iDiv Conference 2024

Wednesday, 13 November 2024 - Friday, 15 November 2024

Leipziger KUBUS Helmholtz-Zentrum für Umweltforschung – UFZ

Book of Abstracts

Table of contents

Wednesday, 13 November 2024

Workshop: Workshop 1: "How to Give a Great Scientific Presentation" - (1) B.01.04 - Red Queen (13 Nov 2024, 13:00 - 16:00)

[174] How to improve a good scientific talk/presentation (13:00)

Presenter: WINTER, Marten

This short hands-on workshop is meant to give you practical help to improve your next scientific presentation (i.e. talk based on slides). Given the timing we could focus on your iDiv conference oral presentations and improve them. But any other presentation purpose is welcome too of course. Three hours are not much and thus I will focus on main principles. It's very little about design principles, colors, style or your content itself. But its also not about vague meta level buzzwords, its hands on using your material. The workshop is meant to be interactive in an informal setting. It's mainly based on my own taste and experiences of listening and giving bacillions of presentations. I want to create an atmosphere of trust, where all participants can give open and honest feedbacks. This workshop should help you. I will show with few real examples of slides and different presentation styles how the 1) way you present your scientific story as well as how 2) different ways of slide structures and elements can improve your presentation skills and the way how your audience perceive, understand and remember your research. You will need a finalized! presentation you want to show and improve, a laptop with the respective software to work on the slides. Depending on the number of participants some (or all) will present examples of these presentations before and after we jointly worked on the slides. Be prepared to present your slides in front of the participants. Be prepared to receive critical feedback meant to improve your presentation. Maybe I can't help you, maybe we as a team don't see potential for improvement. But I hope at the end of this short session, some of the participants leave with a better conscious and confidence how to give a good scientific talk about their research.

Workshop: Molecular network analysis for rapid and visual exploration of MS-based metabolomics datasets - (0) B.00.02 - Brood – Beehive (13 Nov 2024, 14:00 - 16:00)

[158] Molecular network analysis for rapid and visual exploration of MS-based metabolomics datasets (14:00)

Presenter: ANAIA, Redouan Adam (Radboud University - former iDiv)

Metabolomics data is rich and often large, containing far more variables than samples while many features remain unannotated. Therefore, the analysis of metabolomics data is not trivial and calls for approaches complementary to (multivariate) statisticial analyses not only to overcome the metabolite annotation bottleneck, but more importantly, to facilitate the rapid exploration of the chemical space in a (biological) sample. In this workshop, molecular networking (and thus graph theory) concepts will be introduced and real-world examples will be discussed using metabolomics data with special attention to the differences between mass-difference networking, classical, and feature-based molecular networking. During a hands-on session, available computational metabolomics tools for molecular substructure/motif discovery (MS2LDA/MASS2MOTIF) and data visualization (Cytoscape) will be collectively explored. The targeted audience includes experienced, novice and aspiring mass spectromery-based metabolomics users.

Workshop: Exploring bitfields for spatially explicit metadata processing and reuse - (0) B.00.04 - Pollen – Beehive (13 Nov 2024, 15:00 - 16:00)

[136] Exploring bitfields for spatially explicit metadata processing and reuse (15:00)

Presenter: EHRMANN, Steffen

Computational workflows in the earth system sciences are becoming increasingly sophisticated, where data of different types and sources are integrated into large-scale, modelled data products. This is partly a consequence of a competition-driven diversification of tools and approaches, with the desirable side effect that we learn more about the earth's spheres from more distinct perspectives. Ideally, sophisticated and complex workflows are better at mapping the sophisticated interaction networks on our planet with less ambiguity. However, the reality is that practical considerations or a lack of resources or time in our projects demand non-ideal decisions, and how that impacts results often needs to be clarified. We quantify the errors of our output, and software engineering uses so-called unit tests, where the output of the "smallest units" of code are compared against expected results. While error reporting (of the output) is part of best practice in the earth sciences, analysis of intermediate data typically only happens project-internally but is rarely reported, even though intermediate data of one project are often the starting point of another project. With the help of the `bitfield` R-package, one can produce (simple) tests that document data and metadata snapshots along a computational workflow and store them in a very compact form (an integer stored as a column in a table or raster layer). This resulting *computational footprint* could be called meta-analytic or meta-algorithmic data because it allows spatially explicit documentation and re-use of an analysis or algorithm. The bitfield is a promising data structure already employed in the MODIS quality flag that allows vast information to be stored in a single integer. In this workshop, you will learn how to use the tools in `bitfield`, get an introduction to the software logic, and we may discuss possible use cases and the future of this technology. https://github.com/EhrmannS/bitfield

Pau-Hana (16:00 - 17:30)

Thursday, 14 November 2024

Registration (14 Nov 2024, 08:00 - 09:00)

Collect your name badge at the registration desk in the KUBUS foyer.

Welcome note in Hall 1AB (09:00 - 09:30)

Hall 1AB, 1st floor

Keynote Jane Hill in Hall 1AB (09:30 - 10:30)

Hall 1AB, 1st floor

Coffee Break (10:30 - 11:00)

Talk Session: Biodiversity Change - Leipziger KUBUS/1-B - Hall 1 B (14 Nov 2024, 11:00 - 12:15)

[116] Exploring the relation between tree species diversity and forest height heterogeneity across spatial scales using Remote Sensing (11:00)

Presenter: RAHMSDORF, Elisabeth (Helmholtz Centre for Environmental Research - UFZ)

Forests with a high overall biodiversity provide a variety of ecosystem functions and service and are associated with greater ecosystem stability and resilience to disturbance events. To identify and preserve intact forest ecosystems across the country, monitoring forest biodiversity on national scale is essential. Large-scale remote sensing datasets offer the potential to develop novel monitoring strategies on a national level. Within this context, we used high resolution area-wide LiDAR derived tree canopy height models and a national tree species classification map of Germany based on Sentinel-2 satellite data with 20 m spatial resolution to investigate the links between tree height heterogeneity and tree species diversity on different spatial scales and across forest types. Height heterogeneity was derived from the canopy height models whereas biodiversity metrics were calculated from the tree species map. Topographic variables and canopy cover were included in the analysis. First results suggest that the relation between tree height heterogeneity and tree species diversity varies between geographic regions and is partly driven by forest composition. We analysed and evaluated the impact of spatial scale and resolution, as well as forest type specific structural features. We compared our satellite-based findings to results generated from forest inventory data in exemplary regions to provide a comprehensive picture of the potential and the constraints of using remote sensing data products such as canopy height models for forest biodiversity assessment. This study contributes to the development of remotely sensed forest biodiversity indicators and facilitates the integration of remote sensing datasets into large-scale forest assessments to improve the detection of biodiversity changes in forest ecosystems over time and space.

[90] Links between satellite-derived forest health anomalies and biodiversity (11:15)

Presenter: LANGE, Maximilian (Helmholtz-Centre for Environmental Research - UFZ)

The [Forest Condition Monitor project][1] of the Helmholtz-Centre for Environmental Research (UFZ) aims at making information about national scale forest condition accessible to stakeholders, policy makers and scientists. One of its main components is an area-wide estimation of forest condition anomalies from satellite-based land-surface reflectance measurements. Reflectance patterns differ between healthy and damaged vegetation and are widely used to depict vegetation vitality or anomalies. Here, we used a tree species map with 10 *m* spatial resolution to extract species-specific reflectance time series of Germany's tree stands for 2016-2022. The seasonal evolution of these time series serves as reference for the detection of forest condition anomalies. We calculated a similarity metric – further called *forest condition anomaly index* (FCA) - between each reflectance observation and the respective measurements within the reference time series, also considering the natural temporal deviations caused by phenology. A temporal aggregation of these FCA values allows the generation of a spatially comprehensive map with 20 *m* spatial resolution, showing patterns related to drought, fire, storm events and bark beetle outbreaks. We compared this map with the Shannon index derived from tree species information to assess potential links between biodiversity and forest disturbances. Here, we present the FCA's ability to depict forest condition and first results about its relation to biodiversity. [1]: https://web.app.ufz.de/forestconditionmonitor

[34] Effect of non-native flora on natural biogeographic regionalization of global flora (11:30)

Presenter: CAI, Lirong

Human activities have altered the composition of biotas worldwide by introducing non-native species, breaking down biogeographical boundaries. Using global distribution data of 279,437 native and 11,589 non-native seed plant species, we analyzed the impact of species introductions on natural biogeographic boundaries based on taxonomic and phylogenetic compositions of 548 regions. We found that the dispersal of non-native species reshaped natural biogeographical patterns, leading to a reduction of floristic kingdoms. Based on taxonomic dissimilarity, eight natural floristic kingdoms broke down into tropical, non-tropical and Australian regions after species introductions. Geographical distances, accounting for dispersal barriers including water, mountains, or unsuitable climates, important in explaining natural patterns, lost their importance when including non-native species. However, environmental factors consistently exerted a strong influence on native and non-native species. Our findings show that human-mediated dispersal results in the breakdown of biogeographical barriers and redefines the global biogeography of plants.

[16] Land use modulates resistance of grasslands against future climate and inter-annual climate variability in a large field experiment (11:45)

Presenter: KORELL, Lotte (Helmholtz-Centre for Environmental Research – UFZ)

Climate and land-use change are key drivers of global change. Full-factorial field experiments in which both drivers are manipulated are essential to understand and predict their potentially interactive effects on the structure and functioning of grassland ecosystems. Here, we present eight years of data on grassland dynamics from the Global Change Experimental Facility (GCEF) in Central Germany. On large experimental plots, temperature and seasonal patterns of precipitation are manipulated by superimposing regional climate model projections onto background climate variability. Climate manipulation is factorially crossed with agricultural land-use scenarios, including intensively used meadows and extensively used (i.e. low-intensity) meadows and pastures. Inter-annual variation of background climate during our study years was high, including three of the driest years on record for our region. The effects of this temporal variability far exceeded the effects of the experimentally imposed climate change on plant species diversity and productivity, especially in the intensively used grasslands sown with only a few grass cultivars. These changes in productivity and diversity in response to alterations in climate were accompanied by immigrant species replacing the target forage cultivars. This shift from forage cultivars to immigrant species may impose additional economic costs in terms of a decreasing forage value and the need for more frequent management measures. In contrast, the extensively used grasslands showed weaker responses to both experimentally manipulated future climate and inter-annual climate variability, suggesting that these diverse grasslands are more resistant to climate change than intensively used grasslands composed of only a few grass cultivars. We therefore conclude that a lower management intensity of agricultural grasslands, associated with a higher plant diversity, can stabilize primary productivity under climate change.

[23] Consistent species trends across three federal states in Germany revealed by repeated habitat mapping data (12:00)

Presenter: LÜTTGERT, Lina

To determine the winner and loser species of biodiversity change, systematic monitoring data are needed that cover all habitat types, extend into the last century, and are geographically representative. However, such data are lacking, but species trends might be obtained from so far untapped data. Here, we make use of plant species occurrences records that were recorded in habitat mapping programs, with the aim to derive species trends. In Germany, almost all federal states carried out such programs over the past decades, mapping all protected habitat types while also recording plant species occurrences within those habitats. Based on such data, we derived temporal trends within the three federal states Schleswig-Holstein, Hamburg, and Baden-Württemberg from 1977-2021. In addition to trends across all habitat types in each state we also derived trends within broadly defined habitat types. We found consistent negative trends across all states for species that prefer heaths and semi-natural grasslands, meadows and pastures, and coastal and marine habitats. Consistent positive trends across all states were found for species that prefer scrubs, copses and field hedges, and forests. Furthermore, species mostly showed negative trends within their preferred habitat type, while shrub encroachment occurred within most habitat types. We however also found some regional variation in trends between the states. Overall, the mostly consistent trends of species groups across the states point to common drivers of biodiversity change across the studied parts of Germany. Our findings are a conservative estimate of change, as our study included almost exclusively sites that kept their protection status over the study period. Thus, more and stronger species trends can be expected for sites that experienced severe habitat degradation

Talk Session: Biodiversity & Society - Leipziger KUBUS/2-AB - Hall 2 (14 Nov 2024, 11:00 - 12:15)

[63] Forests for Well-being: Exploring public preferences for forest complexity - a European perspective (11:00)

Presenter: GIERGICZNY, Marek (idiv)

Forests are vital for outdoor recreation, benefiting mental, physical, and social well-being. While the importance of forest structure in supporting biodiversity and material ecosystem functions is well-documented, research on its relationship with non-material contributions to people remains limited, and there is a lack of robust indicators for this relationship. Our study addresses this gap by estimating the economic value of recreational benefits provided by forests and quantifying the link between forest complexity and the non-material benefits forests provide. We conducted a large-scale preference survey across 12 European countries (Austria, Belarus, Bulgaria, Czechia, Denmark, France, Germany, Poland, Romania, Scotland, Slovakia, and Switzerland), involving 11,622 respondents. Our findings reveal significant positive correlations between forest complexity and benefits from forest visits. Preferences for older stands with diverse tree species and greater structural complexity were strongly evident across all surveyed countries. Moreover, forests with more complex structures were associated with higher annual visitation frequencies, highlighting the importance of forest quality in driving people’s exposure to nature.

[74] Influence of subjective and objective greenspace exposure on self-reported health & wellbeing (11:15)

Presenter: MEEMKEN, Marie-Theres

Urban living conditions pose a threat to human health and wellbeing, confronting people of all ages with harmful influences like air or noise pollution. This study analyzes the impact of nature experience on four human health outcomes. Longitudinal data was obtained through the deep-phenotyping LIFE Adult study from Leipzig, Germany. Inclusion criteria entailed completeness of datasets and a Leipzig home address, resulting in a sample size of 4000 participants. We analyze self-reported psychological (depression, anxiety) and physical (diabetes, asthma) health via longitudinal cumulative link mixed models (CLMM) in R. We will set up separate models per health outcome to test for effects of several urban characteristics, including greenspace quality and hours spent in greenspace. Land cover, structural characteristics of greenspaces, air pollution and noise levels were collated using geographic information system (GIS) in ArcGIS and extracted for various distances from the individuals’ residences. The impacts of age, gender and socioeconomic status are considered in all analyses. All variables are normalized prior to analysis to provide comparability between models. Our results will contrast (1) perceived and actual biodiversity in urban residential areas as well as (2) their respective influence on health values over a time frame of five years and (3) delineate the impacts of air and noise pollution and socioeconomic background on these relationships. Understanding the link between health and subjectively perceived as well as objective measures of exposure to biodiverse, natural environments is critical for public health — uncovering the potential of preventive and equitable health care.

[123] Assessing the impact of income on life satisfaction in valuing urban nature: A study of 22 German cities (11:30)

Presenter: MARDER, Fabian

The contribution of urban nature to human well-being is well documented, providing benefits such as improved air quality, increased physical activity, enhanced social cohesion, stress reduction and diverse recreational opportunities. These green areas play a crucial role in promoting physical activity and facilitating social interactions. The economic valuation of these natural amenities is essential for environmental and development policy makers. For example, cost-benefit analysis has been used to guide environmental decision making. The life satisfaction approach provides a framework for assessing the relationship between environmental conditions and life satisfaction (LS), as well as the interplay between LS and income. By analysing these relationships, the approach estimates the implicit willingness to pay (WTP) for environmental goods, which is determined by the amount of income required to compensate for changes in environmental quality while keeping LS constant. Thus, an accurate measurement of the income effect on LS is crucial, as it significantly affects the estimated WTP. Using survey data (N=1400) from 22 large German cities, this study compares WTP values for urban green and biodiversity derived from conventional income measures (monthly net income) with those derived from an exogenous income shock resulting from the COVID-19 pandemic. Our results indicate positive WTP values for urban nature in both specifications. However, while conventional methods may lead to inflated WTP estimates, the exogenous income shock approach may provide a more realistic valuation of urban green.

[86] Connecting Stakeholders for Biodiversity: A European Network (11:45)

Presenter: LANGER, Christian (iDiv)

The Europa Biodiversity Observation Network ([EuropaBON][1]) includes one of the largest and most influential biodiversity communities in Europe. The aim of this impressive network of stakeholders is to co-design a seamless European biodiversity and ecosystem monitoring system that integrates existing biodiversity data and fills remaining data gaps. Network members are included in each step of designing the system from identifying user and policy needs, assessing existing European monitoring schemes and identifying data gaps, to defining Essential Biodiversity Variables (EBVs) to be monitored by the system, and demonstrating in a set of showcases how workflows tailored to various EU policies, can be implemented. We therefore developed the [EuropaBON dashboard][2] that allows users to map and interact with data and displays of Europe's biodiversity community, its key actors and their connections. It offers high-level information in one view that can be used to identify occupational sectors (e.g., academia, private industry), realm (e.g., marine, freshwater), or geographic regions (e.g., eastern Europe, southern Europe) with the most connections and pinpoint the central actors within the network. [1]: https://europabon.org [2]: https://europabon.org/members/network-analysis/src/

[59] Integrating Data Cubes for Biodiversity Research and Policy (12:00)

Presenter: ESTUPINAN SUAREZ, Lina

New technologies are enabling scientists to obtain data rapidly and continuously. Examples include camera traps, phenocams, and citizen science apps, among others. These rapidly increasing biodiversity data sets challenge new forms of data access, processing, and documentation. In response to these challenges, we focus on data cubes as an alternative to efficiently handle species occurrence data in tandem with metadata documentation. In an ongoing collaboration between the EBV Data Portal and the Biodiversity Building Blocks for Policy project (B-Cubed), we are developing informatics to facilitate the analysis of species occurrence in a data cube format. We are using the largest biodiversity database, the Global Biodiversity Information Facility (GBIF), although we are not limited to it, to deploy species occurrences in a more interoperable format. Additionally, we leverage the concept of data cubes to standardise access to biodiversity data using the Essential Biodiversity Variables framework. Currently, we are mobilising species occurrence data and calculating metrics for the Invasive Alien Species of Union concern and the Birds Directive from the European Union (EU). The implementation of these occurrence cubes involves harmonising species listed in the EU environmental legislation, creating occurrence cubes through the new GBIF API server, and publishing metrics using the EBV Cube format. The entire workflow is open and accessible via GitHub, with scripts available as Jupyter notebooks. We strongly believe that data cubes will facilitate data sharing and processing and need to be extended to biodiversity stakeholders. For this reason, our results are aiming to support Member States' reporting obligations under the nature directives. Additionally, interoperability with other data cubes is pending. Co-development of tools and approaches with other fields, such as Earth sciences, will undoubtedly benefit cross-cutting research. This is urgently needed for policies that respond to feedback in the coupled crisis of biodiversity loss and climate change.

Talk Session: Flexpool - Leipziger KUBUS/1-A - Hall 1 A (14 Nov 2024, 11:00 - 12:15)

[21] Taxonomic and functional vegetation changes of dry grassland communities in Central Germany (11:00)

Presenter: HORKA, Susanne

Dry grasslands are vulnerable to climate and land use change. Increasing temperatures, drought, grazing cessation or nitrogen deposition result in shifts in taxonomic and functional composition. We resurveyed vegetation plots of dry grasslands after three decades and tested the hypotheses that species richness and diversity decreased both at the scale of the species pool and single communities, functional composition shifted towards more competitive and short-lived trait values and that these responses differed between the different grassland communities, depending on their functional characteristics and the environmental stress level. The size of the regional species pool did not decrease over the last 30 years. The functional turnover of the species pool points to changing precipitation patterns and an increasing frequency of drought events over the study period as main drivers of change. A lower number of species flowering in midsummer and a higher number of early-flowering species in the resurvey suggests the avoidance of summer droughts and taking advantage of more warm and moist spring conditions. At the community scale, species richness and alpha diversity increased over time, in spite of a decreasing plant cover. This increase was mainly caused by annual plant species, indicating drought avoidance as the preferential survival strategy. The studied community types varied in the magnitude of changes in species richness and diversity as well as their species and functional responses, with shifts being independent from the severity of environmental stress. Dry grassland communities have undergone significant shifts in both species and functional composition, in favour of generalist species with faster life-cycles and at the disadvantage of specialist species.

[79] Flexpool Project “Archives4BioDiv” - A Window to the Past: The Use of Archive Data for Collecting Baseline Information on Biodiversity (11:15)

Presenter: WU, ChenHuan

Repeated observations are crucial for understanding trends in biodiversity changes, particularly shifts in species composition. However, next to biodiversity, changes in environmental drivers are of equal importance to understand these. As most monitoring projects only recently started, archival data offer invaluable insights into long-term ecosystem dynamics and environmental changes, revealing perspectives crucial for shaping conservation strategies and enhancing ecological understanding. This project explores advanced AI-based techniques to provide data on the historical development of forest cover, management and age structure, thus, some of the most important drivers for changes in forest biodiversity in time. The goal is to develop innovative, user-friendly methods to extract time-series data, specifically by assessing changes across different years within the same location. We focus on the repeated forest inventory maps of Thuringia from 1850 to 2000, using about 100 maps (out of several thousands) for model development. These maps span diverse geographical and ecological conditions. The research involves several steps: digitizing paper maps through high-resolution scanning to preserve original data integrity, followed by detailed manual annotation to define forest boundaries and features like management type, predominant tree species and age structure. Convolutional Neural Networks are then applied for deep feature extraction and model training, aiming to recognize spatial patterns. Additionally, computer vision techniques enable precise matching between the map features and legends, facilitating comprehensive classification and data integration. This methodology combines deep learning and computer vision to tackle complex map analysis, providing greater accuracy than traditional methods. Our results demonstrate AI's significant effectiveness in image segmentation, legend-feature matching, and text recognition in historical map analysis. This achievement holds substantial potential, offering an automated method for handling historical records of environmental conditions. Future work will enhance model accuracy and expand its applicability to biodiversity conservation efforts, e.g. by identifying areas of high habitat continuance.

[15] Spatial patterns of genomic variation and temporal genomic offset in a common grassland plant and their relation to seed transfer zones (11:30)

Presenter: HÖFNER, Johannes (Helmholtz Centre for Environmental Research - UFZ)

Introduction of large amounts of seeds is essential for restoration of temperate grasslands and is often regulated by seed transfer zones. These zones are often derived from abiotic parameters only. In order to evaluate seed zones as a means for the protection of genetic diversity and to avoid potential detrimental effects such as maladaptation and homogenisation of seed transfer within zones, empirical data on spatial genetic structure is paramount. Here, we focussed on Galium album, a widespread perennial grassland species, which we thoroughly sampled on average once per 25 km x 25 km in all of Germany. Based on 9,403 SNP loci, we described the genetic structure using Bayesian clustering. We identified four spatially coherent genetic clusters that were rarely congruent with the current seed zones. Therefore, current zone-based seed transfer potentially distorts and homogenises some spatial differentiation. Yet, we found significant isolation-by-distance among seed zones, showing that they still reflect a substantial part of spatial genetic differentiation. Seed transfer practice is challenged by climate change that shifts adaptive requirements for populations. We conducted redundancy analysis (RDA)-based genotype-environment association (GEA) analysis, and assessed necessary genomic turnover to maintain current levels of adaptation (temporal genomic offset). The resulting patterns suggest that climate change might impose a risk for regional adaptation in parts of Southern and Central Germany. We found that targeted assisted migration across seed zone borders might in some cases mitigate the most adverse GEA disruptions in seed zones that do not harbour suitable donor material themselves.

[42] PlantCAPNet: A Novel Tool for the Extraction of Plant Species Abundances and Plant Phenology from Images (11:45)

Presenter: KÖRSCHENS, Matthias (Plant Biodiversity Group & Computer Vision Group, Friedrich Schiller University Jena)

The plant community composition and species phenology are important indicators of environmental changes and subject to numerous ecological studies. In most previous studies, data on plant communities was collected by hand, making the data collection process laborious, time-intensive and subject to human error and subjectiveness. Additionally, the amount of work required for this process prohibits a collection in a high temporal frequency, as this would require infeasible amounts of work. Weekly observations are, however, important to generate high-quality data on species phenology. Hence, most studies merely cover data collected in large intervals, leading to temporally coarse subsequent ecological analyses. We introduce a novel tool based on Convolutional Neural Networks called PlantCAPNet, which can be utilized to extract information about the species composition of herbaceous plant communities, and the phenology of all included species automatically from images. In conjunction with automated camera systems, PlantCAPNet offers a powerful way to extract vegetation data in a high quality and temporal frequency with little manual labor required. Therewith, our tool enables temporally fine-grained ecological analyses, offering novel insights into the dynamics of plant communities and their responses. The tool will be made available to plant ecologists as an open-access application. The system is developed in interdisciplinary cooperation between biologists and computer scientists.

[91] Enhancing Nigeria's Biodiversity Strategy: Recent Progress and Future Directions (12:00)

Presenter: BELLO, Abubakar

In the face of an escalating biodiversity crisis, it is imperative to concentrate efforts on developing comprehensive strategies in countries with lower economies, where the rich natural heritage is most vulnerable yet crucial for ecological balance. This aligns with the target set in the Convention on Biological Diversity’s (CBD) Global Biodiversity Framework (GBF) vision 2050, which calls for urgent action to 'put biodiversity on a path to recovery by 2030 for the benefit of planet and people'. Africa, hosting a quarter of the world's terrestrial biodiversity hotspots, is one of the most biodiverse regions on Earth. In light of this, our project specifically focuses on Nigeria, aiming to leverage its unique biodiversity to inform and enhance conservation strategies. The project’s primary objective is to contribute to biodiversity conservation by compiling all domestically and globally accessible data on vascular plants and habitats related to Nigeria, identifying priority plant sites, and providing accessible maps and data to enable local, national, and international stakeholders to direct conservation efforts and resources, thus supporting plant-species-related indicators in the post-2020 GBF. This presentation will provide an update on the progress made so far, highlighting key achievements, challenges encountered, and the next steps in our ongoing efforts to support African biodiversity. Our ultimate goal is to develop a model that can be replicated in other countries, enhancing worldwide conservation strategies and contributing to the global recovery of biodiversity. The project receives support from iDiv’s Flexpool, which prioritizes proposals aimed at capacity building, particularly focusing on communities and regions underrepresented in science.

