Biogeography & Macroecology meeting 2024, University of Marburg
– Schedule –

Session

Keynote Daniele Silvestro: New (un)supervised learning models to infer the evolution and future dynamics of biodiversity

Time:
Thursday, 13/June/2024:
9:10am - 10:00am

Session Chair: **Alexander Zizka**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum für Synthetische Mikrobiologie Karl-von-Frisch-Str. 14 35032 Marburg

https://www.unifr.ch/bio/en/research/eco-evol/silvestro-group.html

Session Abstract

Throughout the long evolutionary history of life, species of all kingdoms have undergone staggering diversification and faced countless environmental changes and extinction events. Since the great majority of species that lived on Earth have since gone extinct, it is difficult to infer how biodiversity dynamics unfolded over millions of years and yet crucial to understand the fundamental evolutionary processes driving them. Today, with over a million species threatened with extinction, biodiversity is facing unprecedented challenges, urging the need for conservation policies that maximize its protection and sustain its manifold contributions to people. Here we present a suite of new supervised and unsupervised models with applications in evolutionary and conservation biology. Specifically, we show how deep learning models can be used to infer biodiversity dynamics in deep time, and test hypotheses on past speciation and extinction based on fossil data. We then present a new semi-supervised framework to improve our understanding of the evolutionary relationships among living species based on the analysis of genomic data. Finally, we introduce a einforcement learning framework to optimize biodiversity conservation policies. Coupling artificial intelligence with evolutionary models holds great promise for advancing our understanding of biodiversity and its evolution across time scales, and for improving biodiversity conservation action in a rapidly changing world.

Session

Macroecological patterns & processes

Time:
Thursday, 13/June/2024:
10:30am - 12:50pm

Session Chair: **Susanne Fritz**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum für Synthetische Mikrobiologie Karl-von-Frisch-Str. 14 35032 Marburg

Presentations

10:30am - 10:50am

Chicken or Egg? Phylogenetic sequences of ecological trait acquisition underpinning alpine biome shifts

Jurriaan M. de Vos, Bram Cladder, Freek T. Bakker, Livio Bätscher

Alpine biome shifts are a model system to understand the factors driving and constraining major ecological transitions. Alpine environments (i.e., above the upper climatic treeline) are particularly exacting e.g., short growing seasons, high UV light radiation, and extreme temperature fluctuations daily and annually. Thus, evolving a trait syndrome that enables becoming alpine involves a multitude of trait complexes, integrating plant architecture (e.g., prostrate growth to leverage boundary layer effects), physiology (e.g., freezing resistance; UV protection), and reproductive traits (e.g., few-flowered inflorescences), jointly relating to these environmental challenges. In this talk, I ask the question if there is some systematic order in which ecological traits underpinning alpine biome shifts were acquired over macroevolutionary timescales. I approach this question in two ways: by analyzing the environmental niches in multiple dimensions of the high- and low-elevation plant species of the European Alps, and by focusing on phylogenetic sequences of acquisition in multiple clades of plants that diversified across mountain systems. Results suggest that trait evolution underpinning phylogenetic biome shifts constitutes a staggered acquisition of the components of complex syndromes, each component of which may exhibit rather strikingly different evolutionary patterns across clades.

10:50am - 11:10am

Dispersal and the generation of diversity

Sarah Sophie Weil, Michaël Nicolaï, Patrick Weigelt

Dispersal is a key process known to influence both speciation and extinction, however, the exact relationships appear to be scale- and context-dependent. Dispersal on ecological scales inhibits speciation due to increased gene flow, whereas dispersal across major barriers may increase speciation due to new opportunities for ecological specialisation and radiations. Similarly, low dispersal abilities have been linked to increased extinction rates, but in meta-populations, high levels of dispersal have also been linked to higher extinction risk due to synchronized population responses. Few studies have explicitly tested these hypotheses at macroecological and macroevolutionary scales across multiple taxa.

Using traits as a proxy for past dispersal ability in state-dependent speciation and extinction models we are linking dispersal to speciation and extinction in reptiles. Ultimately, species richness is the result of the interplay between speciation and extinction. Better understanding the links between dispersal and speciation/extinction will thus improve our knowledge of the origin of biodiversity.

11:10am - 11:30am

Myrejagten: Resource use by ants in Denmark

Julie K. Sheard, Robert R Dunn, Nathan J. Sanders, Carsten Rahbek

What drives variation in resource use among species, trophic groups, and environments? Here, we report on a distributed experiment across Denmark, conducted mostly by children, to address this question in ants. Over two years, children conducted two-hour baiting experiments at 508 sites to investigate how ants foraged for a suite of resources. The distributed experiment, called ‘Myrejagten’ (the Ant Hunt), observed 15,329 workers from 26 species across a variety of environmental and temporal conditions, including building proportion, vegetation density, solar radiation, topographic wetness, coastal distance and Julian date. The experiment revealed that relative resource use varies among trophic levels with primary consumers showing an eight times higher preference for oil and predators a twice as high preference for protein and that environment has a significant effect on resource use. Taken together, our results highlight that engaging children can lead to discoveries at the forefront of ecology, such as the drivers of resource use at geographical scales, among species and trophic levels. Furthermore, we present some preliminary advances on an automated camera trap that can be deployed for continuous monitoring of ant resource use.

11:30am - 11:50am

Opportunistic plant observations reveal spatial and temporal gradients in phenology

Michael Rzanny, Patrick Mäder, Hans Christian Wittich, David Boho, Jana Wäldchen

Opportunistic plant observations collected with plant ID apps such as Flora Incognita provide a rapidly growing source of spatiotemporal plant observation data. Here, we used such data to explore the question whether they can be used to detect changes in plant species phenologies. Examining 20 mostly herbaceous plant species in two consecutive years across Europe, we observed significant shifts in their flowering phenology, being more pronounced for springflowering species (6-17 days) compared to summer - flowering species(1-6 days). Moreover, we show that these data are suitable to model large-scale relationships such as "Hopkins' bioclimatic law" which quantifies the phenological delay with increasing elevation, latitude, and longitude. Here, we observe spatial shifts, ranging from -5 to 50 days per 1000m elevation, latitudinal shifts ranging from -1 to 4 days per degree northwards, and longitudinal shifts ranging from -1 to 1 day per degree eastwards, depending on the species. Our findings show that the increasing volume of purely opportunistic plant observation data already provides reliable phenological information, and therewith can be used to support global, high-resolution phenology monitoring in the face of ongoing climate change.

11:50am - 12:10pm

Species-energy relationships in the climatic mosaic of warmth, moisture and ecosystem productivity

Marco Túlio Coelho, Elisa Barreto, Thiago Rangel, José Alexandre Diniz-Filho, Eliška Bohdalková, David Storch, Yun-Ting Jang, Mikael Pontarp, Fernanda Cassemiro, Pincelli Hull, Catherine Graham

Ecologists have long sought universal principles that govern life's distribution on Earth. One foundational concept is the species-energy relationship, which suggests that areas with more available energy should support more species. However, linking biodiversity to energy metrics like temperature, water, and productivity often yields mixed results due to context dependence. These inconsistencies may stem from overlooking the impacts of spatial and historical processes and the influence of Earth's physical dynamics on climatic conditions, which significantly affect biodiversity patterns. Our study addresses these issues by analyzing the diversity-energy relationship within the framework of environmental space, as defined by Hutchinson's duality. Contrary to geographical analyses, in our approach, species sharing the same climate condition are grouped together even if they are not located in the same geographical area, effectively minimizing the influence of geographical processes on our analysis. Our findings reveal consistent patterns that starkly contrast with the extensive variability and context-specificity reported in previous studies. We confirm the long-standing theoretical predictions of species-energy relationships, highlighting that evaluations of these theories or hypotheses should also exclude spatial processes if they are not accounted for in the original assumptions.

12:10pm - 12:30pm

Unraveling thermal tolerance patterns: a multi-level analysis of physiological traits of arthropods along elevational gradients in Southern Asia

Christian Hof, Imran Khaliq

To understand how species will be able to cope with changing climatic conditions, the integration of thermal physiology and biogeography bears great potential. However, it remains poorly understood whether relationships of thermal traits with the environment observed between species scale down to the intraspecific and scale up to the assemblage level with similar magnitude and direction. Here, we present results from thermal tolerance measurements in over 15,000 individuals representing 116 arthropod species along elevational gradients in Southern Asia. We quantified the associations between thermal traits and their determinants at different taxonomic aggregation levels and for two different mountain ranges.

Our findings show a consistent decrease in all thermal traits investigated with increasing elevation and an increase with the increase of temperature, especially at the assemblage level. Nevertheless, the distributional patterns of thermal traits exhibited greater variation and even contrast along the two elevational transects as well as at lower taxonomic levels. This implies that factors beyond elevation, including vegetation composition, microclimate, or landscape features, exert significant influence on the organisms’ thermal characteristics. Our study highlights this complexity of the interplay of thermal physiology and environment across different habitats and across biological scales.

