could rebuild the world?

Marten Winter

Leipzig University

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

GloNAF – Global Naturalized Online Floras (www.glonaf.org)

This virtual iDiv platform is a dataset providing the Global Naturalized Alien Flora (GloNAF) database. Why is it an iDiv platform? Marten Winter, head of sDiv is one of the eight GloNAF PIs and founder of this dataset. GloNAF started 2011 and was already used in several studies with iDiv participation.

GloNAF represents a data compendium on the occurrence and identity of naturalized alien vascular plant taxa across geographic regions (e.g. countries, states, islands) around the globe. The dataset includes 15,357 taxa, covering 1,339 regions in all continents (including >380 islands). The dataset is based on 319 data sources. For each taxon-by-region combination, we provide information on whether the taxon is considered to be naturalized in the specific region (i.e. has established self-sustaining populations in the wild) and if available, if defined as invasive.

The database also provides a shapefile including polygons for each region, information on whether it is an island or a mainland region, the country and the Taxonomic Databases Working Group regions it is part of (TDWG levels 1-4).

We also provide several variables that can be used to filter the data according to quality and completeness of alien taxon lists. GloNAF has already been used in >50 studies on e.g. historical spatial flows of taxa between continents, geographical and evolutionary patterns and determinants of naturalization across different taxonomic groups. GloNAF is cited more than 4000 times already (see <https://tiny.cc/sdivscholar>).

We intend the update and expand GloNAF presented here to be a global resource useful for studying plant invasions and changes in biodiversity from regional to global scales.

Authors: Marten **Winter**; Wayne **Dawson**; Franz **Essl**; Holger **Kreft**; Jan **Pergl**; Petr **Pyšek**; Mark **van Kleunen**; Patrick **Weigelt**.

Lena Kretz

Leipzig University

Helmholtz Centre for Environmental Research – UFZ

The research arboretum ARBOfun: linking above and belowground traits to tree functioning under climate change

The arboretum ARBOfun is a research platform of iDiv, which was established in 2012 in Großpösna south of Leipzig. It harbours close to 100 different forest relevant tree species being native to Central Europe or frequently planted in plantations. Five individuals per species were planted in a randomized block design with a distance of 5.8 m to each other to exclude competition. ARBOfun is perfectly suited to assess fundamental, species-specific traits and performance rates under the same environmental conditions.

The arboretum was designed to study the relationship between above- and belowground functional traits on the one hand and whole tree structure and functioning on the other hand to predict tree species identity effects in ecosystems. Examples for processes investigated in the past years are effects of root orders on root functional traits, induced leaf defence against insect and mammalian herbivores, and nutrient re-translocation in leaves. The trees have been used as ground truthing for remote sensing of tree physiological rates. Given that trees are growing in isolation and are therefore well coupled to the atmosphere, ARBOfun is also ideally suited to study the effects of the severe drought in 2018-2020 on drought resistance and resilience. Preliminary results on consecutive drought effects on shoot growth indicate that the growth resistance of terminal and lateral shoots is negatively related to tree size and thus growth rate.

For 2022 it is planned to establish a network of sensors measuring soil temperature and moisture as well as the installation of a climate station for future in situ measurement of abiotic conditions within the ARBOfun. To enable access to the upper canopy a lifting platform is now available to reach the tree tops.

Authors: Lena **Kretz**; Ronny **Richter**, iDiv, University Leipzig; Alexandra **Weigelt**, University Leipzig, iDiv; Florian **Schnabel**, iDiv, University Leipzig; Tom **Künne**, University Leipzig; Christian **Wirth**, University, iDiv, MPI.

Aldo Compagnoni

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Helmholtz Centre for Environmental Research – UFZ
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The Global Woody Demography database: a resource for vulnerability assessments and comparative demographic analyses of woody plants

Demographic population models are the golden standard for assessing the population dynamics and the conservation status of plants. Such demographic data mostly come from herbaceous perennial species in temperate environments. For example, in COMPADRE, the largest database containing plant population models, 362 out of the 758 species are herbaceous perennials. However, most plant diversity is concentrated among tropical and subtropical woody species, and these woody plants provide important ecosystem services. We assembled the Global Woody Demography (GWD) database to enable synthesis of demographic data that is available for the world's woody plant species. The GWD database contains data on the survival, growth and reproduction of 4548 (taxonomically resolved) woody species collected across 13 large forest plots. The demographic data in the GWD database is designed to parameterize perfect plasticity approximation (PPA) models – mathematically tractable models of light competition in forests.