Poster Flash Talks - Leipziger KUBUS/2-AB - Hall 2 (14 Nov 2024, 12:15 - 12:30)

[81] Exposure to sealed surfaces and subjective health outcomes: Evidence from longitudinal data in Germany (12:15)

Presenter: KASSOURI, Yacouba (iDiv)

Urban intensification has resulted in an intensive and often uncontrolled increase in artificial and sealed surfaces, reducing exposure to green space and the associated health-enhancing factors. According to the EEA, between 2012 and 2018, the area of newly sealed soil of the EU-27 and the UK increased by 1,467 km2 (European Environment Agency, 2022). This extensive sealing of soil raises not only environmental issues but also societal public health questions concerning exposure to environmental “bads” hazards, mainly because sealed areas have higher surface temperatures compared to green surfaces. As a result, soil sealing is likely to affect humans through urban heat islands, contaminant toxicity, air pollution, and adverse impacts on mental health. This study focuses on sealed soil per capita to proxy green space depletion and uses panel fixed effects model to estimate the well-being impact of green space depletion on different aspects of life in Germany. Estimation results based on the German Socio-Economic Survey data reveal that sealed surfaces negatively influence various aspects of life, including health and social life. We estimate that changes in health satisfaction due to soil sealing correspond to an equivalent income variation of approximately 790.613 EUR/h.h./m2. We argue that urban heat islands can play an important role in explaining the negative impact of sealed surfaces on human well-being.

[80] Biodiverse urban green spaces: Insights from a survey-based hedonic analysis in 14 German cities (12:16)

Presenter: LIEBELT, Veronika (German Federal Agency for Nature Conservation (BfN), German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig)

By offering various benefits, natural amenities play a significant role in enhancing the well-being of urban citizens whose city life is often associated with hecticness and stress. Urban green spaces serve citizens with recreational opportunities, aesthetic enjoyment, contribute to public health, climate regulations, cooling effect, and have an impact on the attractiveness of neighborhoods and housing prices. Thus, in view of global urbanization and biodiversity loss, the valuation of urban green spaces becomes increasingly essential. We analyzed the impact of biodiverse urban green spaces on rental prices across 14 German cities by applying a hedonic pricing analysis. This analysis complements the existing literature by including the diverse measurements of urban green spaces and their biodiversity that we innovatively cluster as 'perceived' -variables retrieved from an online survey and 'objective' -variables, i.e. spatial data computed from satellite images. Furthermore, we analyzed rental prices in contrast to most studies that consider selling property prices. Finally, we incorporated an online survey as a source of perception data with a monetary valuation method. The key preliminary results at the aggregated level suggest that: (i) rental prices are positively correlated with the distance to the next urban green space. This raises the question of whether standard hedonic pricing analysis suffers from omitted variables bias – at least in this case – due to unobserved amenities in cities that are negatively correlated with UGS. (ii) Biodiversity of the UGS as well as around the flat have a positive, albeit not significant, effect on rental prices.

[72] Non-linear relationships between green space characteristics and physical activity in the German National Cohort (NAKO) (12:17)

Presenter: KREISLER, Torvid (Martin-Luther-University Halle-Wittenberg)

Background: Noncommunicable diseases, particularly cardiovascular disease (CVD), account for a large proportion of the global burden of disease. Certain characteristics of biodiverse green spaces such as walkability have been argued to enhance physical health outcomes such as cardiovascular health by increasing the likelihood and intensity of physical activity (PA). However, existing evidence on the relationship is inconclusive. Most previous studies failed to account for non-linearities in the relationship, and they have not systematically considered structural and qualitative characteristics of green spaces. **Aims**: We aim to test for (potentially) non-linear relationships between various green space metrics, including measures of green space diversity and species richness, and various PA outcomes. **Methods**: We used self-reported PA indices from the German National Cohort and objective GIS green space indicators to characterise the neighbourhoods around the respondent’s addresses for different buffer sizes. We modelled the potentially non-linear GS-PA relationship using generalised additive models (GAM). **Results**: The GS metric with the highest explanatory power was NDVI at 1 km radius. There was no GS effect on total PA, but NDVI (1km) was negatively associated with sedentary behaviour. NDVI (1km) had a negative effect on commuting, but a positive effect on leisure time activities. It is possible that these two opposing effects might offset each other. Future research should take into account that different PA outcomes are affected by GS through different mechanisms.

[146] Eco-tourism, insect-perception and mental wellbeing in the Peruvian Amazon rainforest (12:18)

Presenter: AVELLANEDA VERGARA, Adrian Gustavo (FSU Jena)

Arthropods comprise 75% of the earth’s living organisms. At the same time, only 10% of all conservation actions target arthropods — a mismatch that poses a significant threat to global biodiversity. Increasing urbanization in the world reduces nature experiences for city dwellers, effectively alienating people from nature. Urban environments provide few habitats for most insect species. The resulting increased contact with resilient, non-charismatic species can, in turn, lead to generalized misidentification of insects as pests. Simultaneously, peoples' motivation for conservation behaviour rises with stronger nature connectedness. Furthermore, previous research has pointed out the mental health benefits associated with natural environments, necessitating investigations into possible interventions to reduce stigma against insects and enable a positive and nurturing relationship with our environment. This study was conducted in three ecotourism lodges in high biodiversity environments in the Peruvian Amazon Rainforest. We investigate the impact of eco-tourism and participation in citizen science projects on insect perception, mental well-being and willingness to engage in nature conservation efforts. Participants (N=100) were either holidaymakers or enrolled as citizen scientists in *Wired Amazon*, a series of structured citizen science programs offered on site. Participants completed online surveys on mental health and well-being as well as their perception towards insects at different time-points during their ecotourism experience (booking, arrival, departure, follow-up). Our study (1) evaluates the influence of citizen science activity in a high biodiversity environment on insect perception and mental wellbeing, (2) investigates the factors driving nature conservation behaviour and (3) tests the longevity of resulting mental wellbeing benefits beyond duration of the program. The aim of this project is to better understand the perception of insects and its effect on the willingness to protect our biodiverse environment.

[39] FLOW - Citizen science shows that Germany's small streams are in poor ecological status (12:19)

Presenter: VON GÖNNER, Julia (Helmholtz-Centre for Environmental Research - UFZ / FSU Jena / German Centre for integrative Biodiversity Research (iDiv))

Freshwater streams are affected by pesticide and nutrient inputs and severe alterations of the natural water course and riparian vegetation. The goal of the European Water Framework Directive (WFD) to achieve a 'good ecological status' for all surface waters by 2015 has been missed in a large part of German rivers and streams. In the BMBF-funded citizen science project FLOW, over 900 volunteers have assessed the ecological status of small streams between 2021 and 2023. More than 90 groups from NGOs, schools and angling clubs collected data on the hydromorphology and macroinvertebrate community of 137 streams across Germany according to WFD monitoring standards. For this purpose, we developed citizen science learning materials (e.g., identification booklet and video tutorials) and organized citizen science training sessions. A biological indicator (SPEARpesticides) was used to assess the pesticide contamination of the stream sample sites based on the macroinvertebrate data. Results showed that 58 % of the sample sites in agricultural catchments failed to achieve a good ecological status in terms of macroinvertebrate community composition, indicating high pesticide exposure. These streams were classified as 'moderate', 'poor' or 'bad' using the SPEARpesticides index. In terms of hydromorphology, 65 % of the agricultural streams studied failed to achieve good ecological status. Rigorous testing showed that the citizen science monitoring achieved a high degree of accuracy, with results from citizen scientists and professionals highly correlated. We could also show that the citizen scientists' ecological knowledge and collective action to protect streams increased through learning-by-doing in the FLOW project. As a next step, the citizen scientists would like to work on restoring stream ecosystems and monitoring the ecological effects.

[73] How can citizen science support stream restoration? A scoping study (12:20)

Presenter: BISCHOF, Roland

Citizen science (CS) has great potential to advance ecological stream monitoring and restoration. In our scoping study, we aim to investigate how existing CS stream monitoring approaches can best be used and adapted to monitor and implement stream restoration projects together with engaged citizens as a part of inclusive governance. Effective freshwater monitoring and restoration requires not only scientific expertise and practical knowledge, but also the involvement of citizens and different stakeholders in freshwater protection measures. To foster knowledge and awareness about stream health and restoration benefits in local communities, we will establish CS monitoring activities at selected case studies of the EU freshwater restoration project MERLIN (https://project-merlin.eu/). These CS activities will be based on the German CS project FLOW (www.flow-projekt.de), which has mobilized and trained over 90 CS groups to assess the ecological status of small streams between 2021 and 2023. Results show that a large part of Germany's small streams are in poor ecological status. Many FLOW groups are now motivated to take action to improve the health of their streams. We will outline current activities to mainstream the well-tested FLOW method to other European countries. We will also illustrate how CS stream monitoring data can be used as an evidence base to plan and implement low-threshold stream restoration measures (e.g. planting native plants along stream banks, introducing gravel or dead wood to improve flow and substrate diversity). Together with citizen scientists and various stakeholders, we will develop a hands-on guideline for freshwater practitioners on how to successfully establish CS stream monitoring and restoration activities. By involving different stakeholders and tracking the impacts of land use and restoration efforts on freshwater streams, the CS activities can support local decision-making for sustainable water management and stream protection.

Poster Flash Talks - Leipziger KUBUS/1-A - Hall 1 A (14 Nov 2024, 12:15 - 12:30)

[29] Biological species delimitation revisited using the high Andean tree genus Polylepis (Rosaceae) as a model (12:15)

Presenter: OLIVAR, Jay Edneil (Leipzig University)

‘What is a species?’ is a fundamental question in biology influencing many aspects of integrated biodiversity research. The biological species concept, long considered as the golden standard, defines species as reproductively isolated populations in which there is no gene flow and whose genomes diverge due to selection and genetic drift. However, species constantly interact through gene flow, hybridization, and polyploidization. Understanding the drivers and mechanisms of species maintenance is therefore very important, especially in global diversity hotspots such as the South American Andes. In this project, we aim to provide empirical evidence that species identity can be maintained despite continuous and high gene flow, with speciation occurring at the genic rather than at the genomic level. We sampled two morphologically distinct species of the high-Andean genus *Polylepis* (*P. neglecta* in Bolivia and *P. incana* in Ecuador), which occur sympatrically with other species (*P. neglecta* with *P. besseri*, *P. hieronymi*, and *P. subtusalbida*; *P. incana* with *P. longipilosa*, *P. ochreata*, *P. pauta*, *P. reticulata* and *P. simpsoniae*). By generating morphological (40 traits) and genomic (ddRADseq) data for about 170 specimens, we will explore the hypothesis that gene flow between sympatric *Polylepis* species is high and that species will cluster geographically rather than by morphology. If confirmed, this suggests that species identity can be maintained despite gene flow. The results of this project will emphasize the importance of a resolved taxonomy for integrated biodiversity research.

[128] Macroevolutionary insights into the evolution of fleshy fruits (12:16)

Presenter: CLARKE, John (iDiv)

Angiosperms (flowering plants), with over 350k species, represent one of the most spectacular and enigmatic evolutionary radiations on earth. A potential explanation for this evolutionary success may be found in the unique functional traits (i.e. “key-innovations”) of angiosperms that presumably allowed them to colonise and compete in novel environments, establish new biotic interactions, and thus benefit from new “ecological opportunities” for diversification and trait evolution. A key but understudied innovation of angiosperms, in terms of its impact on macroevolutionary dynamics, is the evolution of fleshy fruits, a feature whereby angiosperms commonly entice animals to swallow and distribute their seeds. This innovation is thought to have been particularly crucial to solve a dispersal problem introduced by angiosperms entering rainforests, where shady conditions should create a selection pressure for larger and more energy-rich seeds able to grow taller before becoming fully self-reliant. These larger seeds are then hard to disperse via abiotic mechanisms, increasing the need for a trait, such as fleshy fruits, which delivers a biotic dispersal mechanism. Here, I will present results of the mechanisms by which fleshy fruits evolved, and their impact on species diversification of angiosperms.

[124] Seed microbiome effects on the composition and diversity of organisms colonizing seedlings (12:17)

Presenter: KÖHLER, Michael (iDiv, MLU)

Seeds host highly diverse microbial communities, which colonize the surface but also the internal tissues of the seeds (i.e., seed epiphytes and endophytes). For decades, seed endophytes have gone unnoticed, but recent studies indicate that these microorganisms can have a major influence on the development and health of seedlings. Most of these endophytes seem to be plant-beneficial bacteria and fungi supporting nutrient allocation and offering protection from pathogens. The factors that shape the seedling microbiome, such as drivers of global change, are still under debate. Therefore, we asked how the composition and diversity of the seed microbiome differ among plant species and functional groups; how the seed microbiome determines which microorganisms colonize the roots and leaves of the seedlings, both under aseptic conditions in sterilized media and when grown in “living” soil; and how these processes are altered by global change drivers, such as drought. To answer this, we performed next-generation sequencing on seeds and seedlings grown in sterile tubes on different media to quantify the microbiome of two grassland species (Geranium pusillum and Lolium perenne) originated from the DroughtNet site in Jena. We found that the seed microbiome is significantly different from the seedling microbiome. Nevertheless, our results show that the seed microbiome is an important source for the seedling microbiome. Furthermore, we found that drought has a strong influence on these processes and shifts the community composition (already in the seed).This project was funded by the iDiv Flexpool fund, covering all research areas of iDiv. By using molecular methods to study the microbiome of seeds and seedlings (molecular diversity and complexity), we were able to show that the microbiome changes when exposed to drought (biodiversity change). The topic is very important as we do not yet know what effects these changes in the microbiome caused by global change will have on ecosystem functioning and thus on human life (society) on earth.

[102] Root functional strategies as drivers of the functional composition of soil fungal communities and ecosystem functioning (12:18)

Presenter: HENNECKE, Justus

Ecosystem functions are influenced by various factors. While the role of biodiversity role in maintaining ecosystem functioning is widely acknowledged, there is a significant knowledge gap regarding belowground plant traits. Historically, trait-based concepts have focused mainly on aboveground traits, creating a bias and a lack of understanding of belowground traits. The recent introduction of the root economics space (RES) has improved our ability to integrate root traits into functional plant strategies and biodiversity–ecosystem functioning research. Soil mutualists and antagonists are expected to mediate diversity–productivity relationships. Given the close association of roots with the soil microbial community and the RES collaboration gradient's link with mutualistic mycorrhizal fungi, it is probable that root traits are also involved in these relationships. We hypothesize that plant diversity and root trait strategies along the collaboration and conservation axes of the RES influence the composition of soil fungal communities and ultimately ecosystem functioning. For example, we anticipate that the abundance of plant pathogenic fungi will decrease in more diverse plant communities and those with well-defended plants (associated with root traits linked to high mycorrhization ('outsourcing') and high tissue density ('slow')). In plots of the Jena Experiment, we examined the effects of root trait gradients and plant species richness on soil fungal communities and found a significant decrease in the diversity and relative abundance of plant pathogenic fungi in plant communities with outsourcing root strategies. This highlights the central role of the root collaboration axis in shaping soil fungal communities beyond the direct link with arbuscular mycorrhiza. Changes in fungal and microbial biomass, however, are strongly determined by plant diversity and not driven by root traits. We further analysed a global synthesis dataset on trait-functioning relationships to test how root functional strategies relate to ecosystem functioning across a broad range of systems.

[94] EO4BEF: A global multi-modal Earth Observation dataset for understanding Biodiversity-Ecosystem Functioning (12:19)

Presenter: MONTERO LOAIZA, David (Leipzig University, iDiv)

Terrestrial biodiversity drives ecosystem functions that regulate land-atmosphere interactions. Biodiversity-Ecosystem Functioning (BEF) relationships are critical for ecosystem stability and resilience. While current BEF knowledge stems from relatively small-scale experiments, in-situ data, and theoretical work, Earth Observation (EO) data offer ample opportunities for global vegetation monitoring. However, the extent to which EO data accurately captures BEF relationships remains uncertain. The absence of an integrated dataset combining in-situ BEF measurements with EO products has hindered comprehensive global BEF studies. Here we present EO4BEF, a dataset integrating multi-modal EO data with in-situ BEF data for understanding BEF relationships at a global scale. This integration includes data from optical and thermal satellite imagery at different spatiotemporal scales (Sentinel-2, Landsat, and MODIS), Synthetic Aperture Radar (SAR; Sentinel-1), and climate data across sites spanning the FLUXNET and SAPFLUXNET networks. These networks provide crucial ecosystem function estimates from globally distributed stations that include observations of carbon, water, and energy fluxes and tree-level sap flow measurements. By combining these in-situ observations with multi-modal EO data, EO4BEF enables the upscaling of local BEF relationships to global scales. The dataset includes high-quality, harmonized spatiotemporal data that facilitate advanced Artificial Intelligence (AI) analyses. EO4BEF demonstrates the feasibility of merging diverse data sources and modalities to investigate global BEF dynamics. Furthermore, the utilized approach creates the opportunity to merge multi-modal EO data with additional global vegetation databases such as TRY, sPlot, and the European Vegetation Archive, providing a valuable resource for global BEF studies using AI techniques.

[96] Cryptic diversity and evolution in Orthoptera: A continent-wide perspective (12:20)

Presenter: CASTILLO, Elio Rodrigo (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Puschstraße 4, 04103 Leipzig, DE. Friedrich Schiller University Jena, Institute of Ecology and Evolution, Dornburger Str. 159, 07743 Jena, DE)

Orthopterans, encompassing crickets, bush-crickets, and grasshoppers, are key invertebrate herbivores notable for their genome size (GS) variation and reproductive diversity (RD). Over evolutionary timescales, orthopterans show large-scale chromosome rearrangements. The persistence chromosomal polymorphisms, such as B chromosomes and sex chromosomes in certain lineages but not others, warrants detailed investigation. Orthopterans possess the largest and most variable genomes among insects, and variations in GS can influence cell size and overall developmental processes, impacting organism fitness. Sperm cells are often subject to sexual selection, particularly in species experiencing high levels of sperm competition. This selective pressure can drive diversification in reproductive organs and sperm characters (e.g. size, shape, and structure), thereby promoting divergence among populations. Evolutionary traits like karyotypes, GS, and sperm morphology (SM) are crucial for understanding speciation and biodiversity origins. Here, we aim to characterize karyotypes, GS, and SM across the European orthopteran fauna, providing insights into their evolutionary mechanisms and contributions to biodiversity. Karyotype analyses from more than 30 species revealed variation in both diploid number (2n) and chromosome size between Acrididae and Tettigonidae species. The 2n in Acrididae males ranged from 17 to 23, while in Tettigonidae this trait showed a more stable pattern, ranged from 29 to 31. We compiled the most comprehensive matrix of GS information encompassing over 150 species across Europe, with values ranging from 0.96 pg to 21.96 pg. The study of SM in 10 species of Acrididae, Tettigoniidae, Tetrigidae and Gryllidae, showed noticeable differences in tail length, head morphology, and spermatodesm structure. These data, combined with recent fieldwork, will enable us to reconstruct the evolutionary history of genomic and RD, correlate genomic and RD with species ecological traits, and relate genomic and RD to species richness. This comprehensive analysis will provide insights into the drivers of diversity in Orthoptera on a continent-wide scale.

[71] Integrating High Throughput Molecular and Optical Methods to Study Protistan Abundances in Groundwater Ecosystems (12:21)

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

Heterotrophic protists occupy key nodes in terrestrial food webs due to their high abundance, fast turnover and functional importance as microbial grazers. However, their impact on groundwater bacterial communities and organic carbon transfer to higher trophic levels remains largely unknown. Assessing their role in trophic interactions using molecular techniques has been limited by the variability in 18S rRNA gene copy numbers, complicating the quantification of protists. The key objective of our novel approach is the establishment of protist enumeration by Imaging Flow Cytometry (IFC), combined with qPCR assays and 18S rRNA gene targeted amplicon sequencing, to derive taxon-specific correction factors, facilitating precise estimation of key taxa abundances from molecular data and provide biomass estimates from IFC. In addition, we aim to compare protistan communities between carbonate-rock (Hainich Critical Zone Exploratory) and sandstone aquifers (Saale-Elster-Sandstone Observatory) located in Thuringia, using molecular and cultivation-dependent approaches as well as metatranscriptomics. Protistan monocultures were used to successfully generate initial reference image datasets using IFC, covering sizes from 3 to 50 µm and various morphotypes. Convolutional neural network (CNN) training achieved 85% precision in predicting protistan taxa based on morphological features. Enrichments of groundwater protistan communities initially exhibited predominance of nanoflagellates (3-15 µm) and flagellates (15-20 µm), followed by successional changes in favor of ciliates and amoebae (*Acanthamoeba*, *Hartmannella*, *Vahlkampfia*) within 1-2 weeks where differences between the geological settings were observed. By 4-6 weeks, occasionally heliozoans and *Aspidisca sp.* (Ciliates) emerged. Amplicon sequencing confirmed high abundances of previously identified groundwater taxa such as *Cercomonas spp.*, *Thaumatomonas sp.*, *Neocercomonas sp.* (Cercomonadida), *Sandona sp.*, *Allantion sp.* (Glissomonadida), *Spumella sp.*, *Paraphysomonas sp.* (Chrysomonada), *Rhogostoma sp.* and *Glaucoma sp.* Our results show that IFC enables high-throughput automated quantification. Innovative abundance estimation and community assessment will enhance our understanding of food web structures in aquifers with different geological settings.

[120] Partitioning the arthropod Armageddon: survival of the heaviest (12:22)

Presenter: WILDERMUTH, Benjamin (Flexpool)

Global biodiversity loss threatens a multitude of ecosystem functions. However, not only the diversity of communities drives their functioning, but also the identity and abundance of their members. While arthropods are key indicators of biodiversity and ecosystem functioning declines – e.g. the transfer of energy; often studied through their biomass – it remains unexplored whether such declines are caused by species loss per se, or by the identity and abundances of lost species. Here, we use the ecological Price equation to investigate how temporal changes in arthropod biomass across grasslands of varying diversity and land use intensity can be assigned to the community assembly components of species richness, identity and abundance. Arthropods were sampled over ten years in an experimental grassland site (“Jena Experiment”) and in land use observatories (“Biodiversity Exploratories”). We put a special focus on comparing primary consumers (herbivores) and secondary consumers (predators). Our preliminary results show that decreases in arthropod biomass over time are strongly driven by species richness and abundance losses. Species identity, however, causes counteracting effects, as lightweight species are rather lost than heavyweight species, which persist or even increase in communities over time. These effects are particularly pronounced under high grassland diversity and low management intensity, especially for predators. We conclude that BEF relationships based on species richness account for large proportions of temporal changes in arthropod functioning (biomass), but species identity and abundance complete the picture. While lightweight species diminish, few heavyweight species take over, reducing the functional complexity of the community. Little temporal turnover under low grassland diversity and high land use intensity indicates that these homogenized communities have limited adaptation capacities. Untangling the community (dis-)assembly processes driving temporal arthropod biomass loss, we show that as communities get less diverse and abundant, the heavy members persist, leading to simplified and potentially less adaptable communities.

Poster Flash Talks: Biodiversity Change - Leipziger KUBUS/1-B - Hall 1 B (14 Nov 2024, 12:15 - 12:30)

[97] Writing outreach into your grant proposal (12:15)

Presenter: HAHN, Volker

iDiv’s Media and Communications unit wants to support iDiv researchers in writing outreach into their proposals. Most third-party funders offer the option to include outreach subprojects in grant proposals. For instance, I (Volker) have reviewed outreach subprojects within CRC proposals for the DFG. Aim of this poster presentation is to network with iDiv researchers interested in writing outreach subprojects into their grant proposals and to find out what kind of M&C support they might need.

[40] A biodiversity portal for Germany: Lebendiger Atlas der Natur Deutschlands (LAND) (12:16)

Presenter: ENGEL, Thore

Biodiversity data can be messy, scattered and hard to come by - especially in Germany. As the national research data infrastructure for biodiversity (NFDI4Biodiversity) we set out to make biodiversity data FAIR and open. One of our products is the "Lebendiger Atlas der Natur Deutschlands (LAND)", a national biodiversity portal that provides species occurrence data in Germany to researchers, conservation authorities and the general public. To do so, we joined forces with the Global Biodiversity Information Facility (GBIF) as well as the national node GBIF.de and created the LAND-portal as a GBIF hosted portal (https://land.gbif.de/). The portal integrates species occurrence data from different sources, including monitoring schemes, citizen science, natural history societies, museums and universities. To start with, we mostly stocked the portal with existing datasets from GBIF. Now we focus on mobilizing new datasets. To continue improve the service and mobilize new datasets to GBIF and LAND, we organize annual community workshops with 50-80 stakeholders from different institutions. In this talk, we present the current state of the portal and its functionalities and discuss opportunities for data holders and researchers to get involved.