12:30pm - 12:50pm

Mobile Sensing of the environment: integrating automated plant identification, citizen science, and bio-indication

Susanne Tautenhahn, Michael Rzanny, Martin Jung, Patrick Mäder, Bernhard Ahrens, David Boho, Negin Katal, Hans Christian Wittich, Jana Wäldchen

We introduce mobile environmental sensing as a novel approach for mapping climate, soil, and disturbance factors across scales. Bio-indication allows to infer environmental conditions from plant occurrences based on their ecological niches. Leveraging automated plant identification apps such as Flora Incognita and citizen science millions of opportunistic plant occurrence data become available which will further increase in the future. In combination with recent advancements in pan European bio-indicator value systems this enables us to map environmental factors over large extents.

Currently, mobile sensing achieves resolutions of 0.25° across Europe and up to 100m in urban areas due to a higher citizen participation. Cross-consistency checks against traditional environmental data sources and expert vegetation mappings support a high reliability for temperature, soil pH, and salt variations based on mobile sensing. Importantly, we can also map environmental factors for which traditional data-sets are very uncertain or lacking and therefore allow new insights, such as disturbance severity and frequency, grazing pressure, mowing frequency, soil disturbance, light, soil moisture, and nutrients.

Three applications will illustrate the potential of mobile sensing: mapping of effective bio-environmental regions, high-resolution analysis of urban environments, and a community engagement to better understand ecosystem-atmosphere carbon and water fluxes measured by FLUXNET.

Session

Keynote Florian Hartig: AI in Macroecology & Biogeography – from prediction to inference

Time:
Thursday, 13/June/2024:
1:50pm - 2:40pm

Session Chair: **Alexander Zizka**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum
für Synthetische Mikrobiologie Karl-von-
Frisch-Str. 14 35032 Marburg

https://www.uni-regensburg.de/biologie-vorklinische-medizin/theoretische-oekologie/mitarbeiter/hartig/

Session Abstract

The popularity of machine learning (ML), deep learning (DL), and artificial intelligence (AI) has grown rapidly in recent years. It is often assumed that the advances offered by ML and DL mainly apply to predictive tasks. However, ML and DL algorithms can, at least in principle, also be used for inference, including tasks such as effect size estimation or partitioning of explained variation. In my talk, I will discuss the promise and pitfalls of using AI for statistical inference in macroecological research, using examples from different applications such as species distribution models, community ecology, or the analysis of bipartite networks. I will start by reviewing Explainable AI (xAI) algorithms that can extract effect sizes and variable importance from fitted models, and show how these map to traditional statistical indicators. As a next step, I will discuss how we can provide statistical guarantees such as p-values and confidence intervals for these xAI metrics. A key problem that arises in this context is understanding what inductive biases are introduced by the various ML algorithms and their hyperparameters, and how these affect the bias in xAI effect estimates. These biases can make interpretation of fitted models problematic. On the other hand, well-tuned ML and DL algorithms perform automatic model and complexity selection, and thus may offer better alternatives for dealing with structural uncertainty than statistical model selection tools. I will conclude that there is reason to be cautiously hopeful that ML algorithms may merge with other methods of statistical inference, opening up an exciting new option for macroecological analyses.

Session

AI in Macroecology & Biogeography

Time:
Thursday, 13/June/2024:
2:40pm - 3:40pm

Session Chair: **Jan Hackel**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum
für Synthetische Mikrobiologie Karl-von-
Frisch-Str. 14 35032 Marburg

Presentations

2:40pm - 3:00pm

Deep Species Distribution Models (Deep-SDMs)

Benjamin Deneu

In the field of species distribution modeling, there is often a trade-off between interpretability and performance. This partly explains why the study of species distributions is often based on relatively simple models (GLM, MaxEnt, etc.). The advantage of these models is that they capture easily interpretable relationships between species distribution and environmental factors. In this presentation we describe deep learning-based species distribution models (Deep-SDMs) and their main features. Deep-SDMs have emerged recently and often lead to superior performance for predictions. As for JSDM (Joint Species Distribution Models), Deep-SDMs account for species co-occurrences, and have the ability to model and predict species communities. Deep-SDMs can bring several advantages to the field of SDM and macroecology more generally. In particular, their ability to efficiently predict species communities on big datasets by learning a common latent space and the ability to easily integrate complex data (aerial or satellite imagery, environmental neighborhood information). We show for exemple that Deep-SDMs can capture information about the spatial structure of the environment or the landscape to enable better performance than other state-of-the-art models.

3:00pm - 3:20pm

Spatiotemporal patterns of humans and wildlife: The potential of AI and camera trapping

Manuel Steinbauer

Big data approaches, like large-scale camera trapping studies, are becoming more relevant for studying human-wildlife interactions. In addition, open-source object detection models are rapidly improving and have great potential to enhance the image processing of camera trap data. The resulting large-scale and long-term database enables to understand and predict spatiotemporal patterns of human activities in natural areas as well as their interactions with wildlife.

Building on own results, this talk first highlights the performance of open-source object detection model in visitor and wildlife monitoring. Since the accuracy of the detection model is very high, this approach is suitable for biogeographic analysis of spatiotemporal patterns of humans and wildlife. Besides the great acceleration in processing speed, the approach is suitable for long-term monitoring and allows reproducibility in scientific studies while complying with privacy regulations.

The talk will further show how such long-term monitoring can be used to predict visitor flows along a trail network using multiple spatiotemporal predictors. Building on this, the data allow the assessment of human-wildlife interactions and are thus able to enhanced the adaptation of management measures to reduce social and ecological conflicts.

3:20pm - 3:40pm

Automated redlisting using deep learning

Alexander Zizka

The IUCN Red List of threatened species (RL) is the most authoritative global quantification of extinction risk, and widely used in ecological research and applied conservation. Yet, due to the time-consuming assessment process, the RL is taxonomically and geographically biased, in particular towards the global North and charismatic taxa. One promising approach to speed up RL assessments and overcome these biases is the use of AI to predict extinction risk based on the combination of information from digitized collection specimens and citizen science data with remote sensing information on the environment. Here, I present IUCNN, an approach using deep learning models to predict species RL status from publicly available geographic occurrence records (and other data, such as traits if available).

Session

Island biogeography

Time:
Thursday, 13/June/2024:
4:30pm - 5:30pm

Session Chair: **Maaike Bader**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus --
Zentrum für Synthetische Mikrobiologie
Karl-von-Frisch-Str. 14 35032 Marburg

Presentations

4:30pm - 4:50pm

Global floristic homogenisation on islands during the past 5000 years

Anna Walentowitz, Nichola Strandberg, Manuel Steinbauer, Sandra Nogué

The global homogenisation of floral communities is a characteristic of the Anthropocene. Oceanic islands are especially prone to homogenisation due to their high invasibility and anthropogenically-caused extinctions and extirpations of unique native, and often endemic, species. In existing studies, the time horizon in which homogenisation is analysed rarely exceeds 500 years and pre-human times are often considered as a single point in time. Thereby, the temporal contextualisation of this process is disregarded. We analyse the similarity of island floras across the globe during the past 5000 years using fossil pollen data from sedimentary sequences. We track changes from a global, cross-ocean to a regional scale. While globally a clear harmonization trend can be detected, magnitudes of change in floral similarity differ at regional scales. This study underlines the usefulness of palynological data to support the analysis and contextualisation of biodiversity changes in the Anthropocene.

4:50pm - 5:10pm

Global patterns of functional and phylogenetic diversity and their drivers in island birds

Jan B. Kalusche, Patrick Weigelt, Ana Maria Bastidas Urrutia, Katrin Böhning-Gaese, Christian Hof, Susanne A. Fritz

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 across biogeographic realms. However, functional diversity values were more clustered than expected based on species richness, while phylogenetic diversity was generally lower than expected. Correspondingly, dispersal and biotic and abiotic filters show strong effects that vary considerably 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.

5:10pm - 5:30pm

Island biogeography of fishes in Indonesian marine lakes

Adriana Alzate, Awaludinnoer Ahmad, Noortje Barning, Lisa Becking, Maarten Hoepel, Dea Fauzia Lestari, Stephanie Martinez, Francesco Pelizza, Beginer Subhan

How does marine biodiversity flourish on islands? Our understanding of island biodiversity is predominantly based on terrestrial examples, while processes governing marine biodiversity might differ completely. Here, we tested the effects of island size, isolation and age on fish taxonomic, functional and phylogenetic diversity in a unique island-like marine system - Indonesian tropical marine lakes. Marine lakes are bodies of seawater surrounded by land connected at different levels to the sea. Because of their high degree of natural replication combined with small and manageable sizes, they offer an unprecedented opportunity to investigate the processes shaping biodiversity. Additionally, we investigated whether fish communities in marine lakes are randomly assembled (a random subset from the regional species pool) or whether environmental or dispersal filters are at work (composed of species with similar traits such as high dispersal ability or environmental tolerance). This study is the first attempt to describe marine lake fish communities and to investigate how biodiversity arises and thrives in these isolated ecosystems, relevant in a world where nature is becoming increasingly fragmented.