Here, we show the potential of this database by combining its demographic data with PPA models to produce estimates of generation time – a useful metric for species vulnerability assessments. We perform an example using 241 species studied at the Barro Colorado Island site, in Panama. Our generation time estimates correlate with measures of life-history continua in trees, with the survival of dominant trees, and growth of suppressed trees. Expanding the applications of the GWD database will be straightforward, and we thus believe this data resource can be applied to a variety of questions ranging from understanding variation in the life histories and population dynamics to threat assessments and conservation prioritization for the world's woody plant species.

Authors: A. **Compagnoni**, iDiv, Helmholtz Centre for Environmental Research – UFZ, Martin Luther University; B. **Ohse**, iDiv, Helmholtz Centre for Environmental Research – UFZ; N. **Rüger**, iDiv, University of Leipzig; T. **Knight**, iDiv, Helmholtz Centre for Environmental Research – UFZ, Martin Luther University.

Martin Schädler

Helmholtz Centre for Environmental Research – UFZ

The Global Change Experimental Facility - investigating the consequences of climate change in agroecosystems

Climate change and land-use change are important threats to ecosystems and can be expected to have interacting influences on ecosystem functions directly and indirectly. Knowledge about these interactions is limited due to a lack of experiments which investigate climate change effects under different land-use scenarios. Among the processes involved in ecosystem responses to global change, in particular, those occurring in soils or related to biotic interactions and microevolution were underinvestigated in previous experiments. Examinations of these relationships require spatial and temporal scales which go beyond those realized in the majority of ecological field experiments. We introduce the Global Change Experimental Facility (GCEF), which was designed to investigate the consequences of a future climate scenario for ecosystem functioning in different land-use types on large field plots (400 m²). Climate manipulation is based on projections for the period of 2070–2100 with an increased temperature and a changed precipitation pattern consisting of reduced precipitation in summer and increased precipitation in spring and autumn. We subject five different land-use types (two farming systems, three grasslands), differing in land-use intensity, to ambient and future climatic conditions. The large plot size and the technical configuration allow the establishment of realistic land-use scenarios and long-term observations of responses of ecosystem functions and community dynamics on relevant temporal and spatial scales. Thus, the GCEF provides a well-suited platform for the interdisciplinary research on the consequences of climate change under different land-use scenarios.

Authors: M. **Schädler**, UFZ; Dept. Community Ecology; H. **Auge**, UFZ; Dept. Community Ecology; F. **Buscot**, UFZ; Dept. Soil Ecology; S. **Klotz**, UFZ; Dept. Community Ecology; T. **Reitz**, UFZ; Dept. Soil Ecology.

Maria Fabisch

Friedrich Schiller University Jena

Collaborative Research Centre 1076 AquaDiva – Understanding the Links between Surface and Subsurface Biogeosphere

The Earth's Critical Zone (CZ) is the layer that extends from the vegetation on the surface to the groundwater in the subsurface. The principle aim of the CRC AquaDiva is to increase our understanding of how water (Aqua) links surface and subsurface and how local geology and surface conditions set subsurface functional diversity (Diva) and ecology. Our central questions are: How deep do surface 'signals' penetrate into the subsurface? What is the role of events in the dynamics of the subsurface biogeoreactor? What is more important to subsurface life – land cover or geology? We established the Hainich Critical Zone Exploratory (CZE) in western Thuringia, which encompasses two main aquifer assemblages along a ca. 6 km hillslope transect in alternating limestone–mudstone rock. In addition, we established the Saale-Elster-Sandsteinplatte Observatory (SESO) in eastern Thuringia in acidic sandstone rock with similar surface land cover but different geology. Based on these contrasting geologic settings, we will generalize our concepts and develop predictions about the response of subsurface life to pollution, land-use, and climate change scenarios and the consequences for water resources. In two combined posters, we aim to introduce our facilities, demonstrate how research activities come together addressing AquaDiva's overarching goals, and share our recent research highlights with the iDiv community.

Authors: K. **Küsel**, iDiv, Institute of Biodiversity, Friedrich Schiller University Jena; S. **Trumbore**, Department of Biogeochemical Processes, Max Planck Institute for Biogeochemistry; K. U. **Totsche**, Institute of Geosciences, Friedrich Schiller University Jena; M. **Fabisch**, Institute of Biodiversity, Friedrich Schiller University Jena.