[127] Shifts in the distribution of timber species in Nigeria under climate change and implications for timber availability (12:19)

Presenter: MÜNDER, Nina (Universität Leipzig - Molekulare Evolution und Systematik der Pflanzen)

The temperature increase predicted for the end of the 21st century will affect the distribution of biodiversity worldwide and impact natural resources and the availability of ecosystem services. Given the dependence of humans on certain species and the severity of environmental change, the effects may vary from region to region. The availability of timber is directly linked to the natural occurrence of specific tree species of high wood quality and regional abundance. Therefore, sustainable access to these resources depends, among other things, on how the changing climate will impact the characteristics of species´ current habitats. Understanding the effect of climate change on the distribution ranges of timber species may provide important insights into how to promote adaptation to regional changes in timber availability and sustainable management. In this project, we constructed species distribution models to assess the impact of climate change on the distribution of suitable habitat of 98 important timber tree species in Nigeria. We used occurrence records as well as bioclimatic, topographic, and edaphic variables to predict current and future (2041 to 2070) potential suitable habitats of the species. Our results show a major distribution of timber species in the southern forest and coastal regions of Nigeria, with precipitation of the wettest month being the most important factor influencing the distribution. In addition, the diversity of timber species is predicted to stay stable in the southern forest, while it is declining in the northern regions. While some species lose most of their suitable habitat, others benefit and gain suitable habitat. Although southern forests are important not only for timber production but also for carbon sequestration, local climate regulation, biotic interactions, rapid deforestation and land degradation are currently occurring there, threatening the possibility of range shifts to compensate for habitat loss in the north.

[142] Mongolian vegetation in the past and present - deducting plant occurrences, performance and phenology from herbarium specimens (12:21)

Presenter: VINCZE, Anna (Senckenberg Intitute for Plant Form and Function Jena)

Mongolia, like everywhere else in the world, is currently confronted by the effects of global change. These predominately include increasing average winter temperatures, decrease in winter and spring precipitation and a change in land-use due to increased grazing pressure. Little is yet known about the long-term effects of these developments on plant phenology, species composition and plant functional traits of the Mongolian steppe vegetation. Long-term data on these aspects can be obtained from herbarium specimens, which are valuable sources of historical data on plants’ adaptations to changing environmental conditions. Specimens collected in Mongolia have not yet been utilized for this purpose. To assess possible changes in phenology we are analysing approx. 3.000 herbarium specimens of 16 selected dominant species of Mongolian dry steppes, deposited in herbaria in Mongolia and Germany, as well as digitised specimens available online. In addition, we are using near infrared spectroscopy to determine the contents of carbon, nitrogen and their stable isotopes δ13C and δ15N, which are related to palatability, water-use efficiency and photosynthesis rates. Aside from herbarium specimens phenological data is obtained via a long-term survey in Hustai National Park, which was started in 2003. Additionally, changes in plant composition and functional traits will be assessed by repeating surveys along a precipitation gradient first conducted in 2014/2015. In better understanding the recent impacts of global change on Mongolian steppe vegetation we hope to get a better understanding of future developments. Those might not only have an impact on biodiversity but also on the traditional Mongolian nomadic lifestyle, as changes in precipitation and temperature might cause changes in growth start and duration, which may impact forage availability and quality for livestock.

Lunch Break (12:30 - 13:30)

Talk Session: Biodiversity and the functioning of Ecosystem - Leipziger KUBUS/1-A - Hall 1 A (14 Nov 2024, 13:30 - 14:45)

[138] Effects of Artificial Light At Night extend below ground to limit soil respiration (13:30)

Presenter: HINES, Jes

Terrestrial ecosystems acquire carbon via photosynthesis and lose it predominately through soil respiration. These coupled processes occur rhythmically in diel cycles. Global changes that influence carbon loss vs carbon gain alter ecosystem carbon storage capacity. Yet, the mechanisms underlying the influence of some global change drivers on ecosystem processes remain undocumented. We test how Artificial Light At Night (ALAN) influences realistically diverse grassland plant-soil communities in the iDiv Ecotron. We show that, during peak plant biomass, ALAN reduces soil respiration, a result that was associated with a shift from plant to heterotrophic soil respiration. We detected no ALAN influence on plant photosynthetic responses. Moreover, we found neither soils nor plants were sensitive to ALAN later in the season. These results emphasize the importance of temporal dynamics in coupled plant-soil systems. We suggest that soil and plant responses serve as reciprocal references upon which to gauge ecosystem responses to global change.

[104] Ecosystem Monitoring using Multi-source Optical Remote Sensing Data at Bavarian Forest National Park (13:45)

Presenter: JI, Chaonan (Leipzig University)

Current static mapping approaches of ecosystem conditions are inadequate, given the fast pace of ecosystem transformations under the climate change regime. Our project “Time-varying AI-based mapping of ecosystem conditions and extents using multi-source Earth observation data cubes”, TEE Cube, aims to bridge this gap by developing a dynamic approach for mapping ecosystem conditions. The study focuses on the Bavarian Forest National Park in Germany. We analyse time series of spectral indices and plant biochemical traits using multispectral satellite imagery and hyperspectral data. We use Artificial Intelligence (AI) techniques to assess retrospective changes and to predict missing time steps of plant traits, providing detailed, long-term information on ecosystem dynamics. We collect and process spaceborne multispectral data (Landsat and Sentinel-2) to generate a regional data cube covering the park from 1984 to 2024. Additionally, we combine spaceborne hyperspectral data (EnMAP, PRISMA, EO-1 Hyperion, and DESIS) and preprocessed airborne hyperspectral image archives (HySpex) with biochemical and biophysical traits to generate a regional biological condition data cube. We develop a regional demonstrator data cube using the Earth System Data Cube (ESDC) framework to integrate diverse Earth Observation (EO) data relevant to mapping ecosystem extent and condition (Figure 1). In the next steps, we aim to establish a thorough comprehension of ecosystem dynamics and states by seamlessly incorporating multispectral and hyperspectral data-derived plant traits. The utilisation of advanced AI techniques specifically tailored for the analysis of three-dimensional data cubes will facilitate the reconstruction of plant traits and enable the discernment of long-term trends and patterns. These advancements will substantially enrich scientific understanding in remote sensing, AI, and ecosystem mapping. [Figure 1. Preliminary results of the showcase on the constructed VI data cube and hyperspectral plant traits data cube. (a): Landsat OLI-derived NDVI data cube; (b): EnMAP-derived chlorophyll data cube.][1] [1]: https://drive.google.com/file/d/1t3OI0Xdm3DTXWHlZKfDba3LRrzPPA4jo/view?usp=drive_link

[89] Priority effects in native and exotic European grassland plants are mediated by direct competition and soil fungi (14:00)

Presenter: DIESKAU, Julia (MLU Halle)

In plant communities, species often don´t arrive simultaneously at a new site. The effect of an early-arriving species (EAS) on the establishment, growth and reproduction of a late-arriving species (LAS) is referred to as priority effect. Despite increasing evidence that priority effects play an important role in community assembly processes (Ejrnæs, Bruun and Graae, 2006; Körner et al., 2008), the underlying mechanisms are not fully understood (Fukami, 2015). To achieve a deeper understanding of the mechanisms underlying the priority effects of native and exotic plant species, we conducted a multi-species field experiment, with LAS arriving two years later than EAS. To gain better insights into the role of direct competition and soil fungi accumulation in this process, we implemented two treatments: a fungicide treatment (for the removal of the soil fungi accumulated by EA plants) and an herbicide treatment (for the removal of EA plants and in consequence their direct competitive effects). Consistent with our expectation, we found that the strength of the direct competition effect depended on the biomass of the EAS. Additionally, both the priority effect mediated by soil fungi and that mediated by direct competition were influenced by the origin of the EAS and LAS. Furthermore, we demonstrated that the soil fungi accumulated by the EAS had not only a direct effect on the LAS but also an indirect effect through their influence on the performance of the EAS, thereby affecting the strength of the competition effect. Our results support the assumption that both direct competition and soil-borne pathogenic fungi are important drivers of priority effects, and that both depend on the origin of the interacting species. These results do not only contribute to our mechanistic understanding of assembly processes but are also relevant for the management of invasive species and habitat restoration.

[8] TOWARDS CLIMATE-SMART REWILDING (14:15)

Presenter: SCHWARZ STARK, Gavin

The European Union has set an ambitious target to tackle climate change: achieving net zero carbon emissions by 2050. To achieve this target, it is essential that the EU focuses on increasing carbon storage in our soils and forests. According to most experts, the implementation of nature-based solutions (NbS) is crucial to tackling the climate crisis. Rewilding is a type of NbS that aims to allow nature to regenerate through minimal human intervention. WildE is an innovative Horizon Europe-funded project. WildE introduce a new rewilding strategy called "Climate-Smart Rewilding". The aim is to generate climate-related benefits while achieving other important goals. This can include ecosystem restoration, biodiversity conservation and the well-being of local communities. Climate-smart rewilding could bring numerous economic benefits, particularly through the acquisition of new carbon credits. At a low cost, this strategy could help meet other environmental and societal needs. Our research explores how different rewilding interventions can help mitigate and adapt to the negative impacts of climate change on both ecosystems and human well-being. We develop a conceptual framework that incorporates key components such as land use, biodiversity, climate change mitigation and adaptation, and socio-economic aspects in an integrated re-wilding analysis. This framework can enable policy makers, conservation managers, communities and the private sector to jointly develop climate-smart strategies as effective NbS across the European continent to achieve EU climate and biodiversity targets. The flexibility of the approach and the potential for economic benefits make it a compelling solution to the challenges of the coming century.

[106] Reflecting spectral information: Global leaf and canopy optical dimensions and their associations to traits and the environment. (14:30)

Presenter: JOSWIG, Julia S. (Remote Sensing Centre for Earth System Research, Leipzig University)

Plants mediate - through their traits - between the environment and ecosystem functioning. Plants' optical spectra can directly reflect some of these traits. A series of studies have assessed trait estimates or plant-environment relationships from hyperspectral data. Yet these relationships largely differed in biomes, functional aspects, application context, or for different functional groups. Thus, we still miss a universal and overarching understanding of what the main variations of optical data are and what they reflect in terms of functional traits or environmental conditions. Here we assess the global plant spectral properties with respect to their shared information content with in-situ traits and environmental variables. In detail, we reduced the optical dimensions of a large, global and standardized spectral dataset across leaf and canopy scales to 10 principle components (PCs), and then related these - via models - to a range of traits (individually measured and database extracted) and to environmental variables. We find up to 88% of spectral variation (capturing for leaf 99.2 % and for canopy 99.58 %) explained by database traits and the climate variables. Importantly, how much these optical PCs are associated with traits and climate, is independent from how much they explain the spectrum. In other words tiny spectral variations reflect important aspects of plant function. E.g. the 9th PC is explained by pigments. Since traits explain a larger fraction than the environment, the optical signal appears to vary much within the same climatic conditions. Generally, the information content for optical PCs decreases from leaf to canopy, area to mass-based traits (for canopy), directly measured to database-derived. These findings are based on the largest aggregation of leaf and canopy spectra, and have the potential to improve our understanding about which aspects of plant function are reflected by in-situ, and optical data at different scales.

Talk Session: Biodiversity Change - Leipziger KUBUS/1-B - Hall 1 B (14 Nov 2024, 13:30 - 14:45)

[64] Revegetation across Europe primarily benefits common and generalist pollinator species (13:30)

Presenter: GLENNY, William Robb

Active restoration accelerates the colonization and succession of vegetation communities by using manual methods to introduce plant propagules into a degraded area. To meet the demands for large landscape revegetation, active restoration restricts land practitioners to use plants that are produced by seed suppliers at commercial scales (the ‘Restoration species pool’). Plants from the restoration species pool may therefore become more common across ecological communities as land managers seek to revegetate degraded areas, with unknown consequences for biotic communities in higher trophic levels. For Europe, we surveyed the literature to identify plant genera that are available for restoration, and then used plant-pollinator interaction data from 17 different studies to compare the association between plant commonness and pollinator diversity. We predicted that plants from the restoration species pool would already be common in plant-pollinator interaction networks, and that common plants primarily benefit common and abundant generalist pollinators. Plant genera from the restoration species pool were more common and supported more pollinators, than other plant genera, and only a few genera from the restoration species pool are required to support most of the pollinator species. However, common plants supported pollinator assemblages that were redundant with other co-occurring plants, and contribute little to overall pollinator diversity. Finally, simulated seed mixes of common plant species supported fewer rare pollinators, and more generalists, indicating that active restoration contributes to the functional homogenization of pollinator communities. Increasing the availability plants that support rare, specialized, and unique pollinators can equip land managers to restore ecosystems with taxonomically and functionally diverse communities.

[151] The impact of urban development on diversity, performance and fitness of cavity-nesting Hymenoptera (13:45)

Presenter: ÇELIKGIL, Atilla (Martin Luther University Halle-Wittenberg)

Urban development can affect population dynamics, ecological interactions and fitness, challenging the persistence of many species, including Hymenoptera. Yet, how and which urban environmental features affect Hymenoptera abundance and species richness, as well as fitness, remain unclear. Here, we used a citizen science approach and cavity-nesting Hymenoptera in insect hotels as a model system to study the effects of urban development on Hymenoptera abundance and richness, mortality and reproductive output. In total, 286 insect hotels were deployed in two German cities at sites ranging from the edge to the core of the city, and several environmental variables (i.e., impervious surfaces, temperature, green cover, landscape fragmentation and landscape diversity) were collected from each site. Overall, more than 10,000 and 2,000 individuals belonging to 12 cavity-nesting bee and 23 wasp species, respectively, were sampled in all insect hotels and cities. Statistical analyses revealed a strong negative relationship between impervious surfaces and cavity-nesting Hymenoptera abundance, species richness, reproductive output and survival. Additionally, urban landscape fragmentation negatively affected cavity-nesting Hymenoptera survival, temperature negatively impacted their abundance, species richness and survival, while landscape diversity positively affected their species richness. As cities expand worldwide, our study aims to highlight the main urban environmental factors that influence cavity-nesting bees and wasps and can help guide conservation management to mitigate the adverse consequences of urbanisation on Hymenoptera.

[67] Land use effects on freshwater biodiversity: synthesis based on a new global database (14:00)

Presenter: SHEN, Minghua

Freshwater ecosystems have been heavily impacted by land-use changes, but syntheses on the impacts on freshwater ecosystems are still limited. First, we compiled a global database encompassing 242 studies and 4,653 sites with species abundance data (from multiple taxon groups and geographic locations) across sites with different land-use categories. This database is now the largest database to incorporate the abundance data of freshwater biota across different land-use categories. Then, we analyzed this database to investigate the effects of land-use change on freshwater biodiversity by comparing less impacted sites with more impacted sites across different spatial scales (e.g., α, β, γ), employing multiple biodiversity metrics (e.g., richness, evenness, abundance). Our analysis showed the freshwater ecosystems in urbanization had the strongest declines in species richness, rarefied richness and evenness, while not in abundance. This study will facilitate a better understanding of how land use alters freshwater assemblages on a global scale.

[65] Synthesizing over 30 years of soil biodiversity data in Germany (and beyond) (14:15)

Presenter: RISTOK, Christian

The decline in biodiversity in conjunction with global change poses a threat to human well-being. Soils are home to c. 60 % of species on earth but our knowledge of soil biodiversity change and its drivers is limited. Long-term monitoring data are needed but are scarce or have not yet been analyzed. Here, we present analyses of over 30 years of soil biodiversity monitoring in Germany. In c. 800 plots, physico-chemical and biological parameters of soils have been monitored, partly since 1985. These plots were established in three major land-use types, i.e., agriculture, forest, and grassland, and are monitored in set intervals every few years. We have aggregated and harmonized all data and used time-series and meta-analytical tools to statistically analyze the data. In addition, we performed a literature synthesis of available temporal trends. We show how earthworm diversity in Germany’s long-term observational sites, as well as micro-, meso-, and macrofauna based on literature changed over time. In addition, we link changes in these soil biodiversity variables to important drivers, such as soil pH, nutrients, and pollution. We are able to show how these drivers interact with land-use type. Lastly, we present a statistical approach to deal with heterogeneous monitoring data. Taken together, we present the first time-series of soil biodiversity change for Germany and make a case for the importance of soil monitoring. Furthermore, we show how our results can inform assessments on the state and change of biodiversity, potentially resulting in policies to protect and restore soil biodiversity.

[101] Disproportionate declines of formerly abundant species underlie insect loss (14:30)

Presenter: VAN KLINK, Roel

Recent studies have reported widespread declines in terrestrial insect abundance, but trends in other biodiversity metrics are less clear-cut. We examined long-term trends in 923 terrestrial insect assemblages monitored in 106 studies, and found concomitant declines in abundance and species richness. For studies that were resolved to species level (551 sites in 57 studies), we observed a decline in the number of initially abundant species through time, but not in the number of very rare species. At the population level, we found that species that were most abundant at the start of the time series showed the strongest average declines (corrected for regression-to-the-mean effects). Rarer species were, on average, also declining, but these were offset by increases of other species. Our results suggest that the observed decreases in total insect abundance can mostly be explained by widespread declines of formerly abundant species. This counters the common narrative that biodiversity loss is mostly characterized by declines of rare species. Although our results suggest that fundamental changes are occurring in insect assemblages, it is important to recognize that they represent only trends from those locations for which sufficient long-term data are available. Nevertheless, given the importance of abundant species in ecosystems, their general declines are likely to have broad repercussions for food webs and ecosystem functioning.

Talk Session: Biodiversity & Society - Leipziger KUBUS/2-AB - Hall 2 (14 Nov 2024, 13:30 - 14:45)

[31] Societal Dynamics and Loss of Coastal Ecosystem Biodiversity: A Sociological Multi-Level Review (13:30)

Presenters: YENDELL, Alexander (Leipzig University), JAECKEL, Yvonne (Leipzig University), ROSTEIUS, Pauline (Leipzug University), LERCH, Helene (Leipzug University), BÄR, Giulia (Leipzig University)

In the proposed paper, we present the research that was conducted within the framework of the PRO-Coast project, initiated in November 2023 with funding from Horizon Europe. The study aims to uncover the complex societal drivers of biodiversity loss in coastal ecosystems through an in-depth, multi-level analytical framework. This framework examines demographic, social, ethnic, religious, gender, organizational, and broader societal factors that influence attitudes and actions with regard to the conservation of coastal biodiversity. An extensive review of existing literature was conducted to understand the complex interplay between societal factors and the loss of coastal biodiversity. Our findings emphasize the significant impact that age, gender, socioeconomic status (SES), and education have on conservation efforts, which highlights the need for sophisticated approaches to be taken with regard to the preservation of biodiversity. This paper underlines the critical need for comprehensive conservation strategies that are inclusive and engage diverse social groups in the conservation discourse. The literature review also reveals that the theories underpinning many existing studies, including our own, often lack depth in the context of the social sciences. In contrast, theories that could benefit not only scientific understanding but also practical interventions draw primarily from environmental psychology, personality psychology, and sociological theories at the meso and macro levels of society. For instance, insights from the Sociology of Risk (Beck, 1992; Giddens, 1991), from Social Capital Theory (Bourdieu, 1986; Putnam, 2000), from theories of Social Inequality (Bourdieu, 1984; Douglas et al., 1993), and from Critical Theory (Adorno & Horkheimer, 1944; Marcuse, 1964) prove to have high explanatory power. These theories offer a perspective on the overall relationships that link various aspects to environmental destruction and participation in environmental efforts, including aspects of biodiversity in coastal regions.

[145] Rewilding the Oder Delta, Germany: Envisioning Pluralistic Value Perspectives with Nature Futures Scenarios (13:45)

Presenter: QUINTERO URIBE, Laura Catalina (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Puschstrasse 4, 04103, Leipzig, Germany)

Rewilding has emerged as a restoration approach that addresses societal challenges and promotes the benefits of nature restoration. It aims to restore wildlife, mitigate climate change, and create transformative change. However, scaling up rewilding efforts is challenging due to complex nature-people relationships. Effective landscape management and stakeholder engagement are crucial for successful rewilding. Participatory scenario planning and co-design can help understand the benefits and trade-offs of rewilding. We introduce a novel methodology using the Nature Futures Framework to address opportunities, co-benefits, and trade-offs for rewilding. The German Oder Delta was studied to identify appropriate rewilding actions based on diverse socio-ecological demands. We conducted stakeholder interviews to co-design three distinct scenarios reflecting diverse values of nature and rewilding strategies. The study identified a comprehensive set of actions to be implemented across the landscape. The findings suggest that diverse values related to nature are distributed heterogeneously across the landscape, requiring an adaptive management approach. By evaluating various perspectives on nature, preferred areas for rewilding actions were identified based on their role in providing intrinsic, utilitarian, and relational values. Regions closer to agricultural sites were favoured for carrying out biodiversity-friendly agricultural practices, such as paludiculture, emphasizing restoring natural disturbance dynamics. In the different scenarios, rivers were essential landscape elements for promoting intrinsic and material benefits from nature and landscape connectivity. Finally, rewilding actions, such as allowing a natural succession of abandoned grasslands and old-growth forests, were allocated in less fragmented areas and distant from urban infrastructure landscape areas. The findings emphasize the importance of considering pluralistic values when designing rewilding actions, underscoring the crucial role of stakeholders in highlighting areas with less resistance to rewilding and co-adapting to landscape changes. Recognizing the multiple values of nature can foster the successful implementation of rewilding measures and their upscaling to larger areas.

[33] Multi-objective management of naturally regenerating beech forests – An ecological-economic optimization approach (14:00)

Presenter: SCHORN, Markus Erhard

How can we meet economic objectives of timber harvesting while maintaining the functioning of diverse forest ecosystems? Existing forest models that address this type of question are often complex, data-intensive, challenging to couple with economic optimization models, or can not easily be generalised for uneven-aged mixed-species forests. Here, we develop an ecological-economic optimization model, which integrates a state-of-the-art demographic forest model with a continuous cover forestry harvesting model to optimise efficient and sustainable timber harvesting. As a proof-of-concept, we apply the model to a beech-dominated forest in the Hainich-Dün region in Thuringia, Germany, with the goal of optimising multiple objectives such as timber yield and the biodiversity value of the forest. The ecological module is the Perfect Plasticity Approximation (PPA) demographic forest model that simulates forest dynamics based on individual tree growth and survival rates in the canopy and understory layers, respectively, as well as recruitment rates. We used repeated forest inventory data from a 28-ha forest plot to quantify these demographic rates and validated the predictions of the ecological module against the structure of old-growth beech forests in Europe. The economic module includes the optimization of net revenues (market revenues net of harvesting cost) from harvesting timber. As an indicator of the biodiversity value of the forest, we use the number of retained habitat trees (>70 cm diameter). The forest model delivered reasonable predictions of structural attributes of unmanaged old-growth beech forests. When net revenues from timber harvest were maximised, trees were logged when they reached 55 cm in diameter. This is similar to current management practices in beech forests. We found a linear trade-off between timber net revenues and biodiversity value with about 2.5% of the maximum benefit of timber harvest being lost with each additionally retained habitat tree. We established a generic ecological-economic modelling framework that reliably represents forest dynamics as well as optimising forest management. To our knowledge, this is the first forest model for central European forests capable of identifying optimal harvesting over the full set of feasible strategies, rather than merely comparing predefined management scenarios. The framework can be extended to mixed-species forests and support forest management for diverse ecosystem services.

[129] Expert evaluation: Potential future scenarios for the Common Agricultural Policy (14:15)

Presenter: SCHAAN, Linn

The future Common Agricultural Policy (CAP) (post-2027) is currently under discussion, with the EU Commission set to unveil its proposal in July 2025. Thus, the upcoming CAP will be shaped by a new EU administration, following the EU elections in June this year. The hope is that the next CAP should fulfill, inter alia, ambitious EU sustainability targets defined in the Green Deal, Farm-to-Fork Strategy and the Biodiversity Strategy, considering that the CAP is an instrumental policy to implement some of the listed targets when aligning with agroecological principles. Many scenarios that set out structural changes to the CAP have been proposed, but their potential implications have yet to be evaluated. Following a literature search, we consolidated published visions for the CAP into four distinct scenarios. Using an online survey, we invited experienced CAP experts to evaluate them. We sought over 200 CAP experts from across the EU working from a wide variety of disciplines and backgrounds, including academia, NGOs, farmer organisations, rural community groups, consumer advocacy groups and agricultural cooperatives. Each scenario was evaluated on its strengths, weaknesses, feasibility and barriers to its implementation. The scenarios included in the survey were chosen to cover a wide variety of options and captured the following broad ideas: “Business as usual”, “Strengthening green and social architecture”, “Food System Policy” and a “Substantial reduction of CAP budget”. Experts could also propose their own scenario for the CAP. We also sought insights into the key barriers to reform the CAP and explored potential avenues for overcoming these challenges. We used a qualitative content analysis to analyse the survey responses. In our talk, we will share the findings and political implications derived from the analysis of survey responses collected (so far) from over 50 scientists and more than 15 non-academic participants. Based on the insights, we make recommendations on how the CAP can optimally help scaling up agroecology in Europe.