5:30pm - 5:50pm

Unique and tricky to measure: Functional traits of habitat-specialized succulent plants on edaphic quartz islands in the Knersvlakte

Pia Maria Eibes, Ute Schmiedel, Meline Brendel, Annelise Le Roux, A. Muthama Muasya, Aaron Niekamp, Jens Oldeland, Wanda Thormählen, Daniel A. Zhigila, Severin D.H. Irl

Edaphic islands commonly host high numbers of habitat-specialized or endemic plant species. In the case of quartz islands in South Africa, many of these species are additionally characterized as dwarf succulent shrubs with unusual growth forms. The functional traits of these plants are poorly represented in trait databases and the distinctive succulent growth forms necessitate innovative approaches to trait measurement in addition to conventional protocols. In this study, we investigate whether and how the plant functional and biogeographic traits correspond to the specific soil abiotic and spatial characteristics of the edaphic islands, in comparison to the surrounding matrix. We use quantitative data on various traits of the most abundant perennial plant species (n = 195) found on a quartz island archipelago in the Knersvlakte nature reserve. We explore how a functional approach can enhance the comparison of different types of edaphic islands, enabling us to gain further insights into their unique or shared characteristics. Furthermore, we discuss where deviating from common standardized protocols for trait measurement in succulent plant species is unavoidable and which additional traits provide important information about the strategies of the studied edaphic specialists.

Session

Keynote Jana Wäldchen: Automated plant identification with Flora Incognita

Time:
Friday, 14/June/2024:
9:10am - 10:00am

Session Chair: **Alexander Zizka**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum
für Synthetische Mikrobiologie Karl-von-
Frisch-Str. 14 35032 Marburg

https://www.bgc-jena.mpg.de/person/jwaeldchen/4679062

Session Abstract

The global loss of biodiversity is one of the most pressing environmental issues of our time. Effective conservation efforts require a precise understanding of the spatiotemporal patterns of biodiversity and how they change over time. However, biodiversity monitoring is labor-intensive, heavily relying on individual expertise to correctly identify species in the field. In-situ species identification is almost impossible for untrained people and challenging even for professionals. For these reasons, there has long been interest in developing automated species identification systems. Recent increases in data availability, along with major advances in machine learning algorithms, especially deep convolutional neural networks, have brought these systems to a 'production-ready' state. Automated species identification now has the potential to greatly enhance biodiversity and conservation research. The project partners at the Max Planck Institute for Biogeochemistry and Technische Universität Ilmenau have developed Flora Incognita, an app for automated plant identification. This talk will provide insights into the Flora Incognita project and discuss how automated plant identification can contribute to biodiversity monitoring.

Session

Extinction & conservation

Time:
Friday, 14/June/2024:
10:30am - 12:50pm

Session Chair: **Alke Voskamp**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum für Synthetische Mikrobiologie Karl-von-Frisch-Str. 14 35032 Marburg

Presentations

10:30am - 10:50am

Acceleration and demographic rates behind bird decline in North America

François Leroy, Marta Jarzyna, Petr Keil

Acceleration of human activities over the past century might have caused a corresponding acceleration in the decline of abundance of species, but this has not been empirically assessed. Further, the temporal dynamics of abundance arises from a complex interaction between recruitment and loss of individuals, yet this interplay remains unexplored across large spatial scales. We address these gaps by examining temporal changes, acceleration, deceleration, and vital processes (i.e. recruitment and loss) across much of the North American avifauna from 1987 to 2021. We confirm the continent-wide decline of bird abundance, and pinpoint the regional hotspots of acceleration of this decline in the Mid-Atlantic region, Midwest, and California, matching broad spatial patterns of human activities. We further reveal that the increasing rate of loss is the primary process of acceleration of abundance decline in California and the Midwest, whereas a decrease in recruitment rate dominates in the Mid-Atlantic. Finally, we highlight a worrisome trend: 96% of bird species and 100% of families with increasing abundances are concurrently experiencing a decline in recruitment rate. Thus, we need conservation policies even for species that appear to be thriving. Simply preventing loss may not be enough, as we also need policies that enhance recruitment.

10:50am - 11:10am

Contrasting impacts of non-native and threatened species on morphological, life-history, and phylogenetic diversity in bird assemblages.

Aurèle Toussaint, Meelis Partel, Carlos P. Carmona

Human activities have altered the species composition of assemblages through introductions and extinctions, but it remains unclear how those changes can affect the different facets of biodiversity. Here we assessed the impact of changes in species composition on taxonomic, functional, and phylogenetic diversity across 281 bird assemblages worldwide. To provide a more nuanced understanding of functional diversity, we distinguished morphological from life-history traits. We showed that shifts in species composition could trigger a global decline in avian biodiversity due to the high number of potential extinctions. Moreover, these extinctions were not random but unique in terms of function and phylogeny at the regional level. Our findings demonstrated that non-native species cannot compensate for these losses, as they are both morphologically and phylogenetically close to the native fauna. In the context of the ongoing biodiversity crisis, such alterations in the functional and phylogenetic structure of bird assemblages could heighten ecosystem vulnerability.

11:10am - 11:30am

Determinants of Seed Longevity under Artificial Ageing Conditions

Lea Klepka, Sascha Liepelt, Anna Bucharova

Stored seeds of wild plant species serve as repositories of plant genetic diversity, and are valuable resources for evolutionary research, species conservation, and ecosystem restoration. However, long-term storage inevitably leads to the deterioration and loss of viability of the seed. While seed longevity is known to be species-specific, the significance of intraspecific variability in seed longevity, and how it varies across geographic ranges, remains unexplored. Here, we tested how seed longevity varies between and within species, and how it correlates with the climate in the source region. We focused on 42 common grassland species and 182 accessions from 23 regions across Europe. To simulate seed aging in storage, we exposed the seeds to artificial ageing conditions (60% relative humidity, temperature 45°C). The seed longevity strongly varied between species more than twenty-fold, increased with seed protein content, yet it did not depend on phylogeny. Within species, the seed longevity varied more than ten-fold between the accessions. It increased with the initial seed viability and mean annual temperature in the region of origin. Our results suggest that seed from warmer regions, especially those with high initial viability, survive longer in conservation seed banks.

11:30am - 11:50am

Patterns and drivers of regional plant extinctions

Laura Méndez, Sonja Knapp, Erik Welk, Marten Winter, Markus Bernhardt-Römermann, Helge Bruelheide, Marina Golivets, Matthias Grenié, Ingolf Kühn, Ingmar Staude, Alexander Zizka

In the face of increasing biodiversity threats, understanding the predictors of plant extinction risk is critical for conservation. Global assessments indicate over one-third of terrestrial plant species are rare, with regional extinctions outpacing documented global extinctions. Integrating national and regional Red Lists of vascular plants with plant trait data and phylogenies, we analyze patterns of regional plant extinctions globally, to discern the role of evolutionary and functional uniqueness in species' vulnerability. Specifically, we investigate whether phylogenetic marginality—species' evolutionary distinctiveness—correlates with their risk of regional and global extinction of vascular plants. Additionally, we examine if species that have gone extinct exhibit greater functional trait marginality, meaning they occupy more unique positions in the functional trait space compared to the broader species pool. This approach may prompt early conservation actions across countries, even before species are globally recognized as threatened, addressing the growing importance of extinction risk estimation for enhancing conservation initiatives amid escalating anthropogenic impact.

11:50am - 12:10pm

The Parcel Index of Conservation Attributes (PICA) to predict and evaluate hotspots of old-growth biodiversity in small-scale private forests

Peter Hansen, Andreas Mölder

Endangered forest species often depend on slowly evolving structures of old-growth forests such as large-diameter trees and deadwood, or cautious or absent forest management. Small-scale private forests are particularly important in this regard, offering great structural diversity and varied landscapes shaped by the individual owners, and serve as refuges for forest biodiversity.

The Parcel Index of Conservation Attributes (PICA) is presented as a tool to quantify the value of individual small-scale private forest parcels in terms of crucial old-growth structures that are becoming rare in current forests. PICA values are defined by broadleaf tree volume, broadleaf deadwood, management intensity, biotope values (according to German federal law), and number of large-diameter trees.

The PICA components have been demonstrated to correlate with easily obtainable topographical data such as land use, plot geometry, and forest cover continuity. To aid nature conservation efforts in understanding the spatial distribution of valuable structures, we utilized machine learning algorithms to predict PICA values. We parameterized and evaluated different models using data collected from a field survey of 129 small-scale private forest parcels in the Lower Saxon Hills region. The models were then used to create a map of potential old-growth biodiversity hotspots.

12:10pm - 12:30pm

Threatened at home but naturalized elsewhere: conservation conflict or opportunity?

Weihan Zhao, Trevor S. Fristoe, Amy Davis, Wayne Dawson, Franz Essl, Holger Kreft, Jan Pergl, Petr Pysek, Patrick Weigelt, Marten Winter, Mark van Kleunen

Humans pose threats to numerous native species, while they also have introduced many species outside their native ranges, where some have become naturalized or even invasive. Most of the naturalized species are common at home, but some of them may actually be threatened. Naturalization of threatened species could be considered an accidental kind of ex-situ conservation, but with the potential to become invasive pose a conservation conflict. It remains, however, unknown how many threatened-but-naturalized species there are, what features they have, and in which regions they are native and naturalized. To address this, we combined databases on the global threat status and naturalization success of the world’s seed plants. We found that 231 threatened species have become naturalized elsewhere; most of them are trees or shrubs with economic uses such as provisioning of materials and landscaping. Europe received more threatened-but-naturalized species than expected, whereas Africa, which harbours the largest number, was under-represented. Australasia and Northern America were over-represented as donors of threatened species. Our study shows that some threatened plant species have managed to become naturalized outside their native range, although the number is relatively low. Future studies should test the potential conservation value of these naturalized populations.