Carsten Meyer

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

Strategic project 'iUPDATE' – Iterative Improvements in Understanding, Prediction, and Driver-Attribution of Trends in Ecological Systems

Understanding of long-term biodiversity trends has recently seen a shift from the classical 'biodiversity loss' paradigm to one that emphasizes complex patterns of 'biodiversity change' characterized by winners and losers. Evidence of spatiotemporal and taxonomic patterns of biodiversity change is increasing rapidly, as more regional to global biodiversity-monitoring schemes established over recent decades accumulate long-enough time series, and as more historical field datasets are integrated into global databases (e.g., BioTime, BioDivBank, and sPlot). Similarly, emerging long-term time-series data on anthropogenic drivers are shedding new light on the causes of variability in biodiversity trends among different species groups and regions. The rapid growth of biodiversity databases and the continued pressure on biodiversity from anthropogenic sources requires up-to-date synthesis of patterns and drivers of biodiversity change to support applications in science and policy. Subsequently, the overarching goal of iUPDATE is to foster this updating process within iDiv, i.e., moving from one-off analyses to regular re-analyses that help continuously improve inference and application. To this end, the iUPDATE project develops an integrated system of analytical pipelines that tap into different, continuously growing databases, different showcases studies, and online dashboards designed to communicate regularly updating scientific results. Among the initial showcases of iUPDATE are studies on changes in species communities due to the interaction of land-use and climate change, and policy-relevant national indicators of ecosystem changes.

Authors: Carsten **Meyer**, UL & Jonathan **Chase**, MLU (coordinating PIs of the strategic project), Kimberly **Thompson**, iDiv & Ruben **Remelgado**, iDiv (iUPDATE postdocs), and several iDiv members and postdocs who lead/collaborate on specific studies.

Samira Babalou

Friedrich Schiller University Jena

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

iKNOW: A Semantic Toolbox for Reproducible Knowledge Graph Generation in the Biodiversity Domain

Knowledge Graphs (KGs) are graph-structured knowledge bases storing factual information in the form of relationships between entities, e.g., “tree_species has_trait average_SLA” or “Achillea_millefolium is_observed_in Jena_Botanical_Garden”. Most KGs encode these statements in RDF (Resource Description Framework). With this, data can be easily queried, explored and linked across data sources. Using KGs to manage biodiversity information and develop an integrated knowledge base linking information about species, individuals, traits, projects, people, etc., has been proposed a decade ago, already. Up to now, though, creating such KGs requires large manual effort. Often, the resulting KGs cannot easily be reproduced or updated. In the iKNOW Flexpool project, we aim to provide a semantic-based toolbox to support the creation of reproducible KGs. Together with the PlantHub project, this toolbox will be used to transform important iDiv databases to KGs, facilitating their integration and exploration. Creating a KG from tabular data requires a number of steps: First, data needs to be cleaned. Here, we rely on the existing tools and workflows used by well-curated iDiv databases and will integrate those in our toolbox. For the next steps, we will offer a set of tools for different KG functionalities’ management such as entity linking, RDF creation, and visualizing. Such tools accelerate the cross-links of iDiv databases to the external KGs like Wikidata and also interlink iDiv databases. Owners of data sources that aim to create a KG from their source will be able explore the toolbox and adapt the existing workflows to their needs. Retrieving knowledge in our KG will be possible via either the SPARQL endpoint or free-text search functionality.

Authors: S. **Babalou**, iDiv, Institute for Computer Science, Friedrich Schiller University Jena; D. **Schellenberger Costa**, iDiv, University of Leipzig; F. **Zander**, Institute for Computer Science, Friedrich Schiller University Jena; H. **Bruelheide**, iDiv, Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg; J. **Kattge**, Max Planck Institute for Biogeochemistry, Jena; C. **Römermann**, iDiv, Friedrich Schiller University Jena; C. **Wirth**, iDiv, University of Leipzig; B. **König-Ries**, iDiv, Institute for Computer Science, Friedrich Schiller University Jena.