[26] Persefone.jl: evaluating biodiversity impacts of agricultural policy with a multidisciplinary mechanistic model (14:30)

Presenter: VEDDER, Daniel

The environmental impacts of modern agriculture are a grave concern. Although policies such as the European Common Agricultural Policy (CAP) attempt to mitigate further damage to ecosystems, plant and animal species in agricultural landscapes continue to decline at alarming rates. A major challenge in designing effective agricultural policies is that these must take multiple economic, social, and ecological aims into consideration. In addition, agriculture takes place at the intersection between societal and natural processes; it is influenced as much by legislation and market prices as it is by pollination and weather. Simulation models are a valuable tool to help evaluate policies by exploring the likely outcomes of different scenarios. Agricultural policy-making in Europe has benefitted from existing economic and environmental models, which often explore abiotic phenomena such as climate and hydrology. However, there are few models that study the effects of agricultural policy and practice on biodiversity. We present Persefone.jl, a new model of agriculture and ecosystems currently being developed at iDiv. Persefone.jl simulates agricultural landscapes as social-ecological systems, with interacting submodels of farm management, crop growth, and animal populations. This allows the model to replicate the spatial and temporal dynamics of such landscapes, and study their impact on species abundance and distribution as well as farm production. Thus, it synthesises knowledge from multiple research areas, building on empirical data and established theory to create an integrated process-based simulation. To showcase how Persefone.jl can be used to evaluate policy, we use it to analyse the consequences of this year’s weakening of the CAP’s environmental regulations. We also briefly present our future development plans for including ecosystem services and climate change in the model. By making the software as accessible and adaptable as possible, we hope to establish Persefone.jl as a useful tool for future social-ecological research at iDiv.

Poster Flash Talks - Leipziger KUBUS/2-AB - Hall 2 (14 Nov 2024, 14:40 - 15:00)

[82] Science meets policy: the European Topic Centre on Biodiversity and Ecosystems (14:40)

Presenter: BRASCHLER, Brigitte

Reversing the decline of biodiversity requires that scientists work with society to achieve comprehensive and efficient conservation of habitats and species. Scientists can contribute in many ways, e.g. by informing on current and new policies and aiding their implementation through expert advice, development of definitions, indices and standards, or evaluations of current status. The European Topic Centre on Biodiversity and Ecosystems (ETC BE) is a consortium of 24 European research institutions, organizations, and national agencies with expertise in terrestrial, aquatic, and marine biodiversity and ecosystems. Coordinated by the Norwegian Institute for Water Research (NIVA), the ETC BE supports the European Environment Agency (EEA) and the European Commission in their mission to implement EU directives, strategies and policies, and to provide information to policymakers and the public. Our team collaborates on the implementation of EU biodiversity legislation (e.g. Nature Directives, Invasive Alien Species, Nature Restoration Law, Natura 2000), their data reporting and analysis, as well as in the maintenance and further development of Information Systems (e.g. BISE). Participation in this project requires overcoming challenges related to worldviews and procedures unfamiliar to academics. Exciting, ground-breaking work combines with repetitive technical tasks; with EEA and Commission counterparts often more interested in the latter. Political processes can have massive impacts, such as when adoptions of new data standards were rejected by EU Member States, and when the delayed adoption of the Nature Restoration Law resulted in freezing related actions and budgets for extended periods. Particularities of different Member States result in varying data quality and structure, and render task automation challenging. Furthermore, many tasks draw on the expertise of diverse teams distributed among partner organisations, necessitating coordination within and among scientists and public officers. Although challenging, biodiversity scientists should get involved in policy and implementation, and collaborate in order to impact biodiversity conservation.

[48] How policy can support farmers in restoring habitat connectivity - Simulations on policies for hedge plantings (14:41)

Presenter: KOLB, Lea-Deborah (Helmholtz Centre for Environmental Research - UFZ and German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)

Preserving farmland biodiversity is one of the objectives of the Common Agricultural Policy (CAP) of the European Union. To achieve this goal, it is important to restore landscape connectivity by enriching agricultural landscapes again with accessible habitats for breeding, feeding, and shelter. In intensive agricultural regions of Germany, adding more hedges would be highly beneficial for biodiversity and would also serve for climate adaptation. Most hedges are protected by law and cannot be removed. However, planting and maintaining hedges can be financially disadvantageous to farmers. To offset this disadvantage, some federal states subsidise hedge planting, while others do not. Here, CAP funding is complemented through federal directives. However, there is still much uncertainty about how to optimize subsidy design to maximize ecological impact while meeting farmers' needs and adapting to local conditions This study examines hedge planting subsidies, specifically the effect of subsidy height on farmer adoption and resulting changes in landscape connectivity in Thuringia and Baden-Wurttemberg. For this purpose, we developed an agent-based economic-ecological model. This model simulates how policy payments and regulations affect landscape composition and configuration through farmers' decisions. The work is part of the CAP4GI project that explores restoring Green Infrastructure through better CAP payments. Employing digital experiments, we assess alternative payment schemes that may be implemented with the upcoming CAP reform in 2028 or via the German action plan for natural climate protection. We also explore the importance of boundary conditions such as tenure and non-pecuniary incentives for farmers. From this, we develop recommendations on how policies can be adjusted to account for the current gap between ecological needs and farmers’ challenges. In the future, the model may be coupled to ‘Persefone.jl’, an agro-ecological model, to assess the outcomes for biodiversity.

[22] Country-level determinants of the decision to invest into renewable energy projects (14:42)

Presenter: MARTINI, Christina

Preliminary abstract: "There is substantial variation in investments in renewable energy infrastructure across European countries. This paper examines country-level variables to explain differences in the willingness to accept investments in renewable energy plants. Using survey data and a discrete choice experiment encompassing 13,879 observations from 30 European countries, we analyze whether cultural factors, such as individualism and long-term orientation, as well as variables measuring a country’s environmental performance and climate change risks, influence respondents’ willingness to accept an investment offer. Our findings reveal that respondents in individualistic countries demand higher profits from investment options. Conversely, respondents from countries with a long-term orientation and high environmental performance are more likely to accept lower profits. Notably, we find that individuals’ pro-environmental motivation mediates the relationship between country-level variables and investment willingness. For example, respondents in individualistic countries with low pro-environmental motivation demand higher profits for renewable energy projects than those in less individualistic countries with similar motivation levels."

[149] iDiv for female scientists (14:43)

Presenter: HOSS, Daniela

Women and several minority groups are underrepresented in leadership positions in scientific institutions. How does iDiv compare to the global picture? In general, female researchers face both structural and individual challenges, including lower income, fewer career development opportunities, unconscious biases, discrimination, and harassment. The first step to changing this reality is to promote awareness, and this has been the main goal of the Female Scientists initiative created in April 2023 at iDiv. The initiative is now led by five iDiv postdocs and has grown into a network of more than 110 members. We have accomplished more than 20 activities aimed at increasing transparency and supporting female scientists. During the iDiv Conference, we want to share our experiences and knowledge on gender inequalities in science and engage in an open discussion within the community. We aim to move towards a more diverse, safe, healthy, and equitable environment for all.

Poster Flash Talks - Leipziger KUBUS/1-B - Hall 1 B (14 Nov 2024, 14:45 - 15:00)

[58] Defining the role of spatial sampling in soil biodiversity estimates (14:45)

Presenter: KOSTAKOU, Maria (Department of Applied Microbial Ecology, Helmholtz Institute for Environmental Research-UFZ)

In soil microbiomes, the interplay between dispersal, biotic, and abiotic selection is scale-dependent, but the impact of sampling design on biodiversity estimates is often overlooked. To address this, we studied the effects of spatial sampling designs, including commonly-practiced homogenization (or sample pooling), on microbial diversity estimates by sampling soil microbiomes at 54 sites across grasslands and forests in Germany. Using 16S rRNA gene metabarcoding, we explored how variations in sample size and distribution within plots influence diversity estimates. We assessed the effects of sample extent, aggregation, and sample number on alpha, beta, gamma, and zeta diversity estimates, comparing these to homogenized soil samples from the same locations. Our findings provide valuable insights into the effects of spatial sampling designs on microbial diversity estimates in soils. It underscores the importance of preserving soil cores rather than homogenizing samples, thereby contributing to the development of more robust sampling methodologies.

[162] A framework to model species responses to extreme weather events (14:46)

Presenter: KAUFFELDT, Aaron Hagen (Senckenberg Biodiversität und Klima Forschungszentrum Frankfurt am Main)

Human induced climate change poses a threat to global biodiversity. Broad scale effects of climate change are often assessed on the basis of long-term changes in climatic conditions. However, the effect of increasing frequency and intensity of extreme weather events (EWE) due to climate change on biodiversity remains unclear. We introduce a general framework to investigate the effects of EWE on species. As a case study we train coccupancy models for 132 German bird species of conservation interest (species requiring assessment under the EU Bird Protection Areas guidelines) with monthly specific weather and remote sensing data over the time period of 2000 to 2022. The species-specific models predict the occupancy through time from 1999 to 2022 for each month across Germany. With this approach, the suitability over all non-extreme months can be compared to the suitability in months with climatic extremes, to generate a measure of the impact of an extreme event on the distribution of a species. With this measure it is possible to identify geographic areas, species communities, taxonomic- and functional groups that may be vulnerable towards specific EWE.

[68] Known unknowns and model selection in ecological evidence synthesis (14:47)

Presenter: BLOWES, Shane

Quantitative evidence synthesis aims for general insights into the direction, magnitude and variability of ecological effects. Two common forms of quantitative synthesis are meta-analysis (i.e., analyses of effect sizes collated or calculated from existing studies), and analyses of data compiled to address specific questions. Both approaches frequently quantify the heterogeneity of effect sizes across studies to describe how consistent ecological effects are across studies. However, both these types of quantitative synthesis typically assume constant between-study heterogeneity (meta-analysis) or residual variation (i.e., homoscedasticity for analyses of raw data). This assumption is equivalent to assuming that included studies sample effect sizes from a single population. Despite the rapid rise of meta-analysis in ecology and conservation biology, neither the consequences of this assumption, nor the opportunities available when it is relaxed, have received much attention. Here, I demonstrate the utility of multilevel location-scale models and cross-validation for model selection in quantitative evidence synthesis. First, I revisit a meta-analysis of spatial scale-dependence in plant native-exotic species richness relationships. I quantify relationships among unexplained variation, grain size, and spatial extent, and examine how relaxing the assumption of constant heterogeneity impacts predictive performance. The second case study uses a data compilation of habitat fragment diversity studies. I focus on the relationship between fragment size and local (i.e., patch-scale) species richness, examine whether residual variation is related to fragment size and other study-level predictors, and how heteroscedastic residual variation impacts predictive performance. For both case studies, the assumption of constant between-study heterogeneity limits model predictive performance, particularly the ability of models to make predictions to new studies.

[131] Understanding biodiversity patterns in response to land-use change: Insights from Peneda-Gerês National Park (14:48)

Presenter: JOERGER-HICKFANG, Theresa

Agricultural land abandonment is one of the main drivers of land-use change across Europe, with significant environmental consequences, particularly in regions such as northern Portugal. In the Peneda-Gerês National Park, this phenomenon has led to substantial landscape changes, primarily through secondary natural succession on areas formerly used for agriculture. As a result, the National Park now features a mosaic of young and old oak forest stands, each potentially offering distinct habitats for various species. This study focuses on evaluating the impact of these changes on beetle communities by comparing the effectiveness of classical species-area relationships (SAR) and countryside SAR models in predicting habitat preferences of beetles across different forest patches. To achieve this, we employed window traps to systematically sample beetle populations across various forest stands. The collected specimens were identified using a metabarcoding approach, which allows for rapid and accurate species identification, thus enabling a comprehensive assessment of beetle biodiversity within the park. Our analysis aimed to determine whether the countryside SAR, which accounts for human-modified landscapes, provides a better model for predicting beetle species richness and habitat preference compared to the classical SAR model. The findings show that beetle communities display clear preferences for specific forest ages, with the countryside SAR model showing better performance in indicating these preferences. These results contribute to a broader understanding of the National Park's ecosystem resilience, highlighting the importance of habitat patch characteristics such as forest age diversity and size in shaping biodiversity. This research underscores the need to integrate these factors into conservation and management strategies, particularly in regions undergoing significant land-use changes, to ensure the protection and sustainability of biodiversity.

[69] Heathland restoration measures worsen ground beetle decline, regardless of functional traits. (14:49)

Presenter: FAURE, Mathieu (Martin Luther University Halle-Wittenberg, Université de Bordeaux)

There is growing evidence of a worldwide insect decline, caused by various pressures such as natural habitat loss, chemicals, or warming temperatures. However, not all insects are impacted in the same way, and long-term monitoring coupled with a trait approach can be a powerful tool for understanding the drivers and consequences of these environmental changes. Here, we use data from two semi-natural areas in Drenthe, the Netherlands, where ground beetles (Coleoptera: Carabidae) have been sampled using pitfall traps since 1959. These areas consist mainly of heathland and are isolated in a highly intensive agricultural landscape. Over the years, numerous restoration events have taken place in the form of vegetation burning and topsoil removal. This dataset has already been partially analysed, showing a decline in abundance and biomass, but it is not known which species are the most affected, and what environmental factors might be driving these trends. Thus, using GLMMs, we computed and compared the trends of different beetle groups, based on their habitat preferences, breeding season, and dispersal. We hypothesised that the trends of the first two groups are mainly related to climatic factors, while the trends of the third group might be related to habitat fragmentation. Over the whole period, all the beetle groups were found to decline, with the exception of the forest species and the fall breeders. The fastest declining beetles were the wetland and heathland species, as well as those with lower dispersal ability. Most of these trends were similar with and without restoration, but, overall, we found a significantly steeper declining trend in the sites present in the restored areas. These results suggest that the restoration measures are not sufficient to address the decline of insects. Also, for the low dispersal species more efforts are needed to increase the connectivity to other natural areas.

[100] Wild bee body size as a response trait to anthropogenic disturbance in agriculturally dominated landscapes (14:51)

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

Landscape alteration, agricultural intensification and climate change are considered the most important global change factors driving wild bee decline. However, little is known about whether these drivers have led to 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, population dynamics and the structure of ecological networks. Therefore, variability in bee body size across environmental gradients deserves more attention. To investigate how bee body size changes over environmental gradients of anthropogenic disturbance, we measured the body size of 10 wild bee species collected from 6 landscapes that vary in agriculture intensity and landscape heterogeneity in Saxony□Anhalt, Germany. Our results revealed that i) there is a shift in bee body size between sites with different levels of human impact, and ii) the direction of change is not consistent across species. We discuss the eco-evolutionary implications of the effect of agricultural intensification on bee body size and how different bee species might vary in their vulnerability to environmental change.

[148] Insects in cities: A within-city approach to reveal the ecological drivers that shape urban pollinator assemblages (14:52)

Presenter: FRIEDEL, Selina (Martin Luther University Halle-Wittenberg)

Urbanisation is one of the main drivers of land-use change with overall negative effects on biodiversity. Yet, insect pollinator communities have been shown to have contrasting responses to urbanisation with varying effects on their species richness and abundance. Here, we used a multiple spatial scale (local to landscape scale) within-city approach to investigate the overall impact of urban development on insect pollinators, as well as identify the main urban environmental factors that influence pollinator communities in cities. For this, we used pan traps in the cities of Hamburg, Leipzig, and Halle at 350 sites that spanned from the edge to the city centre and collected several local (i.e., nesting and floral-food resource availability) and landscape scale (i.e., temperature, green cover, habitat fragmentation, impervious surfaces) ecological variables that could affect insect communities. Overall, we collected more than 10,000 insect individuals and identified more than 21 hoverflies, 33 Coleoptera, and 160 Hymenoptera species. Our analyses revealed that different insect pollinator groups had varying responses to different environmental factors in terms of richness and abundance. Our results provide insights into how environmental factors can influence and shape insect pollinators and highlight key processes necessary to inform strategies to restore and maintain diverse urban insect communities.

Poster Flash Talks: Biodiversity and the functioning of Ecosystem - Leipziger KUBUS/1-A - Hall 1 A (14 Nov 2024, 14:45 - 15:00)

[87] Biodiversity increases the stability and resistance of plant communtiy nutrient concentrations. (14:45)

Presenter: BAAN, Patrick (Idiv)

The elemental composition of plants plays a major role in different ecosystem processes (e.g. nutrient recycling) and ecological interactions (e.g. herbivory), and has of recent received increased attention in biodiversity-ecosystem functioning research. While biodiversity can affect plant community nutrient responses, less is known about the role of biodiversity on the stability of these nutrients in plants over time, and whether biodiversity could buffer those against climate extremes. Through long-term data (20 years) from the Jena experiment, we tested whether increasing plant diversity (species richness and functional groups) affected plant community C, N and C:N ratios over time. Furthermore, we incorporated data on plant community composition, soil characteristics and environmental changes to identify the drivers underlying these temporal nutrient responses. Overall levels of plant nutrient concentrations slowly increased over time in the Jena experiment. Plant diversity increased the temporal stability of both C and N concentrations and their ratio. Stability of community C concentrations was mostly influenced by climate events, such as a drought. Temporal stability in N concentrations showed greater sensitivity to changes in plant community composition, especially related to the presence of legumes. Increasing diversity also buffered against climate extremes by increasing resistance and resilience of the plant community concentrations. Both C and N concentrations also recovered faster after climate extremes in plots with higher species richness. These results show that the stability of plant community nutrient concentrations is strongly linked to biodiversity and therefore conserving the latter could be vital in maintaining ecosystem functions and furthermore making ecosystems more resistant against future climate extremes.

[25] Moving forward with energy landscape research (14:46)

Presenter: BERTI, Emilio

Animals move in order to track resources and suitable habitats for their survival. In turn, animal movement promotes ecosystem stability and its functions, generating large scale biodiversity patterns. Animals, and all of us, make decisions on where to go and how to get there, evaluating the optimal travel paths more or less sub-consciously. Perhaps the most clear factor influencing movement decisions is how much effort, or energy, we have to spend to get where we want to go. Energy is the currency of life, with individuals striving to optimize energy costs and gains to maximize their fitness. Therefore, animals should minimise the energetic costs of moving, determining how they use the landscape and affect the environment. Yet, our understanding of how animals optimise their movement strategies remains limited. Our understanding of the importance of energy landscapes for terrestrial animal movement has been limited by the lack of a scalable framework to quantify energy costs of travelling and by data availability. These limitations have been recently resolved: I developed a scalable framework (enerscape) to compute movement costs for terrestrial animals and massive amounts of animal telemetry data have been made publicly available (e.g., https://www.movebank.org/). Here, I propose a new research project for investigating the impacts of energy costs on movement of terrestrial animals and how they use the landscape. Specifically, such research project will investigate: 1. How terrestrial mammals respond to energy landscapes. 2. How energy landscapes, resource availability, predation risk, and human pressure interact to influence animal decisions. 3. The connectivity among European protected areas network from the perspective of energy landscapes. 4. Tools and methodologies to support planned and future research. In this poster, I illustrate such a research project and what it offers to the larger scientific and practitioners community.

[13] Soil Multistability (14:47)

Presenter: JANDA, Zarah

Soil, Earth's vital thin skin, sustains life beyond water and forms the foundation of terrestrial ecosystems. Our project “Soil Multistability” aims to deepen our understanding of soil stability and its crucial role in biodiversity and ecosystem functioning (BEF). Specifically, we focus on multidimensional soil stability, including temporal stability, resistance, and recovery, by examining the biological, chemical, and physical dimensions essential for soil functioning. This research is conducted within the framework of the renowned Jena Experiment, where we explore the short- and long-term effects of plant diversity on the stability of soil microbial properties. Additionally, in the DrY greenhouse experiment, we investigate whether the effects of plant diversity on the magnitude and stability of soil properties intensify with increased abiotic and biotic stress. The ResCUE Experiment further extends this investigation by examining how plant diversity influences the stability of multiple soil properties under extreme drought conditions. Our innovative approach addresses how biotic interactions at the plant-soil interface drive BEF relationships, extending this inquiry to the abiotic level. By analyzing aggregate formation and microbial properties along a plant diversity gradient, we elucidate the interplay between biological and physical dimensions of soil stability and investigate how community assembly influences BEF relationships. This comprehensive study integrates data from long-term and new experiments, utilizing both simple, high-throughput methods like bait-lamina tests and sophisticated analyses of extracellular polymeric substances. By doing so, we aim to reveal the stabilizing mechanisms of soil properties over the long term and under climate extremes, ultimately contributing valuable insights into the resilience and functionality of ecosystems in the face of biodiversity and global changes.

[53] Soil food-web reconstruction across different mycorrhizal type dominated forests using the compound-specific isotope analysis of amino acids (14:48)

Presenter: HAUER, Amelie

Soil food-webs are crucial for nutrient cycling and ecosystem functioning in forests. They involve complex interactions between soil invertebrates, fungi and microbes, and are based on a variety of resources. Forest ecosystems dominated by distinct mycorrhizal associations exhibit significant differences in their biogeochemical properties on a global scale. A critical distinction lies in carbon allocation and sequestration, with ectomycorrhizal fungi (EMF) dominated systems harbouring substantially larger carbon stocks compared to those dominated by arbuscular mycorrhizal fungi (AMF). However, soil functioning in these two forest types depends on the local soil context, and the drivers and ecosystem effects of soil invertebrate communities in these systems are poorly explored. Up to date, there is no knowledge available on whether soil food-web structure and energy channeling across size classes differs between different mycorrhizal type dominated forests or if the feeding preferences of soil invertebrates change depending on the mycorrhizal system in which they feed. Compound‐specific isotope analysis of amino acids (CSIA-AA) is a novel tool to explore complex food-web dynamics. The combined use of δ13C and δ15N of essential amino acids helps to disentangle trophic relationships since it provides comprehensive information on basal resource consumption, and the trophic position of consumers. Here we present the results of our observational study, where we have analyzed nine groups of soil invertebrates in temperate, deciduous forest systems using CSIA-AA. The study aims at describing the use of plant, bacterial and fungal energy channels by different groups of consumers in soil and to elucidate structural differences in soil food webs among different mycorrhizal type dominated forests. As the first empirical quantification of root, bacterial and fungal energy channels in soil food webs across size classes, the study further marks the first application of CSIA-AA to a diverse array of consumers in soil food-webs.

[78] Understanding the impact of aboveground invertebrate decline on soil biodiversity and ecosystem functioning (14:49)

Presenter: CONSTANTINOU, Ioannis (1German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany; 2Institute of Biology, Leipzig University, Leipzig, Germany)

Global change is altering above-belowground multitrophic communities, and this has consequences for ecosystem processes and multifunctionality. The ecosystem-wide effects of such changes depend on the joint interplay of various taxa and their ecological interactions. Our aim is to investigate how above-belowground multifunctionality, multitrophic interaction networks, and energy fluxes respond to aboveground invertebrate decline. Firstly, through data from Insect Armageddon, an iDiv Ecotron Experiment, we will investigate the effects of aboveground invertebrate biomass decline on ecosystem functioning. Secondly, through BadBug, a field experiment in the global BugNet consortium, we will investigate the effects of aboveground insect\mollusc\pathogenic fungi exclusions on ecosystem functioning. Lastly, in FunDrought, another iDiv Ecotron experiment, we have manipulated the structure of the soil communities, under drought stress, and different tree mycorrhizal types, to investigate if there is a causal relationship between soil community structure and ecosystem functioning. Soil microbial respiration, PLFA\NLFA extractions, nematode, mesofauna and macrofauna extraction\sorting\identification, are some of the approaches that will be utilized. For assessing multifunctionality, energy fluxes will be calculated by reconstructing the soil food webs, to quantify the degree to which each treatment provisions integral ecosystem functions, like belowground decomposition, herbivory and predation. Treatments with more diverse aboveground communities, will show more diverse soil fauna, higher microbial biomass and less changes in fatty acid profiles in time, indicating resilience to environmental change. Additionally, more diverse soil communities will be able to simultaneously support high levels of belowground decomposition, productivity, and predation, as measured with the energy flux approach. The results of this study will highlight the importance of soil biodiversity, since Integral ecosystem functions like decomposition and plant productivity are mediated or solely provisioned by the belowground “compartment” of the ecosystems, and yet, we do not know much about how and to which extent this is currently being influenced by global change.

Coffe Break (15:00 - 15:30)

Talk Session: Biodiversity and the functioning of Ecosystem - Leipziger KUBUS/1-A - Hall 1 A (14 Nov 2024, 15:30 - 16:45)

[98] Mycorrhiza in Tree Diversity-Ecosystem Function Relationships: the first nine years of the iDiv experimental platform MyDiv (15:30)

Presenter: FERLIAN, Olga

The widely observed positive relationship between plant diversity and ecosystem functioning is thought to be driven by complementary resource use of plant species. Biotic interactions among plants and between plants and soil organisms are suggested to drive key aspects of resource-use complementarity. The young tree diversity experiment MyDiv aims to integrate biotic interactions across guilds of organisms, more specifically between plants and mycorrhizal fungi, to explain resource-use complementarity in plants and its consequences for competition and multitrophic interactions. Our overarching hypothesis is that ecosystem functioning increases when more plant species associate with functionally dissimilar mycorrhizal fungi (arbuscular and ectomycorrhizal fungi). Here, we present an extract of results from the first nine years of MyDiv. We investigated tree mycorrhization with classical and novel techniques as well as different ecosystems functions ranging from tree productivity to herbivory and energy fluxes through food webs as affected by tree species richness and mycorrhizal type. The studies largely showed that tree species richness and identity effects dominate over mycorrhizal type effects in the early stage of the experiment. Furthermore, tree communities with two mycorrhizal types experienced rather additive effects that were in between that of arbuscular and ectomycorrhizal communities. We showed that plant communities differ in their preferred fungal communities. Overall, the results of the first nine years of the experimental platform reveal strengthening distinct mechanisms of the two mycorrhizal types with time driving life strategies of trees and biodiversity-ecosystem functioning relationships.