12:30pm - 12:50pm

A framework to model species responses to extreme weather events

Aaron Hagen Kauffeldt, Susanne Fritz, Damaris Zurell, Katrin Böhning-Gaese, Alke Voskamp

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 classical presence/absence 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 1999 to 2022. The species-specific models predict the suitability 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.

Session

Species distributions 1

Time:
Friday, 14/June/2024:
1:40pm - 2:40pm

Session Chair: **Manuel Steinbauer**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum für Synthetische Mikrobiologie Karl-von-Frisch-Str. 14 35032 Marburg

Presentations

1:40pm - 2:00pm

Disentangling metacommunity assembly mechanisms from eDNA using joint species distribution models

Maximilian Pichler, Wang Cai, Douglas W. Yu, Florian Hartig

New advances and technologies are leading to an unprecedented high resolution of community data, perhaps making it possible for the first time to unravel the mechanisms of metacommunity assembly. Environmental filtering, species interactions, ecological drift, and dispersal determine community composition in local communities, but disentangling their relative importance has proven elusive, likely due to inappropriate tools. Here, we show that joint species distribution models (JSDM) and variance partitioning can provide a solution. First, JSDM reveals the "internal structure" of communities and species that can be correlated in a second step against environmental and spatial distinctiveness, thereby revealing the importance of metacommunity assembly mechanisms. We demonstrate that this approach can detect environmental filtering and dispersal limitation in a pond metacommunity. We conclude that JSDMs are a powerful tool for metacommunity analysis, especially for large community data.

2:00pm - 2:20pm

Global Inventory of Floras and Traits (GIFT)

Pierre Denelle, Sarah Sophie Weil, Patrick Weigelt, Holger Kreft

The Global Inventory of Floras and Traits (GIFT) is a global database of regional plant checklists that has proven successful in documenting biogeographical patterns of plants. Since the release of the first version of GIFT, the database kept on expanding. GIFT version 3.0 contains 5169 plant checklists referring to 3400 regions worldwide. These checklists include a total of 371,148 land plant species, mostly vascular plants, of which 354,848 have accepted species names, and species-level data for 109 functional traits.

This presentation will first introduce the GIFT database and present its structure with examples showing how to retrieve distribution data for specific taxonomic groups, functional traits at the species level, phylogenetic diversity, and environmental data at the regional level. Second, a comparison of data between the GIFT database and the GBIF repository will be presented.

2:20pm - 2:40pm

spatialMaxent

Lisa Bald, Jannis Gottwald, Dirk Zeuss

Species distribution modeling (SDM) often performs poorly when evaluated against spatially independent test data. One contributing factor to this issue is the neglect of spatial autocorrelation during model training and validation, resulting in inflated performance metrics and the development of overly complex models. Among the SDM softwares used Maxent is one of the most widely utilized methods, largely attributable to its user-friendly graphical-user-interface (GUI). It has been shown that parameter tuning leads to better Maxent models in terms of complexity and performance. However, in nearly all published applications, Maxent is used with the default settings. The lack of model tuning and the ignoring of spatial autocorrelation may be related to the fact that the Maxent GUI does not include such functionalities.

We implemented tuning and validation functionalities that account for spatial autocorrelation in a software extension for Maxent: spatialMaxent (https://doi.org/10.1002/ece3.10635). We compared our results to models based on Maxent's default settings on a dataset with over 200 species. spatialMaxent outperformed the Maxent models in terms of model complexity and performance on spatially independent test data. All tuning functionalities in spatialMaxent are accessible via the user-friendly GUI, ensuring easy access for researchers and conservation practitioners alike.

Session
Species distributions 2

Time:
Friday, 14/June/2024:
3:00pm - 4:00pm

Session Chair: **Manuel Steinbauer**

Location: **SynMikro meeting room**

Marburg Lahnberge Campus -- Zentrum für Synthetische Mikrobiologie Karl-von-Frisch-Str. 14 35032 Marburg

Presentations

3:00pm - 3:20pm

The use of process-explicit models to forecast species distributions

Andrés Lira-Noriega, Lucas A. Fadda, Luis Osorio-Olvera, Luis A. Ibarra-Juárez, Jorge Soberón

Understanding the mechanisms shaping species distributions is crucial for deciphering biodiversity patterns. While correlative models like ecological niche models (ENM) and species distribution models (SDM) have been valuable in predicting potential distributions across various scales, process-explicit models offer a more nuanced understanding of distribution causes, abundance predictions, and dispersal dynamics. These models vary in algorithmic nature and input data requirements. I will discuss the distinctions between correlative and process-explicit models, illustrating with a case study on the invasive ambrosia beetle Xyleborus glabratus, a vector of Raffaelea lauricola causing laurel wilt disease in the southeastern USA. Facing challenges due to lack of demographic data, we developed a process-explicit model in the lab. Our simulations align spatio-temporally with known invasion dynamics and provide superior dispersal estimates compared to correlative approaches. Predictions highlight Mexico's favorable conditions for beetle establishment, particularly in the central west. These findings have implications for agricultural, forestry, and economic decision-making, emphasizing the value of multidisciplinary approaches. I will discuss process-explicit model advantages and limitations, encouraging further exploration in diverse research contexts.

3:20pm - 3:40pm

The key role of vicariance for soil animal biogeography in a biodiversity hotspot region

Xue Pan, Holger Kreft, Jing-Zhong Lu, Yabin Du, Stefen Scheu, Mark Maraun

The extraordinary species richness and endemism of the Indo-Australian Archipelago exists in one of the most geologically dynamic regions of the planet. Application of the biogeographic history and developed processes-based approaches has stimulated an increasing biogeographic work for aboveground animals and plants in this region. But it is basically unknown how the degree of biogeographic isolation may lead to differences in belowground biodiversity. Here, we used geographic distance and beta diversity partitioning to analyze the influence of biogeographic isolation on soil oribatid mite assemblages in eleven regions in the Indo-Australian Archipelago. On average, oribatid mite richness in the eleven regions showed pronounced endemism. The soil oribatid mites' zoogeographic distribution pattern changed gradually from the west and east sides to the central regions, consisted with the combination of Weber's line, Lydekker's line and Holt's line. That dissimilarity pattern, in which species turnover was the most critical driving process, was closely correlated with geographic distance, underlining the importance of biogeographic isolation in soil animal biogeography. Our results, for the first time, elucidate the processes-based soil biodiversity patterns in the Indo-Australian Archipelago and emphasize how long-lasting vicariance structure divergent diversity in this biodiversity hotspot region.

3:40pm - 4:00pm

Intraspecific trait variation of carrion beetle species and communities across elevations

Qiao-Qiao Ji, Zhijing Xie, Yunga Wu, Zhuoma Wan, Caiyi Xu, Donghui Wu, Ting-Wen

Chen, Alejandro Ordonez

Environmental filtering processes are revealed by trait variation in communities, with the community-weighted mean (CWM) being a common metric to indicate optimal adaptive strategy of taxa and directionality of filtering processes. Proximity to CWM indicates of higher fitness, and deviations from this optimal value result in changes in relative abundances of coexisting species. We investigated patterns of intraspecific trait variation in four coexisting carrion beetle (Silphidae) species across elevational gradients in temperate forest ecosystems with distinct natural vegetation zones ranging from 950 m to 1700 m a.s.l.. For seven of the 12 traits, most of the variation was attributed to intraspecific variation. Niche breadth was positively correlated with relative species abundance for most traits. In addition, CWMs of traits associated with long-distance dispersal decreased with elevation, while those associated with microhabitat use showed opposite trends. Soil temperature influenced tibia length after controlling for species identity effects. Nicrophorus quadripunctatus and N. tenuipes supported the CWM-optimality hypothesis for body width and thorax width, while N. maculifrons and N. vespilloides showed an opposite pattern for body width and thorax length. Our study suggests that some functional traits are highly variable, which is likely to help carrion beetles adapt across elevations and vegetation types.

Session

Poster session

Time:
Thursday, 13/June/2024:
3:40pm - 4:10pm

Location: **SynMikro entry hall**

Marburg Lahnberge Campus -- Zentrum für Synthetische Mikrobiologie Karl-von-Frisch-Str. 14 35032 Marburg

Presentations

A cryptic future. Modelling the butterflies Aricia agestis and Aricia artaxerxes under climate change.

Anabel Onay, Christian Hof, Eva Katharina Engelhardt

Under changing climatic conditions, widespread generalists and warm-adapted species may benefit, while specialists and cold-adapted species may decline, with interspecific competition possibly adding to unfavourable conditions. A fascinating example are the cryptic butterfly species Aricia agestis and Airica artaxerxes. Here we investigate the climatic niches of both species to assess competition effects and model probable distributions under future climates. As the multivoltine, generalist A. agestis likely outcompetes the univoltine, more specialized A. artaxerxes, we assessed possible negative effects on the latter by combining both species' projected occurrences in a new framework.