Stefan Trogisch

*German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
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BEF-China Tree Diversity Experiment

Among the current 28 tree diversity experiments, BEF-China (<https://bef-china.com>) is the largest experiment worldwide in terms of the number of planted trees (> 300,000 trees) and species (19 evergreen and 21 deciduous species). Located in the Chinese subtropics (Xingangshan, Jiangxi Province) on a total net area of 38.4 ha of sloped terrain at two sites (Site A and Site B), the experiment features a diversity gradient including tree species richness levels of 1, 2, 4, 8, 16 and 24 species. Trees were planted in 2009/2010 on 566 plots of 25.82 m x 25.82 m, each planted with 400 trees (20 x 20 individuals) with a horizontal planting distance of 1.29 m. Tree species within a plot have been randomly assigned to planting positions, and a broken-stick design ensures that each species occurs the same number of times at every richness level. To account for the understory contribution to forest functioning and to assess the role of shrub diversity, different numbers of shrub species (0, 2, 4 and 8 species) were planted between trees on a subset of plots. The BEF-China platform is complemented by 27 comparative study plots in the Gutianshan National Park (Zhejiang Province).

In the last years, BEF-China has developed into a major platform for large collaborative research initiatives like the International Research Training Group TreeDì (www.treedì.de) at iDiv and the University of Chinese Academy of Sciences. The aim of TreeDì is to understand how tree-tree interactions in local neighbourhoods of varying diversity translate into the observed positive tree species richness effects on key ecosystem functions at the community scale. BEF-China is a member of the global network of tree diversity experiments (TreeDivNet) and welcomes new collaborations.

Authors: S. **Trogisch**, Martin Luther University Halle-Wittenberg, iDiv; XJ. **Liu**, Institute of Botany of the Chinese Academy of Sciences (IBCAS); H. **Bruelheide**, Martin Luther University Halle-Wittenberg, iDiv; KP. **Ma**, Institute of Botany of the Chinese Academy of Sciences (IBCAS); **International Research Training Group TreeDì**.

Anahita J.N. Kazem

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Integrative Biodiversity Data & Code Support Unit (iBID)

Biodiversity science is becoming evermore data- and computationally intensive. Treating data and code as first-class citizens in scientific endeavours is thus crucial to this discipline. iDiv's Data & Code Unit (iBID) aims to support researchers in making our science globally accessible and enabling others to build upon it, with an emphasis on the production of high quality, open and FAIR data, and well-documented open software. To position iDiv in the forefront of the ongoing cultural shift towards more open data and science, we take a two-pronged approach. Firstly, we offer data and code stewardship: providing curation services to enhance the reusability of research results, individual support in publishing data and code, the minting of DOIs, and capacity building. In parallel on the technical side, we run and extend the underlying infrastructure (including multiple public data repositories), as well as supporting iDiv projects by building custom databases and web applications. Drop by to learn more about iDiv initiatives in fostering open science and how we can support you in achieving them.

Keywords: open science, FAIR principles, data repository, archiving, software development

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NEu — Nutrient Network Europe (strategic project)

The aim of the NEu Strategic Project is to realize a European-focused sub-network of the Nutrient Network (NutNet) that is centered in Germany, at iDiv. Our goals are to 1. develop new question-driven science initiatives that focus on regional biodiversity questions and environmental problems, and to advance synthesis by leveraging unique local opportunities to bring in new data that was not previously possible before; 2. actively pursue new German and European collaborations, partnerships and funding opportunities, again leveraging the critical mass of the iDiv community

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The TrophinOak - PhytOakmeter platform

TrophinOak and PhytOakMeter focus on biotic and abiotic interactions with the in vitro propagated clonal Oak tree DF159 (*Quercus robur* L.) under laboratory and field conditions, respectively.

With the TrophinOak platform, we first studied the impact of detrimental and beneficial interactions using collembola, caterpillars, nematodes, fungal mutualists and parasites. Transcriptomic and metagenomic analyses were coupled with growth traits and C/N allocation analyses in order to better understand how the endogenous rhythmic growth displayed by this major forest tree interplays with its complex multitrophic interactions. Four projects were run on this TrophinOak platform. The DFG project TrophinOak itself was complemented with two iDiv Flexpool projects "Mycorrhizal interactions of different fungi with oak trees" and "PlastOak" and a Marie curie EU grant "OakMykEvo".

From 2010 on, DF159 clonal saplings were released in the field as phytometers in two time series over 10 Years on sandy and chernozem soils, respectively. The PhytOakmeter platform also includes sites selected along a European climate gradient from Finland to Southern France. To tackle the influence of water relations, they also included a precipitation gradient along the central German TERENO sites in Saxony Anhalt. Modifications in soil microbial community composition under the influence of the oak clone were studied in 2018 using amplicon sequencing. The data were related to oak growth traits, but also to climatic and edaphic variables. The presented Oak platform is an ideal tool to study acclimation and adaptation of a long-lived forest tree to ecological variations and climate changes in the near future.

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