[75] Tree diversity increases carbon stocks and fluxes above- but not belowground in a tropical forest experiment (15:45)

Presenter: SCHNABEL, Florian (University of Freiburg)

International commitments promote large-scale forest restoration as a nature-based solution to mitigate climate change through carbon (C) sequestration. Accumulating evidence suggests that mixed compared to monospecific planted forests may store more C, exhibit greater stability to climate extremes, and provide a wider range of ecosystem services. However, experimental studies that thoroughly examine the control of tree diversity on multiple C stocks and fluxes above- and belowground are lacking. To fill this gap, we leverage data from the Sardinilla experiment in Panama, the oldest tropical tree diversity experiment which features a gradient of one□, two□, three□ and five□species mixtures. Over 16 years, we measured multiple above- and belowground C stocks and fluxes, ranging from tree aboveground C, over leaf litter C production, to soil organic carbon (SOC). We show that tree diversity significantly increased aboveground C stocks and fluxes, with a 57% higher gain in aboveground tree C in five-species mixtures compared to monocultures (35.7±1.8 vs 22.8±3.4 Mg C ha⁻¹) 16 years after planting. In contrast, we observed a net reduction in SOC (on average -11.2±1.1 Mg C ha⁻¹) and no significant difference in tree-derived SOC (SOC₃) stocks between five-species mixtures and monocultures (13.0±0.9 vs 15.1±1.3 Mg C ha⁻¹). The positive effects of tree diversity persisted despite repeated climate extremes and strengthened over time for aboveground tree growth. Increased tree growth in mixtures enhanced leaf litter and coarse woody debris C fluxes to the soil, resulting in a tightly linked C cycle aboveground. However, the only link between above- and belowground C stocks and fluxes was between leaf litter C inputs and SOC₃ which was positively affected by diversity. Our study elucidates the mechanisms through which higher tree diversity enhances the climate mitigation potential of tropical forest restoration. Restoration initiatives should prioritize mixed over monospecific planted forests.

[46] Inconsistent short-term effects of enhanced structural complexity on soil microbial properties across German forests (16:00)

Presenter: SCHWARZ, Rike Lena

Production forests are managed to optimize timber production, resulting in even-aged stands with few canopy gaps and little deadwood. This biotic homogenization can lead to loss of biodiversity and ecosystem functions with far-reaching consequences for human well-being. To explore strategies for promoting biodiversity and ecosystem functioning while maintaining timber production, the BETA-FOR project studies the impact of experimentally induced structural complexity on forest biodiversity and ecosystem functioning. In total, we investigated 156 plots (each 50 x 50 m) in eight forests in Germany, whereof half was used as a control with forest management as usual, whereas in the other half canopy gaps and various types of deadwood were created. Our subproject examines how these treatments alter soil abiotic variables (soil pH and soil water content) and soil functions (soil respiration, soil microbial biomass, respiratory quotient, and activity responses to different substrates), and how these relationships evolved over five years of treatment. Results indicate that increased structural complexity influences soil water content but not soil pH. The activity, biomass, and substrate response of soil microorganisms appear to be context-dependent, with effects varying across different forest regions in Germany. Within the first five years following treatment establishment, there was no significant change in the impact on soil functions. Despite the lack of significant immediate changes in soil functions, promoting structural complexity in production forests holds promise for enhancing long-term biodiversity and ecosystem health.

[57] Assessing the role of intraspecific and intraindividual variability in tree-tree interactions (16:15)

Presenter: CASTRO SANCHEZ-BERMEJO, Pablo (Martin Luther University Halle-Wittenberg)

Trait-based ecology assumes that functional traits help to understand how organisms influence ecosystem processes. The focus has classically been on trait differences between species, but, as the range of variation within species (intraspecific and intraindividual trait variability) is highly plastic, it may be more likely to respond to species richness in communities to mediate coexistence. However, we lack empirical evidence on how these sources of trait variation shape tree-tree interactions and how they contribute to the functional diversity of communities. We sampled 4,608 leaves from 384 trees belonging to eight tree species along an experimental tree species richness gradient in subtropical China (BEF-China). To assign trait values to leaves, we conducted leaf spectroscopy and used deep learning to predict values for seven leaf functional traits. Functional indices were used to assess intraspecific and intraindividual trait variability and linear mixed-effect models and structural equation modelling were used to study how intraspecific overlap is mediated by intraspecific and intraindividual trait variability along the tree richness gradient. Additionally, we identified which sources of variation within species strongly affect community functional diversity by comparing the functional diversity of observed communities and virtual communities in which different sources of trait variation were randomized. Intraspecific trait variability responded to tree species richness and was the main supporter of intraspecific complementarity. On the contrary, responses of intraindividual leaf variability to tree species richness were weak and were mainly related to the stomatal strategy of the leaves. Last, our results suggest that functional richness was influenced by intraspecific variability while functional divergence was influenced by intraindividual variability, especially at the higher levels of tree species richness. We suggest that trait variability occurring at the finest scales could have ecological relevance for intraspecific interactions, improve the efficiency in the water use strategy and shape the functional diversity of assemblages.

[12] Volatile responses to branch-localized induction of Quercus petraea in a BEF experiment (16:30)

Presenter: ANJOS DE STEFANO ESCALIANTE, Gabriela (iDiv, Friedrich-Schiller-Universität Jena)

Plants produce specific volatile organic compounds (VOCs) to protect themselves against biotic and abiotic stresses. When herbivores damage plant tissues, plants release signals, which attract natural enemies of the herbivores and inform neighboring plants about a possible attack. Intensity of plant-herbivore interactions and plant diversity could shape VOC emissions resulting in the production of specific compounds, possibly over different resource availability due to a diverse community. How exactly plant defense mechanisms and diversity influence the VOCs emissions is unknown. We hypothesized that branch-localized VOC emissions after induction are influenced by treatment repetition and tree diversity, ultimately affecting predation rates. To test this, we studied VOCs from Quercus petrea in the MyDiv BEF experiment during leaf flush and predation rates by arthropods using clay caterpillars before, during, and after treatments. We selected oak trees from monocultures, two and four species mixtures. Branches from five oaks per plot were repeatedly treated with methyl jasmonate to simulate herbivory or with water as control. VOCs were passively adsorbed onto PDMS tubes and analyzed by TD-GC-MS. Sesquiterpenes were up-regulated in MeJA-treated branches when compared to control branches, particularly α-Farnesene, known for attracting natural enemies of herbivores. Repeated MeJA treatment intensified branch-localized induction, positively affecting arthropod predation. Green leaf volatile emissions decreased with time in treated branches, possibly due to lower mechanical damage. The interaction between plot diversity and treatment was significant specifically on a green leaf volatile, showing a more intense decrease for the treatment branches on the four-species mixtures plots and a higher up-regulation of Linalool, released as defense against insects. These results show that localized VOCs induction is affected by plot diversity and amplify Q. petraea’s indirect defense potential.

Talk Session: Biodiversity Dynamics & Complexity - Leipziger KUBUS/1-B - Hall 1 B (14 Nov 2024, 15:30 - 16:45)

[155] Plant macrophenology - from individuals to synchronised group behaviour (15:30)

Presenter: MORA, Karin (Leipzig University)

Plant macrophenology studies large-scale patterns and processes in the timing of plant life cycle events, such as flowering, leaf-out, and fruiting, across extensive spatial and temporal scales. This field aims to understand how climate and environmental changes influence these phenological events. As climate change continues to impact ecosystems globally, understanding these patterns is crucial for predicting ecological responses and informing conservation strategies. To address the challenges of analysing these complex patterns, we developed a novel methodological approach for plant macrophenology using nonlinear ordination techniques [3]. This approach effectively extracts spatio-temporal patterns from large and diverse phenological datasets. Nonlinear ordination reduces the dimensions of complex data, revealing underlying structures and relationships that traditional linear methods might miss [2,3]. Our primary objective is to quantify synchronised behaviour across thousands of plant species. By identifying and analysing these synchronisation patterns, we can better understand the collective responses of plant communities to climate variability and change. This synchronisation offers insights into broader ecological impacts of climate change and helps detect shifts in plant phenology. We demonstrate the versatility and effectiveness of our approach by applying it to various datasets, including those collected by citizen scientists using mobile applications such as Flora Incognita [1]. Incorporating these large-scale citizen science datasets enhances the resolution and accuracy of our analyses, leading to more robust conclusions about the impact of climate variability on plant phenology. This methodological framework advances plant macrophenology and provides a practical tool for researchers to quantify and monitor the effects of climate change on plant phenology. [1] Mäder et al. (2021) Methods Ecol Evol, 12: 1335-1342 [2] Mahecha et al. (2021) Ecography, 44: 1131-1142 [3] Mora et al. (2024) Methods Ecol Evol, doi.org/10.1111/2041-210X.14365

[99] Long-time scale functional trait data from herbarium specimens shows growth strategy trade-offs in plants of agricultural fields (15:45)

Presenter: KÜHN, Paul (Friedrich-Schiller-University Jena, Jena, Germany)

Agricultural fields are a habitat type which can exhibit a high amount of biodiversity depending on the management intensity. They have come under increasing pressure due to the intensification of management practices like pesticide application or fertilization. While it is understood that intensification has a negative effect on the biodiversity of this habitat, it is not clear how the drivers impact plants on an individual level. The respective change happens over long time scales, which makes experimental or “space for time” approaches unlikely to accurately describe the underlying processes. Herbaria, with their large collections of current and historical plant specimens offer a promising solution to this issue. Novel spectroscopy methods allow for the extraction of chemical plant traits without altering herbarium specimens themselves. Additionally, large-scale datasets are now available, which allow us to use the herbarium specimens as base to which both functional trait and distribution data can be tied, and analyzed over a span of decades and even centuries. In this study, we selected specimens from 36 species sampled from agricultural field sites in the herbaria of Jena and Görlitz. Functional traits were measured using near-infrared spectroscopy, and occurrence data was added from the sMon dataset. A general decline in occurrence of the 36 plant species studied was observed. There was a significant positive connection between high values of traits indicating an “acquisitive”, fast-growth strategy, and high or increasing occurrence. Grasses show high values in both regards, whereas typical and iconic agricultural field species like *Centaurea cyanus* or *Consolida regalis* are among the slow-growth, low-occurrence cluster of species. Our results indicate that declining agricultural field species are likely unable to capitalize on increased nutrient availability due to fertilization and are as a result outcompeted by faster-growing plant species or the crops themselves.

[130] Exploring how plant-pollinator network structure shapes the virome of bee communities (16:00)

Presenter: PLUTA, Patrycja (Martin Luther University Halle-Wittenberg)

Survival of wild bees is threatened by multiple factors such as agricultural intensification, scarcity of food resources and diseases. Many pathogens are shared between managed and wild bee species, with flowers as the most likely route of interspecific transmission. An increased density of managed pollinators in the landscape may therefore aggravate pathogen spillover among communities of flower-visitors. This effect, however, likely depends on the density of reservoir and recipient host species, the structure of the plant-pollinator networks and the availability of flower resources. To explore this possibility, we manipulated the density of honey bee colonies across 32 agricultural sites, placing either 4 or 84 honeybee micro-colonies at the centre of each site. We then recorded plant-pollinator interactions, flower abundance and screened bees for common bee viruses: deformed wing virus, black queen cell virus, acute bee paralysis virus, and sacbrood virus. We related the network structure and honey bee viral transmission potential to the prevalence and load of viruses in wild bees. With increasing flower availability, honey bee abundance increased but network niche overlap decreased. Higher network connectance related to higher viral prevalence. Our study provides insights into the dynamics of viral transmission in bee communities, and can inform management decisions by land managers and other stakeholders to reduce the threat facing wild bees posed by pathogen spillover.

[159] Community Dynamics modifies Pollutant-Driven Species Extinction Risk (16:15)

Presenter: DAS, Rajaditya

Chemical pollution is a major driver of biodiversity loss and is projected to triple in the next 3 decades. Traditionally, laboratory measures of toxin sensitivity have been extended to quantify the contribution of chemical pollution to biodiversity loss. However, this approach ignores important biotic interactions and therefore performs poorly when predicting extinctions in nature. To solve this, we employed simulated food webs to assess the importance of biotics interactions in modulating chemically-driven extinction. Specifically, we exposed 200 food webs of varying complexity to 140 different concentrations of a hypothetical toxin. Models including food web traits predicted extinction twice as well as models that only included species’ toxin sensitivity alone. We find that trophic level and eigencentrality are key predictors of extinction risk. Our findings have important implications for wildlife conservation and management practice, where risk assessment is crucial in determining vulnerability statuses.

[60] Fruits and Microbes, Friends or Foes? The hidden role of microbes in fruit chemical signaling to seed dispersers. (16:30)

Presenter: CHRONOPOULOU, Evangelia (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Friedrich Schiller University of Jena, Germany)

Fruit scent plays a significant role in attracting animals, providing information on fruit ripeness, facilitating fruit selection and eventually contributing significantly to seed dispersal. Chemical signaling is often based on “generic” plant volatile organic compounds. But there is a significant exception: aliphatic esters. These compounds are prominent primarily in ripe fruits and mainly in species that rely on scent for disperser attraction. Previous studies assumed that the plant itself was the only source of esters, but is this true? Esters are synthesized from alcohols and acids, both of which can be products of microbial fermentation, and are strongly linked to sugar levels, the main reward animals seek. Thus, microbes may play a critical yet unexplored role in plant-frugivore interactions, turning a bipartite interaction into a tripartite one. However, increased microbial activity can accelerate fruit decay. This leads to the hypothesis that plants that rely on scent-driven animal seed dispersers have evolved to tolerate higher microbial activity to enhance their scent, thus creating a trade-off: increased attractiveness to seed dispersers at the cost of more rapid fruit decline. To establish a link between microbial taxa of interest and aliphatic esters, both chemical and molecular tools were used. Experiments conducted in various fruits including wild fig species belonging to two different groups: lemur-dispersed (lemurs are mainly olfaction-oriented), and bird-dispersed (birds tend to be vision-oriented). Initial results indicate a substantial difference in the microbial communities and occurrence of esters for different wild *Ficus* species from Madagascar. Notably, known fermenting microbial taxa were identified mainly in *Ficus tiliifolia*, the species that also exhibited higher amount of esters. Derived results could unveil a previously unseen key partner, providing a better and deeper understanding of the co-evolution between plants, animals but also microbes.

Talk Session: Molecular Biodiversity and Evolution - Leipziger KUBUS/2-AB - Hall 2 (14 Nov 2024, 15:30 - 16:45)

[144] Unveiling the role of phenotypic plasticity and adaptation using a grassland biodiversity experiment (15:30)

Presenter: DE GIORGI, Francesca

1. In the last years, biodiversity experiments showed how varying plant species diversity and its associated changes in abiotic and biotic environment produce phenotypic changes in plant species. However, it is still not clear what is the role of adaptation and phenotypic plasticity in shaping these phenotypic responses, and whether the environmental heterogeneity typical of highly diverse communities could increase phenotypic plasticity. 2. To test this, we conducted a two generations common garden experiment using seed families of 16 populations of the clonal herb Taraxacum officinale, grown in plant communities of different species diversity in a 17-year-old grassland biodiversity experiment (Jena Experiment). For two generations, we used clones of each seed family, which we previously genotyped, and we assigned offspring of each clone to a light or shade treatment to simulate differences in light availability between high- and low-diversity communities. We then compared their performance and trait expression in relation to their selection history in the biodiversity experiment and the treatment in which they grew. 3. Increasing species richness was associated with an increase in inflorescence length and leaf greenness. We identified significant interactions between species richness and treatment for biomass production, number of inflorescences, leaf length and leaf greenness. Regarding values of phenotypic plasticity, selection in high-diversity communities lead to a decrease in phenotypic plasticity in the number of leaves in the first generation. However, this effect disappeared in the second generation in favor of an effect of parental treatment. 4. Overall, history of selection in communities of different diversity induced adaptive phenotypic responses visible after more than one generation in a common garden. We could confirm the important role of phenotypic plasticity for a quick adjustment to the environment, but we found only weak indications of selection for increased phenotypic plasticity in highly diverse communities.

[117] A wild past? – Phylogenomic reconstruction of the evolutionary history of Cedrela and Toona (Meliaceae) (15:45)

Presenter: JENNERT, Pauline (Department of Molecular Evolution and Plant Systematics and Herbarium (LZ), Institute of Biology, Leipzig University, Leipzig, Germany)

The pantropically distributed mahogany family (Meliaceae Juss.) is globally valued for its timber and other socio-economically and culturally important products (e.g., in medicine). Despite this recognition, members of the family are threatened by habitat destruction (deforestation). The implementation of long-term conservation measures is hindered by taxonomic uncertainties and inadequate species delimitation. Recently, phylogenomic data yielded a phylogeny incongruent with previous phylogenies based on Sanger sequencing data, possibly due to a complex evolutionary history of Meliaceae characterized by gene duplication events as result of ancient hybridization, autopolyploidization or local gene duplication, hardly captured by phylogenies based on a few loci. This is calling for further investigation into intergeneric relationships and clarifying the taxonomic status of some genera. As part of these investigations, we examine the disjunct sister taxa Cedrela P.Browne (Central and South America) and Toona (Endl.) M.Roem. (Asia). Here, we present first results of our comprehensive phylogenomic study based on Hyb-Seq data, including nuclear single-copy genes data of the Angiosperms353 probe set, aimed at elucidating the evolutionary history of these lineages and detecting putative reticulation events.

[103] How do symbionts adapt in novel hosts? Using experimental evolution approach (16:00)

Presenter: SINGH, Pratyaksh (iDiv/MLU)

Symbionts are integral to arthropod biology, profoundly shaping their hosts' phenotypic traits and playing a pivotal role in speciation. While these associations can be costly for insect hosts, they are typically stable and maternally transmitted with high fidelity. However, the absence of co-cladogenesis suggests that many symbiont-host relationships are transient over evolutionary timescales, necessitating recurrent establishment in new/novel hosts via "host shifting." These host shifts are critical evolutionary events, influencing both host and symbiont dynamics. My experiment focused on the evolutionary trajectory of *Spiroplasma* and their effect on host biology. I employed an experimental evolution approach to investigate the impacts of symbionts on host biology via host shifting, including longevity, sex-ratio distortion, and life history traits. My study involved transfecting various strains of the rapidly evolving bacteria *Spiroplasma* into non-native *Drosophila* host species spanning 24 *Drosophila* generations. Phenotypic effects were assessed through fecundity and longevity assays conducted at different experimental stages. *Spiroplasma* will be sequenced by short and long reads, providing insights into genetic variations and their associated phenotypic trait change. I anticipate observing changes in host biology due to the influence of different *Spiroplasma* strains, with expected variability in phenotype and genotype within replicates as the experiment progresses. These findings will elucidate how host shifting affects symbiont evolution in novel hosts, enhancing our understanding of the remarkable diversity and prevalence of inherited symbionts in arthropods. This research offers valuable insights into the evolutionary dynamics underpinning host-symbiont relationships and will further illuminate the "Red Queen hypothesis" of rapid co-evolution, where hosts and symbionts continuously counter-evolve.

[55] Genetic patterns of a grassland plant across a fragmentation gradient of semi-natural grasslands in Europe (16:15)

Presenter: ENDE, L. Marie (Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany; German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany)

Habitat fragmentation is one of the major threats to European ecosystems. It often leads to decreased patch area and increased isolation of populations. Both processes are expected to result in genetic impoverishment and reduced resilience to environmental changes in populations inhabiting fragmented landscapes. In particular, semi-natural grasslands, which represent one of the most species-rich habitats in Europe, are suffering from human-induced habitat fragmentation caused by intensification or abandonment of management. Grassland plant species that depend on external vectors for pollen and seed dispersal and rely on a specific mating system for successful reproduction are most sensitive. In our study, we investigate the population genetics of the heterostylous, self-incompatible and insect-pollinated grassland plant Primula veris using GBS to identify single nucleotide polymorphisms (SNPs). Samples were collected in five European countries spanning most of the species' distribution range. In each country, samples were taken from contrasting landscapes of fragmented vs. connected semi-natural grasslands creating a gradient of grassland fragmentation sites on a European scale. We expect to find reduced genetic diversity in populations inhabiting fragmented landscapes compared to those in connected ones. Genetic differentiation will be more pronounced among fragmented populations with the effect becoming stronger towards the margin of the species' distribution range. Furthermore, we expect a decline in potential mating partners in fragmented populations, possibly leading to an overall decrease in population size and further reduction in genetic diversity. Our study will provide valuable knowledge to the consequences of ongoing habitat fragmentation. It will contribute to develop and reassess management strategies to restore fragmented habitats, to maintain connected ones, and to preserve resilient populations.

[35] Unraveling Local Decline in Antennaria dioica Populations through Herbarium Specimens: The Role of Genetic Diversity, Sex Ratios, and Environmental Factors (16:30)

Presenter: VÖRÖS, Weronika A. (Martin Luther University Halle-Wittenberg)

The conservation of endangered species is crucial to prevent the loss of biodiversity. Genetic studies provide essential insights into population structure and dynamics and help to investigate the cause of genetic diversity loss, which are vital for effective conservation strategies of those species. Our study investigates the genetic diversity changes in the endangered perennial species *Antennaria dioica* over time, utilizing herbarium specimens and recent samples to uncover population dynamics in central Germany. Employing double-digest Restriction-site Associated DNA (ddRAD) sequencing, we analyze herbarium samples spanning up to 200 years from now, with a focus on the last 70 years, as well as fresh samples to track changes in genetic diversity. Field data were collected in 2022 and 2023, recording sex ratios, plant performance, and population parameters such as the number of inflorescences and their capitula, leaf number, plant height, and population size. We aim to relate specimen data to abiotic habitat data such as environmental factors, including data on climate, land use, and soil properties, which connect our study to several research areas of iDiv, especially to 'Molecular Biodiversity and Adaptation'. We hypothesize a considerable decline in the genetic diversity of *A. dioica* over time, likely due to the populations experiencing prolonged genetic isolation. Furthermore, populations with a higher female-to-male ratio, while maintaining the presence of both sexes, are anticipated to demonstrate better overall condition. Our findings aim to elucidate the primary drivers behind the observed population changes, considering genetic diversity loss and sex ratio shifts due to the dioecious nature of the species, alongside environmental influences. The results will provide crucial insights into the genetic status-quo and its historic development of an endangered plant species, potentially offering guidance for effective management and reintroduction procedures.

Poster Flash Talks: Biodiversity and the functioning of Ecosystem - Leipziger KUBUS/1-A - Hall 1 A (14 Nov 2024, 16:45 - 17:00)

[150] Tree Growth Responses to the Central European 2018-2020 Drought: Roles of Diversity, Mycorrhizal Types, and Drought-Tolerance Traits (16:45)

Presenter: SACHSENMAIER, Lena

Climate change forecasts predict an increasing frequency of consecutive drought years, likely negatively impacting tree growth in Central European forests. Although mixing tree species has been found to enhance the temporal stability of growth in tree communities, studies show inconsistent results regarding extreme drought events. Recent research indicates that, aside from climatic conditions, the biotic context, such as the traits of focal trees and their local neighbors, influences biodiversity–ecosystem functioning (BEF) relationships. However, it remains unclear whether functional trait identity and/or diversity can mitigate the effects of extreme drought events. This study investigates how tree growth in experimental forest plantations is affected by tree diversity before, during, and after the Central European drought from 2018 to 2020. Additionally, we examined how these relationships are modulated by mycorrhizal association types and other functional traits. We utilized annual growth data (2015-2022) from 5,120 tree individuals in a young tree diversity experiment in Germany (MyDiv) and measured functional traits related to drought tolerance and resource use of 10 broad-leaved tree species to model BEF relationships under drought. Tree species' drought-tolerance traits and traits related to resource use formed a joint trait syndrome. We found two axes of trait variation mainly driven by cavitation resistance and stomatal control, respectively. Initial results indicated that diversity–productivity relationships are strongly influenced by these trait syndromes, which shift between drought and non-drought years. Further analyses are ongoing, focusing on mycorrhizal association types and the functional diversity of the tree neighborhood. This study contributes toward understanding the biotic context dependency of BEF relationships under drought and provides a functional basis for designing tree species mixtures able to cope with climate change.

[157] Predicting global-scale plant traits from environmental data (16:46)

Presenter: DECHANT, Ben (iDiv)

Relationships between plant functional traits and environmental variables are important to understand the reasons underlying patterns of vegetation characteristics and quantify potential changes due to climate change. However, plant functional traits have been predicted from environmental data only with moderate success and the reasons for this remain partly unclear. Here, we test the prediction of 18 key plant functional traits from climate and soil variables using machine learning and examine differences between datasets and aggregation approaches and the role of plant functional types (PFTs). We use trait data directly from the global plant trait database TRY and from sPlotOpen. We found that for TRY and sPlotOpen, community weighted mean (CWM) traits could be predicted with R2 of about 0.4-0.7 and relative RMSE (rRMSE) of 0.05-1.5. Adding PFT information only increased R2 moderately overall but by more than 0.2 for individual PFTs and some traits. Adding PFT information had notably larger impacts on trait prediction when using PFT-level aggregated traits either at plot-level (sPlotOpen) or at grid-cell level (50 km) for both TRY and sPlotOpen data. The strongest predictability in terms or R2 and rRMSE was achieved when calculating grid-cell-level CWM traits with fractional PFT cover as weighting factors. This led to 0.9 > R2 > 0.6 and 0.05 < rRMSE < 0.4 for all traits when using PFT weighted mean sPlotOpen data and slightly worse performance when using TRY data. Our findings have important implications for upscaling in-situ plant traits to generate large-scale maps and indicate the relevance of PFTs to refine environment-based trait predictions.