Species' climatic niches indicated that A. artaxerxes was evading direct competition by occurring around the niche edges of A. agestis, which may underline the former being outcompeted by the latter at their climatic optimum. While we projected northward shifts in both species, A. agestis showed an increase in range size but A. artaxerxes' range decreased. Including a possible competition effect only slightly heightened the negative prospects for the latter. Contrary to previous assumptions, the hybridization area may decrease in the future, diminishing the possibility of genetic exchange between the cryptic species.

Our analysis provides a glimpse into the possible future of a complex example of species interactions.

AI4WildLIVE Citizen portal, archive and analytic tool for multimodal monitoring data

Martin Jansen, Maya Beukes, Matthias Biber

Audiovisual methods are increasingly being used in monitoring programmes to observe and describe the loss of biodiversity. There are a variety of methods, including camera traps and acoustic recorders among others, which are being used to record both vertebrates (mammals, birds, amphibians) and invertebrates (insects) in aquatic, terrestrial and marine habitats.

With this technology becoming readily available and easily affordable, it is increaingly being used and thus generates very large amounts of data, which must be archived and processed. Although this task is very time consuming, ideally this would be done almost in real time together with a stream-lined data analysis if possible, in order to develop the basis for instant recommended actions for conservation, society and policy makers.

The AI4WildLIVE project tries to achieve this and aims to bring together data repository, processing infrastructure, citizen science and data analysis multimodal monitoring data in one portal for the first time. We present a first showcase of the portal structure & utility using our own camera trap data collected in Bolivia and South Africa highlighting the different steps of the data archiving, data pre-processing (image classification by citizen scientists & AI) and subsequent geo analysis.

An automated pipeline for assessing leaf-associated interactions and leaf traits

Tobias Müller, Stefan Pinkert, Nina Farwig

Phytophagous insects are closely associated with morphological and metabolic traits of tree species. For the pedunculate oak (Quercus robur) alone, at least 700 species of phytophages are known to affect the health and development of the leaves and, in some cases, can lead to severe leaf loss and tree death.

However, due to the lack of standardized methods for detecting components of tree fitness, the complex spatial and temporal patterns in leaf characteristics and phytophage interactions remain largely unknown.

To address this knowledge gap, we propose a novel approach utilizing imaging techniques and AI-based object detection to automate the assessment of herbivory, leaf-herbivore interactions, and leaf health.

Our automated pipeline aims to overcome current limitations in assessing leaf damage, particularly in leaves with non-entire margins. By applying AI-based object detection techniques, we can accurately identify characteristic damages and quantify herbivore and pathogen damage in a standardized manner. Through comparisons with manipulated test data and human assessed estimates, we will evaluate the accuracy of our methods. The proposed approach will offer a wide range of applications and facilitate a spatially and temporally fine scaled monitoring of plants and associated biota.

Antarctic lichen networks modelled in their environmental space

Anna Götz, Matthias Affenzeller, Lea Maislinger, Wolfgang Trutschnig, Mischa Andreev, Roman Türk, Robert Junker, Ulrike Ruprecht

In the climatically harsh areas of Antarctica and the subantarctic areas of southern South America crustose, saxicolous, lecideoid lichens establish a dominant vegetation-form. They form a symbiosis of fungal (mycobiont) and algal (photobiont) partners. It is now widely assumed that the photobiont is primarily determining the climatic niche for the whole lichen organism. Mycobiont species vary in their capability to associate with either one or more photobionts. Therefore, they differ in their ability to extend their climatic niche by a more generalist selection of photobionts.

In this study, we present a circum Antarctic dataset consisting of 662 samples of lecideoid lichens focussing on their associated dominant myco- and photobionts covering a habitat range from the 41°S to the 86°S latitude. We investigated how symbiotic associations between myco-and photobionts are mediated by climatic factors and in which extent the associations are changing in their environmental space along time. Furthermore, we aimed to model past symbiont switches and accompanied niche change based on the phylogenetic relationship of the fungal symbiont. With this approach conclusions can be drawn to what extent symbiotic networks change in their interconnectedness and how the degree of generalization may be an advantageous adaptation to a rapidly changing climate.

Automated ecological data extraction using machine learning-based language models

Selwyn Hoeks, Maarten J. E. Broekman, Marlee A. Tucker

In the field of ecology, scientific literature is a key data source that is vital for generating insights and testing theories across ecological systems. For example, large ecological databases like TRY, FishBase, Compadre or TetraDENSITY are commonly used. The extraction of new data from literature is tedious and time consuming as it often requires researchers to manually process thousands of articles. This hampers our ability to get the most out of existing data and makes it difficult to keep databases up to date. Methods available for text mining are rapidly evolving because of developments in machine learning-based language models. Here we assess the use of a natural language processing framework to parse computable trait data from scientific literature. To optimize and validate the framework, we will use a case study on the automated collection of mammalian home-range values based on the recently published HomeRange database. We will compare the home-range values from the automated data collection with manually collected values to evaluate the accuracy of the framework. Our ultimate goal is to have an automated workflow that can be applied to various ecological fields and will result in robust datasets that can be used to advance of ecological understanding.

BIOfid: accelerating biodiversity research through text mining

Pedro Henrique Dias, Martha Kandziora, Thomas Schmitt, Gerwin Kasperek, Katrin Peikert, Carlos Alberto Martinez Muñoz, Kevin Bönisch, Manuel Stoeckel, Mevlüt Bagci, Alexander Mehler, Thomas Hickler

We are currently facing a global-scale biodiversity crisis, with accelerating rates of extinction, habitat degradation, and ecosystem disruption. Notwithstanding, the recent past of many organisms is poorly known, especially when the available information is fragmented and scattered in old literature. This source of information is often neglected in research as extracting the information is rather time-consuming, e.g. due to language barriers, library or copyright restrictions and the sheer number of existing documents. Technological advances, such as optical character recognition, natural language processing and artificial intelligence can facilitate the acquisition of information hidden in text sources. Here, we present the Specialised Information Service for Biodiversity Research (BIOfid; https://www.biofid.de) which was launched to increase availability, accessibility and usability of contemporary and historic biodiversity information, with a focus on Central Europe. BIOfid helps to find information from historical biodiversity literature through innovative text mining tools based on large language models. BIOfid`s semantic search technology is backed up by taxonomical, morphological, and ecological ontologies. Our tool is currently evaluated for how well we can acquire information on biotic interactions and functional traits. It improves data extraction, knowledge discovery, and ecological monitoring for a better understanding of the past, present, and future of biodiversity.

Burrowing facilitated the distributional success of mammals and imposes contrasting responses to climatic stability

Stefan Pinkert, Lena Krug, Victoria Reuber, Lea Heidrich, Finn Rehling, Nina Farwig, Roland Brandl

Species' ability to cope with climatic instability varies greatly, influenced by factors like dispersal, physiological adaptations, and phylogenetic conservatism. Here, we investigate how burrowing behaviour – a key component of species' endurance strategies and ecosystem functioning – shaped the distributional expansion and diversification of mammalian lineages. Analysing 4,407 terrestrial mammal species and novel trait data on 3,096 species, we reveal distinct responses to climatic factors between burrowing and non-burrowing species. Burrowing lineages are disproportionately species-rich at lower temperatures and productivity levels. Both range size and species richness steeply increase with climate seasonality in burrowing species, as opposed to non-burrowing species. Constituting 47% of all terrestrial vertebrates, the proportion of burrowing species increases latitudinally, and particularly regions with greater Pleistocene temperature changes are almost exclusively composed of burrowing species. Trait conservatism, higher diversification rates, and Eocene peak diversification provide the evolutionary context to these contemporary gradients, underscoring the role of burrowing for mammalian radiations into cold-temperate climates. Our study highlights the potential of readily available behavioural information in improving forecasts of species' responses to climatic changes, and showcases divergences of broad importance for targeted conservation efforts.

Calcareous grasslands and scrubs in Southern Europe: broad-scale plot-based typology and distribution patterns

Denys Vynokurov, Idoia Biurrun, Juan Antonio Campos, Javier Loidi, Itziar García-Mijangos

Southern Europe, characterized by the convergence of several biogeographical regions and diverse climates, hosts diverse vegetation types. Understanding their typology and distribution is crucial for biodiversity conservation and ecosystem management.

Utilizing data from the European Vegetation Archive (27,511 plots, 7,389 taxa), we applied the TWINSPAN algorithm to classify vegetation into broad types: alpine and subalpine grasslands, xeric and meso-xeric grasslands, rocky grasslands and low scrub, subalpine low scrub of Eastern Mediterranean, Anatolian scrub, Western-Mediterranean garrigue, Eastern-Mediterranean garrigue, and herbaceous Mediterranean grasslands.

Our analysis revealed significant correlations between vegetation composition, climatic parameters, and environmental factors. Vegetation distribution primarily followed a gradient from cooler, mesic conditions at higher elevations to drier, xeric environments at lower elevations. Distinct patterns were observed between Western and Eastern Mediterranean regions. Furthermore, shifts in plant life forms were observed, with hemicryptophytes favouring mesic conditions at higher altitudes, chamaephytes preferring warmer and drier climates, and therophytes more common in areas with greater continentality.