[36] Increasing frequency of drought years threatens the viability of beech forests in Central Germany (16:47)

Presenter: RUEGER, Nadja (BioCity Interim II)

Recent recurrent drought years have imposed water and heat stress on trees across Germany. However, it is unclear how demographic rates of broadleaved tree species were affected by the drought. Moreover, it is likely that climate change leads to an increasing frequency of drought years and associated changes of demographic rates, and it is unclear whether current forests will still be viable in the future. To explore these questions, we carried out a forest inventory in 2023 in a 28-ha beech-dominated forest in the Hainich National Park that had previously been surveyed in 1999, 2007, and 2013. We calculated growth, mortality, and recruitment rates for the four most abundant tree species (beech, ash, sycamore maple, and hornbeam, ≥1 cm diameter) before 2013 (1 drought year/decade) and after 2013 (4 drought years/decade) and projected forest dynamics for both climate scenarios until 2100 using a demographic forest model. Growth rates were similar across census intervals. However, mortality rates were increased after 2013 for all tree species, especially strongly for small trees, as compared to mortality rates before 2013. As an example, the annual mortality rate of beech was ~0.5% higher. Model simulations using demographic rates from before 2013 predict that the forest could increase in above-ground biomass from 410 t/ha to >500 t/ha until the end of the century. However, when using demographic rates from after 2013, the forest was predicted to decline to ~300 t/ha. These simulations also suggested that all species except hornbeam would decrease in biomass. We conclude that an increasing frequency of drought years threatens the viability of beech-dominated broad-leaved forests in Central Germany.

[114] Exploring clonal oak tree-nematode interactions under drought and herbivory stress (16:48)

Presenter: LEONAR, April Lyn

Our understanding of the intricate relationships between trees and their holobiont partners in the soil community is significantly expanding. However, the impact of trophic interactions on these biotic drivers is rarely explored. In particular, nematodes represent a wide range of trophic groups in the soil community, including plant parasites, bacterial and fungal feeders, predators and omnivores, making them an indicator of both direct and indirect influences on tree health. Furthermore, all these relationships will vary under climate change. Nematode community composition is greatly linked to abiotic conditions affecting soil moisture and resource allocation. Following abiotic and biotic stress such as drought and herbivory, nematodes cope differently according to their feeding guilds, which can affect above-belowground interactions, soil food webs and tree health. This project, as part of the PhytOakmeter research unit, aims to investigate how soil nematode communities respond to drought conditions and how it may affect the oak tree holobiont directly as plant parasites and indirectly as free-living nematodes. To do this, we are using *Quercus robur*, a foundation tree species of European forests with highly diverse biotrophic interactions. Specifically, we are growing DF 159 *Q. robur* clones in controlled platforms in the Ecotrons with above/belowground herbivory as well as in the iDiv greenhouse manipulating soil biota abundance, all of which will be subjected to drought stress conditions. In addition, potted trees will be placed in the canopies of trees on three height levels in the semi-controlled Canopy Exposition platform. Lastly, we will observe nematode communities across the European Transect platform with a regional climate gradient. Utilizing controlled experimental platforms to natural field conditions, this project will be assessing the direct and indirect effects of soil nematodes on the oak tree holobiont in response to global change.

[137] ARBOfun – Fate and Functioning of Central European Tree Species under Climate Change (16:49)

Presenter: WIRTH, Christian (Leipzig University / iDiv / Max-Planck-Institute for Biogeochemistry)

Our forests are challenged by a suite of stressors associated with climate change, such as extended droughts, heatwaves, ‘false springs’ increasing late-frost risk, storms, heavy rainfall events, and novel pathogens. Our iDiv platform ARBOfun, established in 2012 in Großpösna, was designed to study the responses (e.g., resistance, resilience) to these stressors of individual trees of close to 100 species including angio- and gymnosperms occurring in temperate Central Europe or adjacent biomes. Each species is replicated five times in a randomized block design and planted with wide spacing. To understand responses mechanistically we adopt the traits-rates-states framework. In collaboration with TU Dresden, we have assembled a uniquely comprehensive dataset of functional traits (> 100 morphological, anatomical and physiological traits for leaves, roots, stems). These are used to understand and predict rates (e.g., growth, transpiration) and states (e.g., size, morphology, vitality). Rates, or proxies of them, are derived from regular inventories, leaf carbon isotopes, drone overflights with thermal cameras, and phenological observations for all trees. 120 trees of 40 species are equipped with sap flux sensors, dendrometers, canopy climate loggers, and cameras recording changes in leaf angle distribution. Next to presenting the design and set-up, we will highlight selected results of recent studies, e.g., that (i) gymnosperms are markedly less resistant to drought, (i) fine-root traits are more important predictors of growth responses than previously thought, and (iii) sub-Mediterranean species have a high drought resistance, but suffer disproportionally from late frosts. As a call to the iDiv community, ARBOfun offers unique opportunities for complementary research on biotic interactions (e.g., interaction networks), biodiversity patterns of associated species (e.g., arboreal lichens, soil organisms, insects), soil ecology, and calibration of remote- or proximal-sensing products on tree species functioning.

Poster Flash Talks: Biodiversity Dynamics & Complexity - Leipziger KUBUS/1-B - Hall 1 B (14 Nov 2024, 16:45 - 17:00)

[54] Testing whether new camera methods could detect change in pollinator and pollination biodiversity across different ecological context in Europe (16:45)

Presenter: ZHONG, Yuping (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)

The reproduction of most crops and wild plant species depends on interactions with animal pollinators, which are declining globally due to climate change and human activities. Understanding changes in pollinator populations and plant-pollinator interactions is crucial for predicting and mitigating biodiversity loss. Traditional methods for collecting these data are time-consuming, costly, and require specialized expertise, posing integration challenges due to varying methodologies and scales. Camera vision methods, utilizing machine learning and computer vision, offer a promising alternative for capturing, counting, and identifying pollinators. This study aims to train and test these methods to capture pollinator and plant-pollinator interaction diversity across different biogeographic contexts. The initial focus is on prioritizing plant species for monitoring with limited camera resources, using data from the EU project SafeNet. Three monitoring options were evaluated: monitoring the most common flowering plant species, plants with diverse floral shapes, or plant genera important for pollinators across Europe. Results indicate that monitoring the most common plant species captures the highest pollinator diversity. The second focus addresses whether automated pollinator monitoring can detect changes in pollinator diversity and interaction network structures as effectively as traditional methods across different environmental gradients. This is being tested in the EU project SEPPI with the hypothesis: H0, that network metrics are consistent across methods and taxonomic grains once rarefied for interactions, or H1, that metrics differ if taxonomic identification influences the detection of rare species and biodiversity changes. The final focus is on developing a model to identify hoverflies, crucial pollinators with diverse morphologies and color patterns due to Hymenopteran mimicry. Currently, no AI efforts target Dipteran pollinators. We aim to train and test a model for Syrphid species identification in Germany. This research will enhance our ability to monitor pollinators and understand plant-pollinator interactions, contributing to biodiversity conservation efforts.

[61] Image-based multispectral flow cytometry – a new analytical approach for fast and efficient pollen determination (16:46)

Presenter: WALTHER, Franziska (Helmholtz Centre for Environmental Research - UFZ, Physiological Diversity, Leipzig, Germany & German Centre for integrative Biodiversity Research iDiv Halle-Jena-Leipzig, Physiological Diversity, Leipzig, Germany)

Manual microscopic analyses are traditionally the gold standard for various palynological applications. However, the recent trend is towards automated, database-driven pollen analyses that are expected to be cheaper, less time-consuming and allow better reproducibility than traditional microscope-based methods. One such innovative approach is multispectral imaging flow cytometry combined with machine learning. This method rapidly records microscopic brightfield and fluorescence images, along with various pollen traits such as diameter, fluorescence, and shape. Based on these data, a convolutional neural network classifier can be trained to enable specific pollen identification. This method was tested for main pollen type identification in three monofloral honey samples (*Brassica napus*, *Helianthus annuus*, and *Castanea sativa*). For this purpose, three different classifiers were trained: one with pollen collected from plants only, another with pollen measured from honey only, and a third with a mix of plant and honey pollen. The results showed that honey pollen from different varieties could be accurately predicted using a classifier that included respective honey pollen.In contrast, pollen collected from plants alone was only partially suitable for detecting honey varieties. Combining plant and honey pollen did not improve identification accuracy; instead, it led to a reduction in accuracy. Looking to the future, ongoing advances in automated pollen analysis techniques have the potential to significantly support palynological applications by improving the efficiency and accuracy of pollen type identification. Keywords: honey, melissopalynology, multispectral imaging flow cytometry

[126] Does diet specialization influences the abundance and distribution of oil-collecting Centris bees in the Brazilian Cerrado? (16:47)

Presenter: SOUSA, Paulo (General Zoology, Biology Department, Martin-Luther University Halle-Wittenberg)

Bees vary greatly in their dietary span, ranging from highly specialized species that collect floral rewards (e.g., pollen, nectar, or oil) from very few plant taxa to generalists that utilize a variety of floral hosts. Such diet specialization is hypothesized to constrain both the abundance and distribution of a species, with specialist species having lower abundance and smaller distribution ranges compared to generalist counterparts. Several studies have shown that diet specialization can increase species’ risk of local extinction. Understanding how diet is linked to the the abundance and distribution of bees is thus critical for conservation. Here, we examined whether diet specialization affects the abundance and distribution of oil-collecting Centris bees, key pollinators of a global biodiversity hotspot, the Brazilian Cerrado. Using museum data from the Federal District of Brazil, we analyzed the abundance and distribution, on a local scale, of 15 Centris species across six decades (from 1970 to 2022). By controlling for time and unequal sampling effort, we found that generalist species had higher abundance ($\bar{x} = 10$) than specialists ($\bar{x} = 6$) and specialist species showed higher variation in their abundance than those of generalists. Using the number of grid cells (10 x 10 km) as a proxy for distribution range, generalist species occupied more grid cells ($\bar{x} = 9$) than specialist species ($\bar{x} = 6$). Despite both abundance and distribution results being non-significant, the pattern may support the hypothesis that diet seems to play a role in shaping the abundance and distribution of those bees, albeit other ecological characteristics be equally important.

[143] From Phreatophyte Species to Habitat Probability for Groundwater-Dependent Vegetation - a Multiscale Approach (16:48)

Presenter: EL-HOKAYEM, Léonard (MLU Halle-Wittenberg)

Groundwater-dependent vegetation (GDV) forms globally important biodiversity hotspots, which are threatened by climate and land-use change and require large-scale mapping efforts for their protection. Phreatophyte species are relevant local ecohydrological indicators of groundwater. However, there exists no approach to move from species to plot level to the final large-scale mapping of GDV. A novel mapping approach is presented that aims to identify both species and communities, indicative of GDV and high probability GDV habitats in the Mediterranean biome. The approach presented combines global plant community data from ‘sPlot - The Global Vegetation Database’ and satellite data in the Mediterranean. A list of ~1,080 phreatophyte species was compiled based on literature review. Additional species with high fidelity for groundwater-dependent EUNIS habitats were extracted within Europe. Based on the compiled lists, co-occurring species were extracted in an iterative process. Finally, the coverage of phreatophytes and associated species was calculated plot-wise to account for GDV habitats. Remote sensing criteria at 30 m resolution include 1) vitality during dry periods, 2) seasonal and 3) interannual variation in vitality, 4) high topographic potential for water accumulation, and 5) topography (elevation, slope). Finally, a regression analysis between the plots and the remote sensing criteria pinpoints areas with high phreatophyte cover and hence high probability GDV habitats in the Mediterranean biome. The resulting species list and composition indicative of GDV can support identification in the field. In addition, detailed maps of GDV for the Mediterranean biome will help to ensure sustainable groundwater management and thus protect GDV as biodiversity hotspots.

[49] Temporal variation of canopy functional trait diversity assessed through remote sensing (16:49)

Presenter: MEDERER, Daniel (Doktorand von Prof. Dr. Hannes Feilhauer)

Plant functional diversity is a crucial property for ecosystem dynamics and buffering extreme events. Metrics for plant functional diversity are usually computed using a set of plant functional traits and corresponding species. Due to the scarcity of field data, functional diversity estimates are frequently only available for single points in time. However, seasonal dynamics during the vegetation period are known to cause substantial changes in plant functional traits, e.g. flowering, stress effects, and leaf senescence. Despite the significant impact of seasonal dynamics on plant and ecosystem functioning, their imprint on functional diversity metrics has so far not been thoroughly examined. Here, remote sensing offers an alternative route to calculate functional diversity from plant functional traits without species knowledge. With recent advances in machine learning, multiple plant functional traits can be inferred simultaneously from hyperspectral remote sensing data. Additionally, recent and future hyperspectral satellite missions such as EnMAP, SBG and PRISMA offer a large quantity of scenes across the vegetation period. In this study, we employ machine learning to derive 20 plant functional traits from a global database of hyperspectral satellite images derived from EnMAP, which cover seven major biomes over two years. We calculate various functional diversity metrics for each scene and analyze temporal changes across each biome. Our findings are anticipated to reveal biome-specific variations in functional diversity throughout the vegetation period at a global scale. These approaches are transferable and can serve as an example of how biodiversity can be monitored extensively, standardized, and across the spatiotemporal continuum in the future.

[44] sPlot 4.0: towards a truly global database for understanding vegetation spatiotemporal changes (16:50)

Presenter: DAMASCENO, Gabriella (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany)

sPlot (v4.0) is the most comprehensive vegetation database in the world containing more than 2.5 million plot observations and 53 million species x observation records from 138 countries. To reduce the geographical distribution bias of the previous versions towards the Global North, we actively worked to promote the integration of researchers from underrepresented areas in this new release. Beside embracing more inclusive language during the call for contribution, we adapted our membership rules to better accommodate local cooperation agreements with databases with multiple contributors. We also improved the handling of missing spatial information by manually attributing coordinates (and associated uncertainty) based on the sampling locations provided by the contributors. In comparison to the previous release, the number of plots from the Global South increased by 41% (46,538 new plots summing up to a total of 158,151 plots). More importantly, the data was contributed mainly by local investigators: the number of custodians based in the Global South more than doubled (113% increase, 26 new contributors making up a total of 49). sPlot 4.0 is also a tool for investigating vegetation change due to new time-series data: it includes 264,246 observations of resurveyed plots from which one quarter (69,624 observations) comes from outside Europe. As a result, sPlot 4.0 opens great opportunities for global vegetation research by combining the macro and local scales: extensive geographical coverage with fine-grain data and on-ground insights from local researchers.

[152] A DIGITAL TWIN OF GRASSLAND ECOSYSTEMS (16:51)

Presenter: TAUBERT, Franziska (Helmholtz Centre for Environmental Research GmbH - UFZ)

Grasslands cover 20-40% of Earth’s land and provide important ecosystem functions. While grassland productivity matters for fodder or bioenergy supply, biodiversity is also relevant, e.g. for stability and for support of animal species, such as pollinators. Hence, the relations between these functions, and their responses to climate and land use change, need to be well understood to promote adequate human action. We develop a prototype digital twin of grassland ecosystems that allows comprehensive investigation of grassland dynamics under various environmental and management conditions. Our approach facilitates frequent interplay between real-world ecosystems and their digital counterparts. The process-based model Grassmind lets us simulate how individual plants of different species compete for light, space and other resources as they establish, grow and die. These dynamics are driven by weather conditions, soil properties and management. Therefore, the digital twin infrastructure includes access to and preprocessing of open data on these drivers so that realistic present and future scenarios can be simulated and predictions of grassland biodiversity and productivity made for different locations. Grassland observation data are integrated to validate and improve model results. End-users can explore the digital twin through a graphical interface, provide feedback or their own data to be taken into account, and gain valuable scientific insight for use in policy or management.

[160] Regional aridification drove changes in Asian mammal faunas by the middle Eocene. Implications for the timing and magnitude of the Mongolian Remodelling. (16:53)

Presenter: BENEVENTO, Gemma (BiK-F)

In Asia, previous studies have shown changes across the Eocene–Oligocene Transition (EOT, a global cooling event; 34 Ma) from perissodactyl-dominated faunas to those dominated by smaller-bodied Glires, better adapted to dry environments with limited resources (the Mongolian Remodelling). However, recent paleoenvironmental records and novel climate models show drying already occurring in Central Asia during the mid-Eocene due to global cooling, the growing Tibetan Plateau, and the retreating Paratethys Sea. We calculated sampling-corrected fossil mammal taxonomic richness across the Paleogene of Central Asia. We recover substantially lower diversity in the mid-Eocene, concurrent with the onset of regional aridification. Mammal richness increased throughout the remainder of the Eocene, but declined again across the EOT and throughout the Oligocene. In addition, we recover increased mammal turnover and decreases in mean and maximum body size in the mid-Eocene and across the EOT, concurrent with shifting environmental conditions. This suggests that regional mid-Eocene aridification in Central Asia may have driven faunal shifts similar in magnitude to those linked to the EOT global cooling event. Furthermore, our analyses indicate declines in both perissodactyl and rodent diversity across the EOT, suggesting that the Mongolian Remodelling may be partially influenced by sampling biases in the fossil record.

Poster Flash Talks: Molecular Biodiversity and Evolution - Leipziger KUBUS/2-AB - Hall 2 (14 Nov 2024, 16:45 - 16:55)

[32] Refining DNA extraction and metabarcoding techniques of soil nematode communities (16:45)

Presenter: WANG, Lu (UFZ Leipzig)

Nematodes are abundant and diverse in soil, and they can influence microbial community composition, plant performance, and nutrient cycling, serving as vital bioindicators for soil ecology and health. While metabarcoding techniques have become highly standardized in the identification of microbial (i.e., bacterial and fungal) communities, similar techniques are still under development for soil animals. As metabarcoding techniques become increasingly popular for characterizing soil animals, establishing protocols that are adapted to larger organisms is necessary. To improve the quality of nematode metabarcoding data, we explored the effect of various DNA extraction procedures adapted to larger soil samples on soil nematode biodiversity estimates. We extracted total DNA from soil samples and sequenced a nematode-specific 18S rRNA primer set (Nemf/18Sr2b; N1F/18Sr2b), and a general 18S rRNA primer set as reference (1391f/EukBr) with an Illumina MiSeq. We tested different DNA extraction methods for large soil samples (10 g), focusing on the effectiveness of different lysis buffers, bead beating durations, and enzymatic digestion applications. Sequencing data obtained from different protocols were filtered, trimmed, merged using the DADA2 pipeline, followed by taxonomy assignment using the PR2 reference database. Our results highlight varying extraction efficiencies from each technique, and their effects on soil nematode alpha and beta diversity assessments. Protocols employing 1% SDS lysis buffer with longer bead beating times yielded the highest concentration of DNA extracts. This study serves as a guide for the selection of DNA extraction methods for DNA-based studies of soil fauna.

[132] Introducing iDiv’s metabarcoding Support Unit iBarc - integrating molecular approaches to explore biodiversity (16:46)

Presenter: HERRMANN, Martina

Metabarcoding is a versatile, powerful and widely used tool for the identification of taxonomic entities, uncovering hidden diversity, assessing of community composition in space and time, elucidating species interactions and food webs, and monitoring biodiversity changes. Metabarcoding allows the monitoring of biodiversity over the whole taxonomic range - bacteria, protists, fungi, animals, and plants - using short variable gene sequences, and it is applied within the realms of ecology, conservation biology, invasion biology, and biomonitoring. The goal of the Support Unit iBarc is to enable more iDiv researchers to benefit from metabarcoding while making molecular approaches and advanced sequence data analysis an integral part of their biodiversity assessments. iBarc will provide direct access to metabarcoding services, starting from project planning via molecular lab support and services to downstream bioinformatics analysis, and offer expert support and advice for data analysis of a broad range of taxonomic groups commonly targeted in metabarcoding studies. In addition, we aim to use the joint interest in metabarcoding to foster scientific integration and initiate new collaborative projects across diverse taxonomic groups, iDiv research areas, and iDiv locations. To achieve these goals, iBarc comprises a Support & Service Center and a Research Network. The Support & Service Center offers a broad range of services, ranging from molecular lab services, provision of state-of-the art analysis pipelines and reference databases to courses for the iDiv consortium. The Research Network will include a communication platform to ensure regular exchange between working groups using metabarcoding, a think tank for the discussion of theoretical questions and unifying concepts associated with molecular biodiversity assessments, and meetings and workshops to foster new collaborative projects. In this poster presentation, we invite everybody interested in metabarcoding to learn more about our mission and services.

[14] iCONNECT, the integrative CONyza NEtwork for Contemporary Trait evolution (16:47)

Presenter: ROSCHE, Christoph (Martin Luther University Halle-Wittenberg)

Contemporary evolution is a common occurrence where plant species colonize non-native ranges and encounter novel interaction partners. However, our understanding of contemporary evolution is limited because most native vs. non-native range comparisons overlook within-range variation among populations and lack interdisciplinary frameworks utilizing multi-omics approaches. The integrative network iCONNECT addresses these research gaps. Here, we introduce the framework and present results from an initial study conducted within iCONNECT. We performed a greenhouse experiment with 108 native and 176 non-native *Conyza canadensis* populations, collected across broad spatio-environmental gradients in both ranges. The populations were exposed to a competition × drought treatment combination. The samples from this experiment were analyzed in a coherent manner to study their 1) phenotype (competitive ability under dry and mesic conditions), 2) eco-metabolomics (mass spectrometry analyses of root exudates), 3) root-fungal interactions (amplicon sequencing), and 4) population genomics (ddRADseq). 1) Interspecific competition had more detrimental effects on native than non-native populations and experimental drought exacerbated the effects of competition. 2) Drought led to increased metabolomic diversity in non-native but not in native populations. 3) Drought altered the composition of root-colonizing fungal communities in non-native but not in native populations, and these changes correlated with the effects of drought on plant performance in the non-native populations. 4) Bayesian clustering revealed significant correlation of the population genetic structure with spatio-environmental gradients and with the phenotypic and eco-metabolomic traits measured in the greenhouse. Integrating multi-omics data can help unraveling how belowground mechanisms determine contemporary evolution in complex biotic interactions. Future research may focus on identifying metabolites and genomic regions associated with competitive ability and root-fungi interactions under dry and mesic conditions. We encourage collaboration with interested researchers who want to use our sampled populations in order to perform add-on studies that investigate drivers of contemporary evolution in diverse biotic interaction traits.

[156] Plot-level steroidal glycoside diversity and chemotype affect plant performance, herbivory and buzz-pollination in S. dulcamara (16:48)

Presenter: ANAIA, Redouan Adam (Radboud University - formerly iDiv)

Intraspecific phytochemical diversity (‘chemodiversity’) affects plant-environment interactions. However, the ecological mechanisms maintaining chemodiversity remain largely unknown. Here, the effects of steroidal glycoside (SG) chemodiversity and chemotype on plant performance, seed progeny, herbivory and buzz-pollination were assessed. Plot-level SG chemodiversity was manipulated using a replacement series (four plants/plot) of two Solanum dulcamara chemotypes producing saturated (*S*) and unsaturated (*U*) SGs, respectively, creating homogeneous (*4S* and *4U*), heterogeneous (*3S+1U* and *3U+1S*) and balanced (*2S+2U*) plots. Berry counts were higher in chemo-diverse balanced plots (*2S+2U*). Herbivory was interactively affected by herbivory-type, chemotype and chemodiversity. *U*-chemotype plants had longer stem lengths, lesser herbivory by leaf-chewers, more and faster ripening berries, less progeny albeit with higher germination rates, and received more buzz-pollinations from *Bombus lapidarius*. Our results indicate that SG chemodiversity enhances plant performance and reproduction, suggesting that frequency-dependent selection pressures play a pivotal role in the maintenance of genetic polymorphisms leading to SG chemotypes.

[165] The impact of metabolomics - EcoMetEoR (16:49)

Presenter: GABRIEL, Jennifer (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig)

Eco-metabolomics is an emerging interdisciplinary field that combines ecological and metabolomic methodologies to investigate the biochemical basis of ecological processes and their responses to environmental changes. By examining how environmental factors such as climate, soil conditions, and interspecies interactions influence the metabolic profiles of organisms, eco-metabolomics provides insights into how plants, animals, and microorganisms adapt to or cope with their surroundings. This approach is particularly relevant in understanding species interactions—such as plant-insect dynamics, symbiosis, and competition—as well as in assessing biodiversity and ecosystem functioning. To support and advance research in this domain, the **EcoMetabolomics Platform for Ecology & Biodiversity Research (EcoMetEoR)** was established. EcoMetEoR provides the necessary infrastructure, expertise, and guidance to implement both targeted and untargeted eco-metabolomic analyses in ecological studies. The platform offers comprehensive support across all stages of research, from experimental design and sample preparation to analytical measurement, data processing, and compound annotation. Our facility routinely analyzes plant secondary metabolites in various tissues to capture biochemical interactions and reveal patterns of metabolite changes that are biologically relevant. By making metabolomics analysis accessible to scientists at all career stages, EcoMetEoR enables researchers to address their specific ecological questions more comprehensively by using molecular data. The platform’s combination of analytical tools and support ensures that researchers can effectively explore the potential of metabolomics in ecology, thereby contributing to a deeper understanding of biodiversity, ecosystem resilience, and the complex biochemical interactions that underpin ecological processes.

[133] Building a macrogenetics database for insects (16:50)

Presenter: DOVYDAITIS, Emily

Genetic diversity is a fundamental component of biodiversity that contributes to the capacity of populations to cope with environmental change. Understanding the extent to which population genetic processes are consistently associated with environmental factors across species is a powerful way to examine the processes maintaining patterns of biodiversity. The field of macrogenetics addresses these types of questions by synthesizing publicly available data to study population genetics at broad spatial and taxonomic scales. Macrogenetics research predominantly focuses on vertebrates, particularly mammals, and rarely features invertebrates. From a biodiversity perspective, this is a major knowledge gap because invertebrates, especially insects, account for ~80% of all animal species and an estimated 300 metric tons of the planet’s biomass—a figure comparable to humans plus livestock. We therefore know little about the broad scale spatial distribution of insect genetic diversity across species, or how such patterns covary with environments, latitude, population structure (eusocial vs. solitary), dispersal ability, and human-caused environmental change. To address this issue, we are harvesting insect nuclear genetic data from public data repositories to build an insect macrogenetic database. The collection will be added to a global macrogenetic database, MMPop!, which is comprised of microsatellite genotypes from vertebrate wildlife populations. Microsatellites, touted for their highly polymorphic and neutrally evolving characteristics, are a commonly used nuclear genetic marker in population genetics. This approach differs from many existing macrogenetics studies which mobilize mitochondrial DNA barcoding sequences. Despite their abundance and low-cost, mtDNA barcodes are not generally suitable for testing questions about intraspecific genetic diversity. Using a list of over 50,000 insect genera and common names, we queried the Dryad data repository for microsatellite genetic data. We then selected data to include in the database based on *a priori* inclusion criteria. The poster will showcase the database building process along with preliminary analytical results.

[95] InsectMobil: Impacts of landscape on insect diversity and composition through the use of citizen science and DNA metabarcoding (16:51)

Presenter: PETERS, Birte

Abstract: Urbanization and agricultural practices account for some of the most drastic modifications to natural habitats as a result of anthropogenic land cover change. The relative importance of different land covers for shaping insect communities, however, remains unclear. In this study, we combine large spatial scale sampling by using citizen scientists car net data collection (nets installed on vehicle roofs) and DNA metabarcoding to investigate the effect of landscape patterns of insect community composition and richness along with land cover heterogeneity. During June and July in 2018 & 2019 volunteers collected 334 car net samples on 67 roads in 7 federal states of Germany. To estimate taxonomic composition of insect bulk samples, DNA metabarcoding protocols were used, and the results compared to known data on flying insect richness and occurrence. The richness and diversity of flying insects were examined across main land cover types. Our results indicate a strong negative association of urban cover on insect populations, implying that urbanization may contribute as a main driver to insect decreases. As a consequence, conserving and extending protected natural and semi-natural habitats should be the primary priority for temperate insect diversity conservation. By conducting a simple, standardized citizen science initiative, we managed to sample flying insects at a broad geographical scale within one month, with a response rate of more than 86% of samples returned. Therefore, car net sampling with citizen scientists can serve as a promising approach for tracking flying insects at a landscape scale.

[19] The ecology and evolution of fruit functional traits (16:52)

Presenter: NEVO, Omer (iDiv/FSU Jena)

Fleshy fruits have evolved to attract seed-dispersing animals to ingest the seed and disperse it away from the mother tree. Fleshy fruits evolved independently multiple times across all major angiosperm families and dispersal by frugivorous animals is the major dispersal strategy of a majority of woody flowering plants, particularly in tropical religions. These fruits interact with a diverse set of frugivores: from the smallest songbirds to elephants; from ground-dwelling foxes through tree-climbing primates to flying bats; and from visually-acute birds and lizards to color-blind lemurs that prefer to use their noses. This functional diversity in animals drives their foraging and food selection behavior, and in turn exerts selection pressures on functional fruit traits, driving trait-matching between animals and plants. The talk will provide the background to these processes and introduce the work conducted at the Evolutionary Ecology workgroup. It will cover projects using metabolomics to understand the evolution of fruit chemical diversity; microbiology to uncover the role of the fruit microbiome in animal-plant interactions; behavioral ecology to understand how fruit traits drive animal-behavior; chemistry to identify drivers of variation in fruit nutrient profiles; physiology to explore the ecology and evolution of fruit maturation processes; and macroevolution to reconstruct the processes driving the initial evolution of fleshy fruits in deep time.

Postersession with drinks and buffet (14 Nov 2024, 17:00 - 20:00)

Friday, 15 November 2024

Registration (15 Nov 2024, 08:30 - 09:00)

Collect your name badge at the registration desk in the KUBUS foyer.

Talk Session: Biodiversity and the functioning of Ecosystem - Leipziger KUBUS/1-A - Hall 1 A (15 Nov 2024, 09:00 - 10:15)

[141] Soil food web states across successional stages, climates, and land use types (09:00)

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

Soil biogeochemical cycles are regulated by soil food webs. However, variations in soil food web structure and functioning across major environmental gradients remain largely unknown, hampering generalisations of links between soil fauna and biogeochemistry. Here, I summarise our several recent projects applying energy flux approach to explore successional development of soil animal food webs and responses of their structure and functioning to climate type and land use. Aligned with the classical ecosystem development theory, we show that along a secondary succession in China, soil food webs develop from fast turnover systems with high herbivory and predation (‘green’ state) to low turnover systems based on detritus consumption (‘brown’ state). We further found a similar trend while comparing energy distribution across micro-, meso- and macrofauna in temperate (Germany, Russia) and tropical forest soil food webs (Vietnam, Indonesia). We show that tropical soil food webs have high energy flux, predation rates and herbivory, while temperate food webs have high bacterivory and litter feeding. Finally, comparison of forests versus agricultural systems in Indonesia and Argentina shows that land use does not result in reduced energy flux in soil food webs, but strongly restructures energy pathways depending on land-use type. In intensively managed systems a drop in predation and an increase in basal consumption typically is observed, mainly explained by earthworm dominance. Our studies show how the functioning of soil animal food webs changes across ecosystem stages and types, summarising functional roles animals play in different biomes.

[119] Functional traits explain growth resistance to successive hotter droughts across a wide set of common and future tree species in Europe (09:15)

Presenter: KRETZ, Lena (University Leipzig)

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 tree functional traits related to drought tolerance, growth, and resource acquisition. We assessed growth resistance, that is, growth 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 for gymnosperms and angiosperms. 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 resistance, while acquisitive species suffer stronger under drought.

[113] Drivers of nutrient pools and concentrations in globally distributed grasslands with nutrient addition (09:30)

Presenter: SIEBENKAES, Alrun (PHYDIV)

Increasing nutrient input may have detrimental effects on the biodiversity and ecosystem functioning of grassland ecosystems. However, which mechanisms affect nutrient pools and concentrations at the community level is not always apparent, as an increase in nutrient availability is not necessarily reflected in an increase in biomass and diverse communities often consist of morphologically and physiologically different functional groups. We studied community aboveground biomass, tissue nutrient concentrations and contents (pools) of functional groups at sites of a globally replicated grassland experiment (Nutrient Network). We analyzed how N (nitrogen), P (phosphorus), and K (potassium) as single nutrients or all possible combinations facilitated variation in nutrient concentrations ([N], [P], [K], carbon [C], calcium [Ca] and magnesium [Mg]) and pools depending on mean annual precipitation (MAP), mean annual temperatures (MAT) and soil acidity (pH). We assessed if observed variation was due to changes in community composition (turnover) caused by nutrient availability or the specific variation in the tissue chemistry of functional groups (graminoids, forbs, legumes, woody species and bryophytes). Communities with either N or P addition had higher biomass and pools of all nutrients. Singularly, added N increased [N], [K] and [Mg], while P lowered [C], but promoted [P] and [Ca]. K addition led to increased [K] and K content, but decreased [Mg] and [Ca]. Singular effects of nutrient addition mostly outweighed combined effects and combined nutrient effects were additive. Covariation of turnover and FGV was mostly negative except for [Mg] and [Ca], while variation in nutrient pools was mainly driven by functional group-specific variation (FGV). For most concentrations except [Ca], the effects of turnover and FGV were more balanced. MAT affected functional group-specific variation in [P], K and Ca contents. Our study highlights the importance of functional group-specific variation of tissue chemistry to nutrient addition and site effects in globally distributed grasslands.

[163] Functional and phylogenetic diversity of island birds in the Anthropocene (09:45)

Presenter: KALUSCHE, Jan (Department of Global Change Ecology, Biocenter, University of Würzburg, Sanderring 2, 97070 Würzburg, Germany)

Global changes in biodiversity and their drivers are a major focus of scientific research. Recent studies have shown that taxonomic, phylogenetic and functional diversity can be combined to disentangle the drivers of community assembly. Due to their nature, islands are ideal biological model systems to study the effects of filters on diversity patterns. Although bird community assembly on islands are a popular subject of study, studies have been limited to single archipelagos or a few islands. We used a comprehensive global dataset of 2719 islands and analysed the diversity of 4624 terrestrial breeding bird species. We calculated functional diversity as well as phylogenetic diversity and corrected both for species richness using null models. To analyse diversity patterns we used multivariate models. We found a correlation between functional and phylogenetic diversity in all biogeographical regions. However, in regions with strong anthropogenic influences, functional and phylogenetic diversity values were more clustered than would be expected from species richness. Thus, dispersal, environmental and anthropogenic filters show strong effects that vary between biogeographical realms. Our results show strong regional effects on community assembly and highlight the importance of the interplay between different filters which a combined analysis of phylogenetic and functional diversity can disentangle.

[147] How Knowledge Graphs can support your synthesis work - a case study integrating PlantHub trait data, public occurrence data, GBIF checklists, and environmental information (10:00)

Presenter: AL MUSTAFA, Tarek (Heinz Nixdorf Chair for Distributed Information Systems, Friedrich Schiller University Jena, Leutragraben 1, 07743 Jena, Germany, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Puschstr 4, 04103 Leipzig, Germany)

In biodiversity research, synthesizing data from different sources is frequently needed as a prerequisite to answering important questions. Performing these integrations remains a tedious process requiring significant human effort. Often, results of these efforts are not easily reusable for other questions. Knowledge graphs have been proposed as an approach to alleviate this problem in the literature, but have gained little traction in biodiversity research practice so far. Our contribution showcases the approach to knowledge graph creation, management and usage implemented in the context of PlantHub and the former iKNOW project. We present a knowledge graph combining plant trait sources within the PlantHub project (planthub.idiv.de) including preprocessed data from TRY, a plant trait database, with citizen science occurrence data from naturgucker.de and add taxonomic and additional information from multiple sources (e.g., Wikidata, GBIF, OpenElevation, ...). We present the workflow needed to create such a graph and show different options for its management using features from Ontotext Refine for data cleaning, API & URL fetching, RDF mapping and export, as well as SQL mapping and export and Ontotext GraphDB for hosting, virtualization, querying, and visualization. For data that is already stored in databases, we also explored the option to directly integrate those into the knowledge graph via Ontop. This tool enables knowledge graph like access to datasets stored in traditional databases without the need to transform them into RDF. All that is needed is a mapping connecting the data points to show their relationship. Our experiences suggest that this might be easier than the creation of a knowledge graph from scratch and thus lower the barrier to their adoption in biodiversity research. We present our work and its application in the biodiversity research domain and contribute to bridging the gap towards advanced computer science technologies.

Talk Session: Biodiversity Dynamics and Complexity - Leipziger KUBUS/2-AB - Hall 2 (15 Nov 2024, 09:00 - 09:45)

[134] Synthesis of recovery patterns in microbial communities across environments (09:00)

Presenter: JURBURG, Stephanie

Disturbances alter the diversity and composition of microbial communities. Yet a generalized empirical assessment of microbiome responses to disturbance across different environments is needed to understand the factors driving microbiome recovery, and the role of the environment in driving these patterns. To this end, we combined null models with Bayesian generalized linear models to examine 86 time series of disturbed mammalian, aquatic, and soil microbiomes up to 50 days following disturbance. Overall, disturbances had the strongest effect on mammalian microbiomes, which lost taxa and later recovered their richness, but not their composition. In contrast, following disturbance, aquatic microbiomes tended away from their pre-disturbance composition over time. Surprisingly, across all environments, we found no evidence of increased compositional dispersion (i.e., variance) following disturbance, in contrast to the expectations of the Anna Karenina Principle. This is the first study to systematically compare secondary successional dynamics across disturbed microbiomes, using a consistent temporal scale and modeling approach. Our findings show that the recovery of microbiomes is environment-specific, and helps to reconcile existing, environment-specific research into a unified perspective.

[76] Metacommunity processes shape multi-scale patterns of biodiversity in fragmented landscapes (09:15)

Presenter: HAJIAN-FOROOSHANI, Zachary

Habitat loss and fragmentation are interacting phenomena that are appreciated to shape patterns of biodiversity. While this fact is widely acknowledged, it remains difficult to make statements about their effects on biodiversity generally. This may be due in part to the scale dependent approaches that are taken to understand their impact on biodiversity, where some studies focus on patterns across a landscape, and others on the scale of individual fragments. These different approaches can provide conflicting intuition regarding the effects habitat loss and fragmentation on biodiversity. Here we take an approach that focuses on the underlying ecological processes of the biodiversity to parse apart the mechanisms that create the scale-dependent patterns observed in empirical studies. Using a theoretical approach, we explore how competition, dispersal and habitat specialization in metacommunities structure biodiversity dynamics in fragmented landscapes. At the landscape scale we find that habitat loss/fragmentation can drive both positive and negative responses in richness depending on both the strength of dispersal and degree of habitat specialization in the metacommunity. At the fragment scale we find that competition and dispersal are the main processes influencing the relationship between fragment size and biodiversity. We suggest that explicitly taking into account metacommunity processes can help parse conflicting empirical patterns of biodiversity response to habitat loss and fragmentation at multiple spatial scales.

[140] Graphical representation of coexistence in a variable environment (09:30)

Presenter: SYNODINOS, Alexis

Competition for shared resources has been shown to support species coexistence given trade-offs between resource consumption and resource supply. However, the number of coexisting species cannot exceed the number of resources when the latter do not vary over time. Allowing for resource fluctuations overcomes this competitive exclusion limitation and two species can coexist on a single resource. The trade-offs required are similar to those in the constant resource case, though certain subtleties distinguish the variable environment case and highlight the complexity of species coexistence. We present a graphical analysis of pair-wise species coexistence competing for a single resource, which fluctuates due to external environmental variability. We explore how differences in the growth functions of the two competitors can alter the likelihood of coexistence. Further, we demonstrate how positive feedbacks between the growth functions and resource fluctuations can induce priority effects. Finally, our analysis illustrates how species do not simply exist in an environment. Rather they shape it in ways that can make it favourable or unsuitable for other species. These, other species, further alter the environment creating a dialectical species-environment relationship. Our study links existing mathematical explorations and long-standing ecological intuition to elucidate how resource variability can support multi-species coexistence. We hope this analysis will help clarify the agreement and divergence between different theories of competition-mediated coexistence, ultimately pointing towards future research directions that will enhance our understanding of biodiversity responses to changing environments.

Talk Session: Flexpool - Leipziger KUBUS/1-B - Hall 1 B (15 Nov 2024, 09:00 - 10:15)

[161] Using machine learning for PROSAIL inversion to retrieve functional plant traits of intensively and extensively managed grasslands (09:00)

Presenters: DOKTOR, Daniel (Helmholtzzentrum für Umweltforschung - UFZ), IAKUNIN, Maksim (Helmholtz Center for Environmental Research (UFZ))

Grasslands, representing the most extensive terrestrial biome, are increasingly subjected to management intensification, particularly in Europe, where they play an essential role in agricultural systems. The ecological and environmental functions of these grasslands are affected by management practices, which vary in intensity according to environmental conditions. While intensified management enhances agricultural productivity, it often results in negative environmental impacts such as reduced biodiversity and soil nutrient depletion. Traditional biodiversity monitoring methods, despite their precision, are resource-intensive and inadequate in isolation for addressing these challenges. Consequently, remote sensing has emerged as an indispensable tool, providing comprehensive and continuous data for monitoring grassland management and biodiversity. This study explores the relationship between grassland management regimes and remote sensing signals through the inversion of the PROSAIL radiative transfer model. The aim is to retrieve community-averaged plant traits from canopy hyperspectral reflectance observations. A machine learning model trained on a look-up table generated from various combinations of plant traits and reflectance spectra, facilitates the estimation of management intensity and biodiversity richness. Fieldwork was conducted in experimental grasslands sites (GCEF) with different management regimes to collect functional plant traits and in-situ canopy reflectance spectra throughout a complete vegetation period. The findings illustrate PROSAIL limitations when retrieving plant functional traits (leaf pigment contents, LAI, leaf mass to area ratio) especially for extensively managed grasslands and advanced phenological stages. The purely empirical categorisation of management types based only on observed spectral signals worked well. This indicates i) that the hyperspectral measurements capture substantial information on traits and the underlying management, but also ii) that standard in-situ sampling schemes and radiative transfer modelling approaches lack components to more exactly capture and quantify the increased ratio of ripe/senescent plant parts in diverse grasslands.

[18] Population Genomics of a Cosmopolitan Weed (09:15)

Presenter: LUCAS, Marilia (German Centre for Integrative Biodiversity Research (iDiv))

Understanding genetic mechanisms of high throughput data facilitates landscape genomic approaches to infer how dispersal is controlled by adaptive vs. non-adaptive drivers of gene flow. Invasive plant species are suitable study models because non-native populations are often prone to rapid genomic changes as a result of colonizing a novel range. However, many studies on invasive plants compared only a few populations in large distributions, underestimating variation within each range, and restricting their ability to predict the native source region and the identification of drivers of gene flow. We explore the genomic structure of 103 native and 177 non-native populations of Conyza canadensis across the Northern Hemisphere using ddRADseq. C. canadensis is an interesting model to investigate global gene dispersal because it is a successful invader with a cosmopolitan distribution and an economically significant agricultural weed. We test the hypothesis that an interplay between environmental gradients and non-adaptive, demographic processes dictates its global genomic structure. Results suggest strong differentiation among populations and low variation within populations. We also found pronounced differentiation between the genomic structures of native vs. non-native populations. Partial Mantel tests showed a significant correlation between genetic distances and both spatial and climatic distances of the populations. However, isolation by environment was more pronounced in the native ranges whereas isolation by distance was predominant in the non-native ranges. Furthermore, clustering analysis using admixture coefficients shed light on how population history dictates biotic interactions across large spatio-environmental scales. Our results suggest that high selfing rates determine the global genomic structure. Gene flow among native populations is controlled by functional connectivity whereas non-deterministic dispersal probabilities drive genetic differentiation in the non-native ranges. Upcoming analyses will be presented at iDiv Conference 2024 including gene flow to illustrate the magnitude of relative migration rates and the clustering of similar sampled areas.

[24] Met-Total: Towards an unbiased survey of habitat-dependent metabolic diversity (09:30)

Presenter: FRANKE, Katrin

Plant secondary (specialized) metabolites play an important role for ecological interaction of organism and responses to environmental factors. Up to now, comprehensive studies of the complex metabolome of whole plant communities are lacking. Little is known with respect to the most abundant plant secondary metabolites, habitat specific metabolite groups and their function, and correlation between chemo- and biodiversity. To approach these questions, we performed a pilot study to compare the metabolome of two climatically contrasting habitats. For this purpose, the plant community of a humid mesophilic evergreen broadleaf forest and a dry microphyll forest in a mountain region of Cuba were chosen. The metabolite profiles of all plant species within randomly selected plots were analyzed using different analytical methods, including thin-layer chromatography, nuclear magnetic resonance spectroscopy and liquid chromatography-high resolution mass spectrometry. The investigations were supported by DNA barcoding of all collected samples and accompanied by data mining for known natural products and plant species of the region. From a methodical point of view, compliance with the Nagoya regulations posed a main challenge for this experimental approach, as the species addressed could not be defined in advance. We hypothesize that although rain forests have a high biodiversity and are therefore considered the most valuable source for new natural products (e.g. for medicine), dry areas might provide a higher abundance of natural products with stronger activity effects due to adaption to harsher environmental conditions.

[118] Ecomechanics - Small animals need shaky grounds, but how shaky? (09:45)

Presenter: WÖHRL, Toni (Flexpool)

Many organisms rely on vibration detection to communicate, navigate, find food, and reproduce. However, the presence of human-made, or anthropogenic, noise through moving machine parts and silence by human-made solid structures, raises concerns about its impact on their locomotion patterns, metabolism, social interaction, development, distribution, food web, and thus resource turnover and ecosystems. However, it is not yet clear how anthropogenic vibrational noise impacts animals, or with other words, whether animals can sense typical human-made vibrations and change their behavior accordingly. A systematic quantitative aggregation and alignment of ground vibration data from the geophysics/civil engineering research community with vibrational sensitivity and behavioral experiments from the life-sciences is currently lacking. The present talk aims to approach this missing link between typical noise characteristics and insect sensation capabilities by presenting a compiled novel dataset based on existing literature data from diverse experimental settings. The aims are to i) illustrate potential interferences of vibrational noise pollution with insect vibration detection thresholds and ii) highlight zones of interest of vibrational frequency-amplitude combinations, which should be picked up in behavioral experiments to quantify potential stress reactions in insects. Based on this, some preliminary results on the locomotion behavior of ants under vibrational stress of our ongoing vibrational playback experiments will be presented as an example. As ecosystem engineers, ants are of particular interest. Through their tunneling and generalist foraging behavior ants contribute significantly to resource turnover and are therefore potentially good candidates for generic energy budget modeling, which has been developed by the iDiv corecenter.

[115] Biodiversity effects on Plant-Atmosphere interactions analysed with Remote Sensing (PARSe Biodiversity) (10:00)

Presenters: FEILHAUER, Hannes (Remote Sensing Center for Earth System Research, Department of Remote Sensing in Geo- Ecosystem research, Leipzig University), MAHANAND, Swapna (German Centre for Integrative Biodiversity Research (iDiv))

Monitoring the biodiversity of the Amazon forest poses significant challenges due to its remote location and limited data availability. Remote sensing promises an efficient solution, utilizing advanced sensors to identify biodiversity patterns in vegetation across vast areas. The Spectral Variation Hypothesis (SVH) suggests a correlation between spectral heterogeneity and biodiversity, with unique spectral entities identified as spectral species. We subjected PlanetScope imagery from the dry season to a principal component analysis and K-means clustering to map plant diversity spectrally. The optimum number of clusters was determined using the Silhouette and Elbow methods. Alpha diversity, assessed as Shannon diversity, was estimated at 1 ha grids, while beta diversity mapping at 4 ha grids was achieved through the Bray-Curtis Distance Matrix and Non-Metric Multidimensional Scaling (NMDS). Field plots revealed a maximum species richness of 129 and species abundance of 1006 individuals per plot. The alpha diversity map highlighted significant spatial patterns, with R^2 values of 0.45 and 0.57 for $k = 40$ and $k = 81$, respectively. Beta diversity characterization using spectral data proved inconclusive, as cross-verification with Detrended Correspondence Analysis and Mantel Test did not yield significant results. Vegetation health and stress were assessed through 69 vegetation indices and principal component analysis. Interestingly, regions with moderate biodiversity exhibited healthier vegetation compared to highly diverse areas, possibly due to similar species clustering into different groups. Ongoing analysis aims to understand the interaction between spectral diversity and biogenic emissions, providing insights into the ecological dynamics of volatile organic compounds. The study demonstrates that spectral diversity is promising for monitoring and conservation efforts, offering valuable insights into biodiversity patterns in the Amazon forest and beyond.

Talk Session: Biodiversity & Society - Leipziger KUBUS/2-AB - Hall 2 (15 Nov 2024, 09:45 - 10:15)

[121] Mapping the global polycrisis (09:45)

Presenter: PEER, Guy

Scholars increasingly point out that the multiple current crises build up toward a global polycrisis. Yet what exactly are its components? How are crises interlinked, and what are its ultimate drivers? A systematic mapping of the polycrisis seems essential for finding a way out. Based on the literature and iterative discussions we identified eight global crises: climate change; biodiversity loss; water insecurity and contamination; a human health crisis; food insecurity; an inequ(al)ity crisis; malfunctioning financial systems; and democratic backsliding. We further distilled five nexus elements (nexi) that indirectly link the crises: land- and sea-use change; land- and soil-degradation; emissions and pollution; unhealthy diets; and social unrest and armed conflicts. Through two expert surveys we mapped the links among the crises and nexi (n=54), and identified ultimate drivers (n=30). We found that most crises are directly linked to one another, reinforcing and exacerbating each other, implying that we need to address the polycrisis in its entirety. Climate affects all other crises most strongly, while human health and inequ(al)ity are most impacted. The nexi are linked to all eight crises, with armed conflicts, and land degradation, having the greatest impacts. The experts identified two ultimate drivers: our prevailing, growth-oriented economic system; and our prevailing norms and values. Political and societal responses that focus on single crises separately, bear the risks of failing to address the polycrisis, accelerating it or even generating new risks or crises. We highlight the challenges of addressing the ultimate drivers, requiring out-of-the-box solutions to overcome challenges such as societal and economic lock-ins. We call for societal, political and economic actors to act jointly, on the basis of robust science, to secure the future for Earth’s inhabitants.