Our research provides valuable insights for revising habitat and vegetation classification systems and developing effective conservation and management strategies. These findings contribute to the broader understanding of biodiversity patterns and their underlying drivers in Southern Europe.

Does mapping transitions between spectral communities reflect ecological reality?

Vincent Wilkens

Understanding global patterns of species richness requires reliable mapping of the composition, steepness, and extent of ecological gradients. Existing paradigms for land-cover classification of remote sensing imagery tend to favor sharp boundaries between biogeographical units, whereas gradients would better reflect reality. Consequently, transition zones are rarely considered when mapping habitats, ecosystems, or biomes. However, research suggests that these transition zones, also known as ecotones, could be centers of biodiversity and drivers of speciation. Therefore, reliable mapping and monitoring of ecotones across large spatial scales is a prerequisite to developing effective conservation strategies for these biodiversity hotspots, especially in the face of climate change-induced range shifts. Spectral communities, based on the spectral species concept, could offer a reliable method for mapping ecotones. With the recent availability of medium-resolution (30 m) hyperspectral satellite imagery (EnMAP), differentiating between even the most visually-similar ecosystems, such as laurel forest and fayal-brezal on the Canary Islands, becomes feasible. Using a global dataset of island and continental ecotones, we test the reliability of the spectral communities algorithm in mapping ecotones by comparing spectral gradients to both climatic (e.g. temperature and precipitation), topographic (e.g. elevation, aspect, slope), and biotic (e.g. species and traits) data.

Enhancing Plant Phenological Monitoring Through Automated Annotation of Opportunistic Observations

Negin Katal, Michael Rzanny, Patrick Mäder, Hans Christian Wittich, David Boho, Jana Wäldchen

Plant phenology, examining key life cycle events such as budburst, flowering, fruiting, and senescence, provides valuable insights into environmental responses. However, documenting these events across vast spatial and temporal scales presents ongoing challenges.

While global phenological networks collect individual-scale data, a decline in observers threatens these datasets. Conversely, plant identification apps collect abundant occurrence data with time stamps and images across large spatial scales. To derive nuanced phenological stages from these records efficient annotation methods are essential which ultimately allow harnessing this data for phenological monitoring.

This study aims to automate phenological stage annotation of images obtained from opportunistic plant observations. We extract deep features from annotated plant images using the Flora Incognita neural network to train a Support Vector Machine (SVM). Subsequently, the model will annotate a large corpus of images according to various phenological stages.

Furthermore, we used the day of year of each image to employ a predictive model to estimate the timing of several phenological stages based on geolocation and elevation. This enables the automatic linkage of observation data to respective phenological stages, facilitating phenological monitoring. Subsequently, we compare the opportunistic data with systematic records over multiple years and phenological stages.

Exploring Regional Insect Trends: A Macroecological Approach

Christian Zehner, Eva Katharina engelhardt, Christian Hof

Biodiversity loss is a main driver of global change and “insect decline” one if its current hot topics. Despite numerous studies, a clear identification of the causes and their relative importance, as well as regional variation and the effect of habitat protection measures, is hard to get. While there are many studies on very large or very small areas facing these topics, few address actionable spatial units and long-term trends for various insect species.

My doctoral project will narrow this gap. Utilizing a long-term dataset (> 30 years) from a governmental insect monitoring program in the state of Bavaria, Germany, I will employ spatially explicit occupancy modeling to (1) capture regionally diverse trends on insect species level. Further, I will (2) explain these insect trends with habitat variables such as remote sensing-based land coverage, climate data, and management tools like protected areas.

By understanding the influence of these habitat variables, (3) future insect trends can be modelled, using existing land cover and climate models. The insights gained from this research not only advance the use of spatial occupancy models for biodiversity research methodologically but also provide crucial insights for practical conservation efforts at the regional level.

Forgotten biodiversity - distribution and ecology of Orchidaceae in Madagascar’s open

ecosystems

Jakub D. Wieczorkowski, Landy R. Rajaovelona, Alexander Zizka, Caroline E.R. Lehmann

Orchids constitute nearly 10% of Madagascar’s plant diversity but the majority of species may be threatened with extinction. Commonly, they would be often associated with forests rather than with open ecosystems, which happen to be significantly under-protected. Here, we conducted a review of all orchid species in Madagascar and assigned their ecosystem types as closed (forest) or open (grassland, marsh, savanna, Tapia woodland, ericaceous scrub, and rocky outcrop) using herbarium specimens, online biodiversity databases and taxonomic literature. We find that even up to 30% of species can be found in open ecosystems, and 15% of species are found there exclusively. We also assess the bioregionalisation patterns across the island which point to the spatial differences in the distribution of closed vs open ecosystem specialists. Finally, using data on species flowering times, we provide a direction for sampling efforts inclusive of the species phenology and past spatial bias. The results highlight Madagascar’s open-ecosystem orchids as a distinct but underappreciated source of biodiversity and demonstrate that conservation efforts should expand beyond the Madagascan forests.

Global biogeography of bat-associated viruses

Simon Biedermann, Anna Walentowitz, Nicolai Nürk, Stephanie Thomas, Carl Beierkuhnlein

Bats (Chiroptera) are one of the most species-rich orders of mammals and harbour a highly diverse virome. Some bat-associated viruses have spilled over to humans, livestock, and other mammals, causing zoonotic diseases. However, a comprehensive overview on the diversity and biogeography of bat-associated viruses is missing, but highly relevant for Planetary Health. Here, we provide a biogeographic overview of global hotspots and biogeographic patterns of bat-associated virus richness in relation to biomes and continents. Publicly available data on bat-associated viruses was combined with data on global bat distribution to identify hotspots and biogeographic patterns of bat-associated virus richness. These patterns were linked to biomes and continents to detect underlying drivers. In general, bat-associated virus richness increases from the poles to the equator, following bat species α-diversity. Southeast Asia, tropical Africa and Central America form distinct hotspots of bat-associated virus richness. Biogeographic patterns for virus families differed. Biomes and continents as potential underlying drivers only explain a low amount of the observed variance. However, these hotspots need to be considered with caution due to biases and knowledge gaps especially in tropical regions. Future research efforts are needed to sharpen our understanding of the bat virome and to identify areas at risk.

Global hotspots of butterfly diversity in a warming world

Stefan Pinkert, Nina Farwig, Akito Kawahara, Walter Jetz

Insects and their key ecosystem functions are in decline, but the distribution of global insect diversity and its threats from climate change remain little understood. Butterflies have the potential to serve as global insect model system given their ecological importance and extensive data. Here we show that tropical and sub-tropical mountain regions emerge as centers of butterfly richness, rarity, and phylogenetic diversity and that the geographically restricted temperature conditions underpinning these hotspots make them highly exposed to projected global warming. Integrating comprehensive phylogenetic and range data for 12,119 butterfly species, we find that while mountains only cover 38% of the Earth’s surface at our grain, butterfly hotspots are 3.5 times more likely to be located in mountains than in lowlands. Hotspots of butterfly diversity face more severe impacts of global warming than non-hotspots, with as much as 64% projected niche loss in tropical realms until the year 2070. However, only 14%-54% of the realm-level richness and rarity hotspots (top 5%) in butterflies overlap with current vertebrate-based conservation priorities. Our study identifies critical conservation needs for butterflies and illustrates how the consideration of at least select global insect systems is key for gaging biodiversity loss in a rapidly warming world.

Global patterns of and biotic and abiotic factors affecting specialised metabolites

Maximilian Hanusch, Robert R. Junker

The availability of trait databases enabled global analyses on the distribution and variation of trait values and the biotic and abiotic factors influencing them. In contrast to morphological trait values and their intraspecific variability, the distribution and responses of chemical traits to biotic and abiotic factors have been less well explored on global scales considering multiple species. However, the few global analyses on the distribution and variation in plant specialised metabolites show clear trends. Previous analyses showed that the plants’ metabolism responds to various environmental parameters including temperature, precipitation, CO2 levels and nitrogen levels. For floral scents, clear effects of environmental parameters have been found. Thus, analyses on and the assessment of global trends in the chemical phenotype of plants revealed general patterns and rules advancing the understanding of the ecology of plant metabolomes. However, chemodiversity, which is the richness, evenness, and disparity within plant metabolites, has not been considered in similar studies and basic information on the factors affecting chemodiversity is still lacking. Based on a well-documented literature survey, we aim to conduct a global analysis based on published data on the global distribution of plant chemodiversity and the biotic and abiotic factors influencing it.

Nature in a mesh: common problems with gridded biodiversity data, and proposed solutions

Petr Keil, Florencia Grattarola, Francois Leroy, Gabriel Ortega Solis, Carmen Soria, Friederike Wölke

Gridded biodiversity data (e.g. country-level or regional atlases) play a prominent role in macroecology, particularly in the study of patterns of species occupancy, geographic ranges, biodiversity, and their drivers and temporal dynamics. However, managing, exploring, and analyzing data in grids comes with problems.

We have reviewed the problems with gridded data, and the existing solutions. We identify problems of sampling (e.g. varying sampling method and effort in space and time, imperfect detection), geometry (e.g. varying grid cell area and shape, positional errors), taxonomy (e.g. misidentification, taxonomic splits and merges), and scale (e.g. unspecified or varying spatial and temporal grain).

The first type of solutions happens prior to gridding of the data; this includes selection of geographic projection, grain, and grid cell shape. The second type of solutions involves manipulation of the gridded data; examples are aggregation of cells to coarser grains or cell filtering. Third type of solutions is done during data analysis, usually by representing the problem by a covariate in statistical models. We hope to provide guidance particularly to early career biogeographers and macroecolgists who may otherwise struggle to make sense of the various solutions scattered through the literature.

Only the tough are good enough - Evidence for selection towards insular woodiness on ancient tephra fields

Simon Biedermann, Anna Hollweg, Anna-Maria Seiverth, Nicolai Nürk, Alessandro Chiarucci, Carl Beierkuhnlein

Secondary woodiness that originates on oceanic islands, insular woodiness, is a remarkable island syndrome that evolved independently throughout the angiosperm tree of life. One of several hypotheses explaining this phenomenon states that burial of vegetation through tephra from volcanic activities on the island is a selecting driver towards insular woodiness. However, there is currently no conclusive evidence for this hypothesis.

Here, we test the role of volcanic tephra deposits as a driver for insular woodiness by analysing vegetation patters and plant functional traits related to three craters that erupted in historic times (75 a, 378 a, and 5 ka) on the island of La Palma.

Vegetation on lapilli fields is dominated by secondary woody and archipelago-endemic woody species, with younger tephra fields highly dominated by secondary woody species and older fields more dominated by ancestral woody species. Furthermore, the functional trait space seems constraint in lapilli vegetation in comparison to pine forest in the same elevation range. These observed patterns indicate potential abiotic filtering of tephra burial towards (insular) woody species and their traits. Our results thus provide the first empirical evidence for the “volcanic selection” hypothesis of insular woodiness.

Patterns of spatial autocorrelation for species distributions and diversity across time and spatial scales

Carmen D. Soria, Gabriel R. Ortega Solís, Vojtěch Barták, Friederike J. R. Wölke, Mutsuyuki Ueta, Karel Šťastný, Vladimír Bejček, Ivan Mikuláš, Petr Voříšek, Petr Keil

Understanding biodiversity change across spatial scales is crucial in the Anthropocene. While existing analyses primarily focus on species range size (i.e. occupancy), spatial structure remains understudied. Spatial structure, indicating the degree of clustering or dispersion in distributions, can be quantified through spatial autocorrelation. This metric, influenced by endogenous (dispersal, demographic) and exogenous (environmental, climatic) processes operating at different spatial scales, can help identify species threatened by population isolation and separation.

Here, we explore spatial autocorrelation patterns of bird distributions across the Northern Hemisphere over time and spatial scales, using data from temporally replicated Breeding Bird Atlases. We computed multiple measures of spatial autocorrelation, including global Moran’s I and Join-counts, for both species’ distributions and richness at different grain sizes and analysed their trends over time and spatial scales. We observed a consistent decrease in autocorrelation with increasing spatial scale across all study areas and periods. Notably, there was no discernible temporal trend in the average spatial autocorrelation of species distributions or richness. Our analyses revealed that temporal trends in spatial autocorrelation were independent of occupancy, highlighting the distinctiveness of range size and structure and the importance of studying both.

Phenotypic and genetic variation within the barley Hordeum murinum across Europe.

Helene Villhauer, Timo Hellwig, Sandy Jan Labarosa, Laura Libera, Ann-Sophie Schmitt, Maria von Korff Schmising, Anna Bucharova

Intraspecific genetic variation between plant populations is common and can reflect local adaptation. Understanding the phenotypic and genetic variation along a geographical gradient is crucial for predicting a species’ adaptive ability and assessing its vulnerability to climate change.

In this ongoing project, we study genetic variation in Hordeum murinum, a common wild annual with different ploidy levels. We combine common garden experiments with genetic tools to identify adaptive variation and its underlying genetic regions.

In 2023 in collaboration with researchers from Europe, we scored H. murinum in wild across Europe to define its ecological niche and collected seeds. H. murinum grew in a wide range of environments and plants were larger in wetter and colder areas. In a preliminary common garden, we found significant phenotypic differentiation between populations in root traits and an increase in the root to shoot ratio in populations originating from warmer sites. The preliminary results from this year’s common garden experiment indicate that plants from warmer and drier areas flowered earlier than plants from colder regions.

Quartz Islands II - Cross-scale determinants of plant diversity and endemism in quartz island archipelagos in southern Africa

Alexander M. Bürger, Pia M. Eibes, Katharina Meyer, Jens Oldeland, Ute Schmiedel, Severin D.H. Irl

Quartzite sites in southern Africa can be considered as terrestrial habitat islands due to their distinct environmental conditions, well-defined boundaries, and unique vegetation hosting a high number of endemic species. These quartzite islands are scattered across various regions of southern Africa, spanning different biomes such as Succulent Karoo, Nama Karoo, and Fynbos, across a wide bioclimatic spectrum. Thus, they present a promising subject for investigating key aspects of island biogeography and ecological dynamics on different spatial scales. This newly funded project aims to investigate and compare six spatially distinct island systems, regarded as archipelagos, located along a broad bioclimatic gradient with different precipitation regimes. For each archipelago, an extensive species survey will be conducted alongside the establishment of a functional trait database encompassing the majority of perennial plants inhabiting quartz islands. The study will be conducted at different spatial scales. At the island scale we will elucidate the influence of island biogeographic drivers on taxonomic diversity, functional diversity and endemism. Additionally, we will test the effect of regional climate on the expression of traits at the archipelago scale. Finally, we will perform a macroecological analysis of the quartz island flora in southern Africa.

Subsampling plants to assess biodiversity patterns

Ludwig Baldaszti, Samuel Pironon, Neil Brummitt, Peter Moonlight, Tiina Särkinen

More than 40% of the world’s plant species are rare and threatened by extinction. While destruction of the natural world has accelerated dramatically over the past decades, our knowledge of global plant biodiversity patterns has not increased at similar rates. As our understanding of plant biodiversity remains incomplete, all global studies of plant diversity patterns are based upon subset of species. Digitally available plant data suffers, however, from strong biases which severely distort our view of global diversity patterns.

In our study, we aim to better estimate plant diversity patterns from incomplete data by determining the number of species needed to accurately represent plant diversity distribution patterns at a global scale using the World Checklist of Vascular Plants as a baseline. We use the information available to determine how well datasets such as the IUCN Red List of Threatened Species and openly available plant occurrence data (GBIF) represent different dimensions of plant biodiversity such as species, taxonomic, phylogenetic, and functional diversity. The results have important implications for macroecology and conservation.

The effect of small stream restoration on terrestrial biota

Lena Lerbs, Anna Dotzert, Sven Portig, Sascha Liepelt, Stefan Pinkert, Anna Bucharova

Stream restoration projects aim to improve water retention in the landscape and increase the ecological value of water bodies around the globe. In Europe, most restoration projects take place on small streams, yet the ecological benefits of such projects are poorly documented. This study focuses on the effects of small stream restoration on terrestrial biota, in particular plants, insects, and birds, as they provide important ecosystem services and have high conservation value. We compare 50 restored small stream sections in Hesse, Germany, with adjacent non-restored sections, using plant and bird surveys and malaise traps with DNA metabarcoding for insect identification. In preliminary field work, we found a significant increase in wetland plants and an increase in bird diversity and abundance in restored sites. With this ongoing study, we now aim to determine the value of different restoration measures across trophic levels. Findings will contribute to increase the ecological value of future restoration projects.

Towards predicting temporal biodiversity changes from static patterns

Friederike J. R. Wölke, Carmen D. Soria, Gabriel R. Ortega Solís, Mutsuyuki Ueta, Karel Šťastný, Vladimír Bejček, Ivan Mikuláš, Petr Keil

The world is undergoing significant environmental transformations, impacting biodiversity and ecosystem functions. Yet, obtaining temporal biodiversity data is challenging due to cost and monitoring limitations. To address this, we aimed to develop a machine-learning model that infers temporal trends of species’ occupancy without requiring temporally replicated data.

The approach involved analyzing static snapshots of species spatial distributions and their covariates to infer temporal change in occupancy for temperate breeding birds in the Czech Republic, Japan, New York state, and the whole Europe (N = 841 species). Although static patterns are only partially able to predict temporal change, we found that the predictive strength of static patterns is lower when predicting past change as compared to future change. Interestingly, geometric constraints of the study area and the species distribution explain a high proportion of the predicted change in occupancy.

Our results suggests that the importance of processes that drive change in species spatial distributions through time does not stay constant, and that characteristics of the study area, such as shape and size may determine the amount of change that can be predicted from data.