[10] Future fishing potential under climate change in the Western Baltic Sea (10:00)

Presenter: VOSS, Rüdiger (iDiv)

Climate change is a major challenge for biodiversity as well as sustainable fisheries management. Scientific advice needs to take modifications in stock productivity into account to safeguard healthy stocks, and to secure viable fisheries, which provide economic and social benefits. We include temperature-dependent stock-recruitment relationships into an ecological-economic multispecies optimization model for major Western Baltic fisheries. Climate-driven temperature increase negatively impacts stock productivity of cod and herring, the two most important fish stocks in the area. We combine three climate change scenarios (RCP4.5, RCP8.5, constant climate) with two management scenarios (multispecies maximum sustainable yield (MMSY), and multispecies maximum economic yield (MMEY), to explore the potential development of key fisheries indicators. Spawning stock size, catch potential, fishery profits as well as total economic surplus are evaluated in the short- medium- and long-term. Western Baltic herring shows potential for stock recovery and commercial exploitation under all investigated scenarios, but only if allowed for an initial stock rebuilding moratorium. Accordingly, all models suggest a total fishing ban for herring of 4 years, before exploitation can restart. Catch opportunities for cod are less optimistic. Given climate change, catch levels will stay below 5.000 tons (historically >40.000 tons), even under optimal management. Differences between RCP 4.5 and RCP 8.5 become obvious from mid-century onwards. Acknowledging climate change in the scenarios strongly changes optimal management (and management outcomes) as compared to assuming a constant climate. Ignoring this might trigger overexploitation. Under climate change, MMEY management is superior to MMSY management in terms of stock size, catch, and total economic surplus, but will result in lower fishing mortality.

Coffee Break (10:15 - 10:45)

Talk Session: Biodiversity and the functioning of Ecosystem - Leipziger KUBUS/1-A - Hall 1 A (15 Nov 2024, 10:45 - 12:00)

[17] Temporal stability of grasslands under climate change and underlying mechanisms (10:45)

Presenter: HERION, Yva (Helmholtz-Centre for Environmental Research – UFZ)

A better understanding of how climate change affects the stability of grassland biomass production is important to ensure future ecosystem functioning. Since 2015, data on grassland biomass production have been collected in the Global Change Experimental Facility (GCEF) – a large field experiment in Bad Lauchstädt (Saxony-Anhalt, Germany) with different land use types under future and ambient climate treatment. We divided the biomass data time series of the species-rich extensively used meadows into overlapping time windows of three years to capture short-term variations in community biomass stability. For each time window, we determined the temporal stability of the community biomass production (inverse of the coefficient of variation) and different potential biotic stability mechanisms such as species asynchrony, species diversity, and temporal stability of common species biomass production. In addition, we identified extreme dry years and quantified the resistance and recovery of community biomass production. After an establishment period of a few years, grassland community biomass production of the spring harvest tended to be less stable under future climate treatment compared to ambient climate treatment. This might be due to tendencies towards more synchronous species dynamics and lower stability of common species biomass production under future climate treatment in comparison to ambient climate treatment. In the year after the two extreme dry years (2018 and 2019), community biomass production (relative to the mean community biomass production of normal years) was significantly lower under future climate treatment than under ambient climate treatment.

[30] Seasonal patterns in flowering intensity in herbaceous species are strongly influenced by their competitiveness and phenological niche (11:00)

Presenter: RAUSCHKOLB, Robert (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany)

Plant-pollinator interactions are important for maintaining diversity and ecosystem services. In recent years, however, mismatches have arisen due to phenological shifts in plants and insects because of climate change. To evaluate these interactions and their future development, it is important to consider not only the beginning and end of flowering but also the course of its intensity (i.e. via flowering curves). In this study, we used flowering intensity data weekly collected in botanical gardens by the PhenObs network to characterise the flowering curves of 215 perennial herbaceous species. We modelled flowering curves and derived four properties per species: maximum flowering intensity, flowering duration, skewness of the curves and number of flowering events. We aimed to show that these properties can be predicted by easily measurable plant traits. We used leaf trait measurements (leaf area, leaf dry matter content and specific leaf area) to derive the competitiveness and stress tolerance of a species using the global vascular plant CSR calculator StrateFy. We further extracted the temporal niche per species using the phenological data. We found that flowering curves of herbaceous species are mostly normally distributed or right-skewed. Early-flowering or competitive species invest resources in single but intensive flowering events, whereby the flowering duration is shorter in the competitive species and the curves are more left-skewed, indicating slow investment into flowering. For early-flowering species this can result in a greater risk of future mismatches, as they shift their onset of flowering more strongly and the flowering period follows an "all-in-one" strategy (i.e. single and intense flowering events). Based on the results, we suggest that characteristics of flowering curves should be considered when analysing plant-pollinator interactions. This information should be included in databases or at least predicted with the phenological niche or competitiveness of the species studied.

[93] Are space-for-time substitution approaches appropriate in phenology research? (11:15)

Presenter: SILVA-CALA, Andrea (FSU Jena)

Knowing and understanding plant phenology patterns is important for three main reasons. 1. Plant phenology is sensitive to climate change, 2. It influences the dynamics and interaction between species, and 3. It drives essential ecosystem functions. To unravel spatio-temporal patterns in phenology, long-term data covering the spatial distribution of species is necessary. However, typically, data is locally limited and contains restricted phenological records (e.g., flowering only). An alternative to overcome this disadvantage is the space-for-time substitution method (SFTS), where the relationship between climate and phenological variables is used to predict phenological responses to climate changes over time. We evaluate the SFTS approach on 42 herbaceous species, by comparing the spatial and temporal variation in flowering phenology in response to temperature and precipitation. For this, we use phenology data of 24 species from the European PEP725 database, and 20 species from the US NPN database, as well as temperature and precipitation data from the Era5-Land product. We evaluate linear models of the spatial-temporal relationship of the day of the year of flowering (DOYFlowering) with three timescales of temperature and precipitation data: annually, January to DOYFlowering, and month of DOYFlowering. We extracted the slopes as an indicator of flowering phenology response to climatic variables, and compared the spatial and temporal variation of slopes using a t-test. Results indicate that phenological responses to changes in temperature and precipitation are significantly different between spatial and temporal scales. This means that there is no spatio-temporal equivalence in flowering phenology, suggesting that SFTS cannot easily be applied to predict phenological responses to changes in temperature and precipitation. In addition, it is shown that the phenological response to temperature and precipitation presents greater variation over time compared to space. Finally, the results highlight that the timescale of temperature and precipitation influences the direction of the phenological response.

[51] Linking Plant Biomass to Herbivore Dynamics: Integrating Remote Sensing and Camera Trap Data to Assess Livestock Impacts on Wild Ungulates (11:30)

Presenter: ZULEGER, Annika Mikaela (Institute of Biology, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany)

Agricultural land abandonment in Southern Europe offers both opportunities for habitat restoration and conservation challenges, including potential human-wildlife conflicts, particularly in regions where extensive farming and free-ranging livestock persist. Livestock can pose threats to wildlife by degrading habitats, competing for resources, and altering habitat use patterns, which may lead to reduced densities or exclusion from grazed areas. This study extends previous research in the Peneda-Gerês National Park in Northern Portugal, where significant rural depopulation and agricultural abandonment have occurred over the past 60 years, while free-ranging cattle and horses are still prevalent. Prior results utilizing occupancy models indicated that cattle and horses share similar habitat preferences, but do not significantly affect the spatial distribution of wild ungulates, suggesting ecological independence between domestic and wild species despite spatial overlap, potentially due to different feeding strategies and ample resources. To further investigate the influences of habitat quality and food availability, we examined the role of plant biomass in determining the distribution patterns of both domestic livestock and wild ungulates. Our methodology involved systematic sampling of plant biomass across various habitat types, measuring dry weights of shrub and herbaceous biomass. This data was integrated with high-resolution remote sensing data, including digital surface and terrain models, NDVI, and vegetation height data obtained from drone imagery. We used generalized additive models (GAMs) to analyze the relationships between plant biomass and remote sensing data, predicting shrub, grass, herb, and total biomass across the entire study area. By correlating these biomass estimates with herbivore occurrence and abundance data from camera trapping, we aim to assess potential resource competition between domestic livestock and wild ungulates, focusing on the impacts of different feeding strategies and resource availability. Our findings aim to enhance the understanding of domestic-wildlife interactions, which is crucial for wildlife conservation and sustainable landscape management.

[9] Rewilding indicators across Europe (11:45)

Presenter: WEISSGERBER, Magali

Unsustainable use of ecosystems has led to the degradation of biodiversity and ecosystem services including reduced carbon sequestration, reduced pollination, and an increase in natural disasters. Widespread restoration of these ecosystems is crucial to address the biodiversity and climate crisis. Rewilding is a form of restoration aiming at improving the condition of ecosystems by recovering natural ecological processes. It intends to restore functional and self-sustaining ecosystems that provide multiple ecosystem services and require little to no human management in the long term. In this context, we seek to develop a set of spatially explicit indicators for monitoring rewilding trends and outcomes. Mapping wildness across Europe is essential to identify priority areas for rewilding and to support the implementation of restoration targets at national and European levels. We consider that the wildness of an ecosystem depends on its ecological integrity and the extent of human pressure. The former relies on three main components: trophic complexity, connectivity, and stochastic disturbance regimes. The more natural these components are, the higher the ecological integrity. We relate trophic complexity to the extent of defaunation: the presence of large-sized fauna – based on Europe wide database and species distribution modelling – in relation to its potential. In terms of connectivity, we consider terrestrial landscapes fragmented by urban fabric, linear infrastructure, and intensive agriculture, and aquatic landscapes fragmented by dams. Natural stochastic disturbances (e.g. floods and fires) are considered through the forestry, agricultural, and grazing impacts on primary productivity. Human pressure is captured through human presence and artificial interventions. Mapping such wildness indicators provides insight into the potential areas for resilient and self-sustaining ecosystems and identifies areas where restoration efforts should be focused.

Talk Session: Biodiversity Change - Leipziger KUBUS/2-AB - Hall 2 (15 Nov 2024, 10:45 - 12:00)

[153] Wildlife on the Edge: Health and Fitness of Wild Macaques in Forest-Oil Palm Plantation Habitats (10:45)

Presenter: HOLZNER, Anna (University of Leipzig; Max Planck Institute for Evolutionary Anthropology)

The expansion of agricultural land into natural habitats harms global biodiversity, especially when unsustainable practices are employed. In Malaysia, pig-tailed macaques (*Macaca nemestrina*) have adapted to this altered environment, regularly entering oil palm plantations adjacent to their remaining forest habitat. Within these plantations, macaques feed on palm fruits and provide an ecosystem service by reducing populations of plantation rats, the primary pest species of oil palm crops. However, the use of plantations also poses risks to these primates: our research has uncovered significant impacts on the health and fitness of a population of wild macaques inhabiting a rainforest-oil palm matrix. Long-term demographic data (2014-2023) revealed an exceptionally high mean infant mortality rate of nearly 60%. The reasons for this elevated mortality are likely complex, but survival analysis indicated that, in particular, prolonged visits to the plantation increased the risk of infant death. Our results further suggest that exposure to agricultural chemicals, which may enter the macaques' food chain via plantation rats or water, plays a significant role. Certain harmful herbicides are known to gradually accumulate in mammals, increasing pesticide exposure for developing offspring, particularly those born to first-time mothers and after prolonged interbirth intervals. Consistent with this, chemical analysis based on 91 samples of macaque body odour revealed changes in their chemical profiles following herbicide exposure in the plantation, indicating metabolomic changes caused by pesticides. Our future work aims to develop a 'One Health' project, considering threats emanating from anthropogenic activities, such as exposure to environmental pollutants or zoonotic disease transmission, and their impacts within a broader context. Our goal is to understand how these threats impact the inextricably linked health of wildlife, humans, and the environment, providing a basis for establishing stakeholder awareness and informing feasible management strategies for sustainable, wildlife-friendly oil palm plantations in Malaysia.

[122] Pan-European Connectivity for Large Mammals: Connections for Continental Resilience (11:00)

Presenter: DERTIEN, Jeremy (German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany)

Continual fragmentation of terrestrial and freshwater habitats can produce multiple negative impacts to wildlife populations, plant community persistence and overall ecosystem functioning. 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 omnidirectional circuit theory methods to model the Pan-European connectivity of ten different large mammal species. From these results we identified key ecological corridors and then used a combination of graph theoretic models and ecological indicators to prioritise corridors for conservation across the continent. We found that models of large herbivores showed more diffuse movement of wildlife across the landscape, indicating the difficulty in identifying key movement corridors for these species. In contrast, meso-predator and apex predator models identified narrower critical corridors for conservation. Despite these relative differences our results found several consistent spatial overlaps in local corridors prioritized for the predator and herbivore species. These results point to the need to prioritize the conservation of multiple key corridors that still exist, most prominently in Italy, Spain, Slovakia, Romania and the Balkans. In addition, our results highlight the need for restoration of fractured connections between protected areas across much of heavily fragmented Western Europe, especially in France and Germany.

[83] War, Peace, and Potato: A retrospective analysis of 250 years of change in forest, defaunation, and recolonization in a rewilding landscape in Europe (11:15)

Presenter: SHARMA, Sandeep

Rewilding has become an established concept of restoring natural processes, while enhancing biodiversity potential of the landscape. Rewilding creates resilient, self-regulating and self-sustaining ecosystems, while promoting human-wellbeing. The Oder delta is one such landscape chosen for rewilding. It is located at the Baltic coast between Poland and Germany, where the complex ecosystems spanning forests, agricultural land, peatland, and lagoons create ample opportunities for rewilding of a diverse assemblage of biodiversity and recolonization potential for locally extinct species such as the European Bison (Bison bonasus) and Moose (Alces alces). Here, we present our findings of a retrospective time-series analysis of ~250 years of change (1780 - 2020) in forest cover within a selected region in this landscape. We also present our findings of defaunation events in the past, and more recent recolonization and reestablishment of populations of iconic key-stone species in this region. We analyze various factors including human population dynamics that has affected defaunation, landcover-change, and rewilding success in the Oder delta. We elaborate on change in trophic complexity as a rewilding indicator for this landscape, and suggest various rewilding pathways.

[27] A time-series exploration of linkages between species diversity, functional diversity, and spectral dissimilarity in a temperate floodplain meadow (11:30)

Presenters: RAHMANIAN, Soroor (iDiv), FEILHAUER, Hannes (Remote Sensing Center for Earth System Research, Department of Remote Sensing in Geo- Ecosystem research, Leipzig University)

Remote sensing is frequently used to assess biodiversity, particularly species and functional diversity. Common approaches rely on the spectral diversity of plant canopies. Spectral diversity, however, exhibits temporal dynamics that remain inadequately understood. We investigated these dynamics in a nutrient-rich floodplain meadow in northern Germany, characterized by dense grassland vegetation and tall forbs. Using thirty-six 1 m² diameter circular plots, we quantified species diversity using the Shannon index and functional diversity using Rao's quadratic entropy, which integrates plant traits like leaf size, specific leaf area, leaf dry matter content, leaf mass, and canopy height from the LEDA dataset. Spectral diversity across six dates during the growing season was measured with a field spectrometer in five spots of each plot’s canopy and quantified using dissimilarity between these five subplot measurements across 166 wavelengths (405 nm to 2445 nm). Early in the growing season, we observed a strong positive correlation among species, functional, and spectral diversity. As the season progressed, the initially positive relationship between spectral diversity and other dimensions weakened and, in some cases, turned negative. This shift reflects changes in vegetation structure affecting spectral response. Initially, with sparse and uniform vegetation cover, spectral signals were influenced by species diversity and their unique light absorption properties, alongside functional traits of early-season plants. As the season progressed and canopy density increased, spectral responses became less sensitive to ground-level variations. Dominance of signals from higher canopy components led to a more uniform spectral signature, despite ongoing species and functional diversity at ground level. This likely explains the observed decline or reversal in the correlation between spectral diversity and other biodiversity metrics. Our study emphasizes the importance of considering temporal dynamics in studying biodiversity and spectral diversity relationships. Insights can improve remote sensing for accurate biodiversity monitoring across different growing season stages.

[164] Utilizing multi-objective decision support tools for protected area selection (11:45)

Presenter: VOSKAMP, Alke (Senckenberg Biodiversity and Climate Research Centre)

Establishing and maintaining protected areas (PAs) is a key action in delivering post-2020 biodiversity targets. PAs often need to meet multiple objectives, ranging from biodiversity protection to ecosystem service provision and climate change mitigation, but available land and conservation funding is limited. Therefore, optimizing resources by selecting the most beneficial PAs is vital. Here, we advocate for a flexible and transparent approach to selecting PAs based on multiple objectives, and illustrate this with a decision support tool on a global scale. The tool allows weighting and prioritization of different conservation objectives according to user-specified preferences as well as real-time comparison of the outcome. Applying the tool across 1,346 terrestrial PAs, we demonstrate that decision makers frequently face trade-offs among conflicting objectives, e.g., between species protection and ecosystem integrity. Nevertheless, we show that transparent decision support tools can reveal synergies and trade-offs associated with PA selection, thereby helping to illuminate and resolve land-use conflicts embedded in divergent societal and political demands and values.

Talk Session: Molecular Biodiversity and Evolution - Leipziger KUBUS/1-B - Hall 1 B (15 Nov 2024, 10:45 - 12:00)

[154] Genome size and trait flexibility influences evolutionary radiation of palms (10:45)

Presenter: BHADRA, Sreetama

Biodiversity of the world flora is shaped by evolutionary radiations. Radiations are influenced by the interplay between functional trait flexibility (evolvability of traits over macroevolutionary times) and genomic factors. However, this has never been tested in a quantitative macroevolutionary framework. Using ca. 2,600 species of palms (Arecaceae) as a model system, we test the hypothesis that evolution of genome size (the total amount of DNA in the nucleus of a cell) influences evolutionary radiation both directly and indirectly mediated by trait flexibility. Applying macroevolutionary models we show that palm speciation rates increased rapidly c. 10 million years ago, coinciding with the increased rates of genome size and trait evolution. Structural equation models applied to the tip-derived rates reveal that lineages with larger genomes show faster genome size and leaf size evolution, which led to increased speciation rates in palms. Rates of stem evolution were negatively influenced by genome size that, interestingly, led to increased speciation. Genome size evolution positively influenced fruit size evolution, likely facilitating animal-mediated dispersal of palms promoting lineage persistence, but not necessarily speciation. Our findings suggest that comparable interplay between genomic factors, traits and diversification may underlie some of the most enigmatic evolutionary radiations observed in angiosperms and the ecological success of certain plant lineages.

[92] Megafauna affects the genetic structure and demographic history of a megafruit palm in Africa (11:00)

Presenter: PU, Yuanshu

The largest animals in ecosystems (megafauna) can feed on mega-fruited plants (fruits diameter > 4 cm) and disperse massive loads of large seeds across long distances, thus playing a vital role in maintaining biotic connectivity and population structures of mega-fruited plants. However, it remains unclear how the global extinction of most megafauna since the late Quaternary (last ~10k years) affected mega-fruited plant populations. Here, we hypothesize that the loss of specialized megafaunal seed dispersers led to dispersal limitation of mega-fruited plants, resulting in high population genetic structure and decreases in population sizes and migration rates that coincided spatially and temporally with the decline and extinction of co-occurring megafauna. We focus on the megafaunal palm *Hyphaene coriacea*, which naturally occurs in savannas in Madagascar (where all seed-dispersing megafauna – e.g. giant lemurs, elephant birds – have gone extinct) and mainland Africa (where more intact elephant populations are still functioning as seed dispersers of *H. coriaceae*). Using RAD-seq from 22 populations and 151 individuals, we found that *H. coriaceae* population structure is shaped by extant and extinct fruit-eating and seed dispersing animals (frugivores), and we detected signatures of population size declines in both Malagasy and mainland African populations. This suggests that current and past interactions with megafauna have left signatures in the genome of megafruited plant populations, and reduced seed dispersal may have led to a loss of biotic connectivity and population size declines. Furthermore, alternative dispersal mechanisms, such as human-mediated dispersal and dispersal by surface runoff, may have substituted dispersal functions by past megafauna, explaining the persistence of *H. coriaceae* in Madagascar. These results provide important insights in the role of frugivores in maintaining seed dispersal and population structure of African plants, and how megafruited plants have been able to persist since the late Quaternary extinction of most primary seed dispersers.

[43] Evolution of Wolbachia nutritional symbiosis – The Enigmatic Case of the Biotin Operon (11:15)

Presenter: PREUSS, Leopold (iDiv, MLU)

The obligate intracellular endosymbiont *Wolbachia* (Alphaproteobacteria) is considered the most abundant symbiont with an estimated 40 % of Arthropod species infected. In most Arthropods, *Wolbachia* exert negative fitness effects on their host, causing for instance reproductive aberrations which facilitate the symbiont transmission. However, recent genomic analyses have revealed the presence of an operon responsible for biotin (vitamin B7) production to be present in *Wolbachia* from several insect hosts, including solitary bees. For some of these host species a nutrient-providing symbiont is advantageous given the monotonous diet of these hosts, and a nutritional mutualism has been demonstrated in rearing experiments. Solitary bees are a diverse and ecologically important group of insects, comprising 604 different species in Germany. Despite the fact that solitary bees appear to be a hotspot for biotin operon-containing *Wolbachia*, the role and evolution of biotin supplementation by *Wolbachia* in bees remains enigmatic. The aim of my project is to investigate the distribution, evolutionary history and functionality of this biotin operon in order to understand the evolution of a potential nutritional mutualism and to elucidate the relationship between *Wolbachia* and their solitary bee hosts. To this end, a comprehensive screen for *Wolbachia* symbionts carrying the biotin operon was performed. Our results show that the phenomenon is even more widespread than previously thought. A large set of Illumina WGS data from a variety of bee hosts will be screened for the presence of the *Wolbachia* biotin operon and extracted, including surrounding gene regions, for phylogenetic and comparative analysis. The role of *Wolbachia* mobile genetic elements, including phages, as potential vectors for the spread of the biotin operon will be investigated.

[20] Little evidence for latitudinal genetic diversity gradients within or between species (11:30)

Presenter: GRANJON, Anne-Celine

The latitudinal gradient in biodiversity is a long-observed phenomenon, where many components of global biodiversity, including species richness, phylogenetic diversity, and functional diversity, decrease from the Equator to the Poles. Though nuclear genetic diversity is an important component of biodiversity that underlies species’ adaptive potential, whether it also varies latitudinally with other forms of biodiversity is unclear. Additionally, unlike other forms of biodiversity which are typically measured at the species level, genetic diversity has both within- and between-species components that may each be predicted to covary with latitude. Within-species genetic diversity patterns emerge in part from population-level microevolutionary processes, while spatial patterns of between-species genetic diversity are products of species-level variation and species turnover. Together, within- and between- patterns of genetic diversity can contribute to a more comprehensive understanding of the evolutionary and ecological processes maintaining global biodiversity patterns. The increasing availability of publicly accessible genetic data worldwide allows us to investigate whether a latitudinal gradient also exists in genetic diversity. Here, we use a unique dataset of 67,000 individual genotypes sampled from 112 species and 1697 local populations to investigate latitudinal patterns of neutral nuclear genetic diversity in mammals. Preliminary results suggest that there is no evident latitudinal gradient in genetic diversity either within or across species. We will discuss the lack of genetic latitudinal gradient in light of theories underlying the species richness gradient and their predictions regarding population-level processes.

[11] Sources of Variation in Plant Chemical Diversity (11:45)

Presenter: NGUYEN, Linh Mai Nhat

Plants, like many other organisms, produce a tremendous variety of secondary compounds that are crucial to interspecific and intraspecific interactions, as well as to adaptation to environmental changes. This chemical diversity has been attributed to multiple factors such as function (e.g. defense, pollinator attraction), tissue-specific needs, various constraints, and phylogenetic history. Yet the interplay between these multiple factors driving plant chemodiversity is still unclear, primarily because the vast majority of studies focused on a single organ - (mostly leaves), or when comparing different organs, focused on single taxa. As such, the interplay between function and phylogenetic effects remains unclear. Using a novel model system of wild figs from Madagascar, this study tests (a) the degree to which phylogeny explains variation in fruit and leaf chemodiversity (b) to what degree phytochemical diversity is explained by tissue-specific function. We applied an untargeted metabolomics approach to unripe fruits and leaves from eight species of wild figs (Ficus spp) sampled in a tropical rainforest in Madagascar. We characterized their chemical profiles using ultra-performance liquid chromatography-mass spectrometry and, using six genetic markers, reconstructed their phylogeny to understand the patterns of chemodiversity. We found a significant, but moderate phylogenetic effect in fruit chemodiversity, and no phylogenetic effect in leaf chemodiversity. Fruit and leaf metabolomes were more similar to the same tissue in other species than to the other tissue within the species. Our results indicate that, while phylogeny plays a role in plant chemodiversity, functional convergence of tissue-specific metabolites is a major driver of plant chemodiversity.

Lunch Break (12:00 - 13:00)

Keynote Susanne Fritz in HAll 1 AB (13:00 - 13:45)

Hall 1AB, 1st floor

Wrap-up and Award Ceremony: Wrap-up and Award Ceremony in Hall 1AB (15 Nov 2024, 13:45 - 14:15)

Hall 1, 1st floor

Workshop: iDiv GMA and Governance Workshop (members only) in 1AB - Leipziger KUBUS/1-A - Hall 1 A (15 Nov 2024, 14:30 - 16:00)