Training and Interpreting Deep Neural Networks with the cito R Package

Maximilian Pichler, Florian Hartig

cito is an easy-to-use R package for deep learning that allows users to build neural networks using the familiar formula syntax of many other R packages. Yet, cito allows flexible modification of network architecture and hyperparameters, allowing users to test and apply most deep learning techniques without having to focus on coding. In addition, cito includes many user-friendly functions for model interpretation based on explicable AI and additional features such as confidence intervals (p-values). We explain how to extract effects (similar to linear effects from regression models) and variable importance (similar to ANOVA) from the fitted DNN and how to interpret these effects. Finally, we will show how cito can be used to fit CNNs for image classification and regression.

VAT: Bridging GIS, AI, and FAIR Data for Biodiversity Research

Henri Dümpelmann, Bernhard Seeger, Frank Förster, Dominik Brandenstein

VAT is a web-based GIS system that offers an interactive and intuitive way to visualize, analyze, and transform spatio-temporal data in NFDI4Biodiversity to serve the biodiversity community. In this workshop, we present a novel VAT workflow for joining spatio-temporal thematic environmental raster data with spatio-temporal species occurrence data from GBIF. The workflow shows the unique features of VAT exploring spatio-temporal data and deriving advanced FAIR data products. Through its seamless connectivity to Jupyter Notebooks, VAT also takes advantage of Jupyter's powerful AI offerings. In addition, VAT, with its docker container-based implementation, is one of the fully integrated critical services in the RDC, the cloud-based research infrastructure of NFDI4Biodiversity. This enables VAT to manage large amounts of data in the underlying object storage ARUNA and to offer outputs of its workflows as new FAIR data products. Overall, this showcases the synergetic value of the RDC with all its interconnected components like VAT and ARUNA.

Comparative phylogeography of Himalopsyche (Trichoptera, Rhyacophilidae) in the Tibeto-Himalayan Region: An assessment of the mountain-geobiodiversity hypothesis

Xiling Deng, Sami Domisch, Steffen Pauls

The “mountain-geobiodiversity hypothesis” explores the interaction of topography, climate, and biology in the evolution of mountain biodiversity. We tested this hypothesis in the Himalayas and the Hengduan Mountains on a group of local caddisfly species. We investigated one caddisfly species pair from each mountain respectively, each pair containing one species inhabiting high elevation and one inhabiting low elevation. We incorporated genomic and ecological evidence to reveal population structure, demographic history, and potential habitat range at present and during the last glacial maximum. The results indicated that the high-elevation species showed strong local differentiation, while the low-elevation species were shaped by hydro-morphology. Caddisfly species in the Himalayas generally exhibited an East-West oriented dispersal, while species from the Hengduan Mountains showed greater connectivity on the North-South orientation. Results of demographic history and species distribution modelling demonstrated that a cold climate leads to an increase in potential habitats, thus causing population expansion. Moreover, most of the divergence and admixture events aligned with the climatic cycles from the middle Pleistocene until the present, suggesting a species-pump effect. Our study demonstrates that mountain topography and climate fluctuations interact and influence the diversification of caddisflies differently in the Himalayas and Hengduan Mountains, thus supporting the hypothesis.

Using global vegetation data and remote sensing to identify groundwater-dependent vegetation

Léonard El-Hokayem, Gabriella Damasceno, Helge Bruehlheide, Francesco Maria Sabatini, Christopher Conrad

Groundwater-dependent vegetation (GDV) is an important global biodiversity hotspot facing threats from climate and land-use change, requiring large-scale mapping efforts. A novel medium-resolution mapping approach is presented that aims to identify GDV in the Mediterranean biome using global plant community data (sPlot) and remote sensing.

Approximately 31,000 vegetation plots have been extracted from ‘sPlot - The Global Vegetation Database’. An expert system is being built to evaluate plots likely to represent GDV based on functional species groups. Lists of species were compiled regarding phreatophyte coverage, moisture values or climatic parameters. These lists will be used to extract species compositions indicative of GDV and to classify vegetation plots accordingly.

The remote sensing approach implements criteria aimed at 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) derived from Sentinel2 and SRTM. The reclassified vegetation plots will be used to train machine learning algorithms for the pixel-wise classification of GDV in the Mediterranean biome.

Species compositions indicative of GDV would support identification in the field. Furthermore, detailed maps of GDV will ensure sustainable groundwater management and thus protect GDV as local biodiversity hotspots.

Understanding the Impact of small-range species extinctions on biodiversity across biomes

Beatriz Prado-Monteiro, Tabea Giese, Wassila Ibrahim Seidou, Aboubacar Oumar Zon, Julius Köhler, Andressa Cabral, Miguel Inácio, Stefan Porembski, Luiz Bondi

It is observed an alarming trend of declines on biodiversity globally due to anthropogenic activities. However, those activities impact ecosystems and biomes differently and as a consequence, some species could be more threatened than others. It is known that small-range species are disproportionately more threatened, due to their expected lower tolerance to environmental changes and lower capacity to move to new suitable locations. In this study, we aim to estimate the impact of the loss of small-range species on biodiversity using desiccation-tolerant plants as model species. We performed sequential extinction simulations, from the small-range to broad-range species, to estimate decreases in phylogenetic diversity in all world biomes. The contribution of small-range species varied across taxonomic groups and biomes. Overall, the loss of small-range Pteridophytes was similar to the loss of broad-range species. Conversely, the impact of the loss of small-range Angiosperms was critical in three world biomes, such as tropical and subtropical moist broadleaf forests. Our findings suggest prioritizing small-range species from these biomes for conservation. Nevertheless, we also recognize the importance of assessing and monitoring small-range species from other biomes, since the loss of phylogenetically more redundant species reduces the options for the maintenance of ecosystem function and services.

Rethinking the relationship between desiccation-tolerant vascular plants and water deficit

Luiz Bondi, Beatriz Prado-Monteiro, Luiza F. A. de Paula, Bruno H. P. Rosado, Stefan Porembski

Water deficit is one of the main drivers of plant mortality and is projected to be more critical owing to climate change. Because desiccation-tolerant vascular plants (DT plants) can cope with water deficit, a paradigm emerges associating those species to locations characterized by water deficit conditions. However, this paradigm is not supported by earlier studies, hampering our understanding of the species–environment relationships and the vulnerability of DT plants to climate change. Here, we tested this paradigm and provide an evaluation of the vulnerability of DT plants to climate change. We estimated the diversity and distribution of DT plants along water deficit gradients and assessed species vulnerability to climate change from a climatic perspective and over broad phylogenetic and macroecological scales. We found that the diversity and distribution of DT plants were neither associated with, nor restricted to, locations characterized by water deficits. Our findings suggest that the desiccation events DT plants undergo are rather promoted by topo-edaphic conditions than by climate, reinforcing the need for studies that investigate processes that operates across different scales. Moreover, species with narrow niche breadth might be the most vulnerable to climate change, we suggesting that ecologically restricted species should be prioritized for conservation.

The centers of diversity and endemism for desiccation-tolerant vascular plants in Africa.

Wassila Ibrahim Seidou, Luiz Bondi, Stefan Porembski, Edson Lezin Bomisso

Biodiversity is threatened worldwide by anthropogenic activities, and the identification of relevant areas for biodiversity is highly valuable to cope with cost-benefits trade-offs in conservation efforts. Such information is highly desired in the African continent. Therefore, we attempted to identify the African centers of diversity and endemism for desiccation-tolerant plants, a group of plants with a remarkable response to drought and largely neglected for conservation. For that, we compile a list of all known vascular species that occur in Africa and estimated the taxonomic and phylogenetic diversity, besides endemism richness and phylogenetic endemism, from a niche and spatial perspectives. We identified Southern Africa (e.g., Eastern highlands and the Great Escarpment) and the Eastern regions of the continent (e.g., East African Rift – Eastern Highlands – Drakensberg), as well as in Madagascar (e.g., Central Highlands) as centers of diversity for this continent. Our findings reveal priority areas for the diversity conservation in 19 different ecoregions of 3 biomes. However, we should not neglect regions rich in endemic species. Those areas covered 32 ecoregions of 4 biomes, extending the need for attention and monitoring in other regions like Ethiopian parts of East African Rift, Namibian Khomas Hochland, and in the Mascarene Islands.

Automated Red List Assessment Provides Efficient but Optimistic Estimates of Plant Species Extinction Risk in Germany

Hannah Spieker, Alexander Zizka

Automated Red List assessments (AA) are rapidly developing approach to support extinction risk assessments. A major strength of AA is that they can speed up the time-consuming Red Listing process by helping experts to identify species for prioritisation and thereby mitigate a sever bottleneck for conservation practice . However, it is unclear how accurate AA reproduce expert-based Red Lists and for which species they can be applied reliably. Here, we present the results of an AA for Germany based on modelled distributions of 2,136 plant species at three time slices. Based on the modelled species ranges and changes in occurrence probability among time slices, we approximate indicators for three official Red List criteria (current population status, short-term trend, and long-term trend), which we then automatically combine into extinction risk assessments. Overall our AA agreed well with the expert-based Red List for Germany, with an average difference of only one category. In general, the automated Red List was more optimistic (suggesting lower extinction risk), although with some variation related to region and extinction risk category. Our results suggest, that AA can provide a reliable data-driven baseline to support expert Red Listing, in particular for species with medium to large distribution ranges.