ABSTRACTS

THE INTERNATIONAL BIOGEOGRAPHY SOCIETY

12th Biennial conference

Aarhus, Denmark, January 2026

AARHUS UNIVERSITY

THE INTERNATIONAL BIOGEOGRAPHY SOCIETY

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AWARD PRESENTATIONS

1. Reflections on the evolution of historical biogeography

Michael Donoghue, *Yale University, New Haven, United States*

The grand aims of historical biogeography are to infer where species originated, when and how they moved around, how this influenced diversification, and how all of this relates to underlying biological, geological, and climatological factors. There have been major changes over time with respect to analytical approaches and interpretation, especially with the advent of evolutionary thinking, of continental drift, and of phylogenetic biology. The greatest progress over the past several decades has been in reconstructing biogeographical events on phylogenetic trees for individual clades. With the dramatically increased availability of relevant environmental data, progress has also been made in inferring ancestral environments and biome occupancy through time. I will highlight advances in this area with examples of the incorporation of information on the distribution of biomes in the past, on the sizes and distances between area, and on organismal information related to fundamental niches. As this work continues, we need to also focus on identifying general biogeographic patterns across multiple clades and their underlying causes. As illustrations of progress in this area, I will highlight studies of the latitudinal diversity gradient and of Laurasian biogeography through the Cenozoic. Finally, I will touch briefly on other promising areas, including the integration of historical biogeography into studies of co-evolution and community ecology.

2. Anomalies and Alchemists in the Geography of Life

Mark V. Lomolino, *State University of New York, Syracuse, United States*

This award is a humbling honor, but more than that, especially in this perhaps uniquely integrative field, I view it as a tribute and homage to the many visionary scientists and colleagues that have inspired and guided me throughout my career. Here I attempt to provide a brief, albeit woefully incomplete summary of the prescient scientists that have nurtured and expanded my visions far beyond what I could achieve alone. I then illustrate how, by following their advice and focusing, not just on general trends but on the anomalies of nature, we can often provide key insights into the forces driving some of the most intriguing patterns in the geography of life.

3. The geography of plant life

Barnabas Daru, *Stanford University, Stanford, United States*

An open challenge in biology is to elucidate the mechanisms by which plant diversity is generated, distributed, and maintained. My team addresses this question through four aims.

First, studying biodiversity requires understanding the evolutionary processes behind modern-day plant diversity patterns. My research shows these patterns are shaped primarily by in-situ speciation, with dispersal connecting regions and extinction playing a minor role. I also found geographical biases in plant occurrence data, which distort true diversity patterns. Second, to address these sampling biases, I applied informatics approaches to generate high-resolution native range maps for ~200,000 plant species worldwide. This dataset revealed how species introductions and native extirpations are homogenizing plant communities in the Anthropocene. Third, to overcome analytical challenges, I developed phyloregion, an open-source R package for biogeographical and macroecological analyses. It is now used in biodiversity assessments by conservation organizations and taught in workshops across four countries. Going forward, I will build on this work by leveraging herbarium specimens as untapped sources of functional traits to explore shifting functional biogeography across ecological scales, identifying mechanisms driving community changes underlying ecosystem shifts. In parallel, I will focus on seagrasses, the only flowering plants to secondarily transition to sea during early monocot evolution. This research will investigate the evolutionary adaptations and structural changes required for survival in saline marine environments. Ultimately, I aim to support conservation and inclusive stewardship in both biosphere and ocean ecosystems so that our understanding of nature leads to meaningful societal and policy impact.

4. Applied primate biogeography: from the role of geographic barriers to implications for the human health

Alisa Aliaga Samanez, *The Spanish National Research Council, Spain*

The distribution of species is being reconfigured by deforestation, climate change, and human activity, with profound consequences for both biodiversity conservation and global health. In this dissertation, I address these challenges by integrating cutting-edge biogeographical methods with conservation science and human health. Throughout my thesis, non-human primates serve as a unifying thread, providing a unique perspective to explore the spatiotemporal dynamics of species distributions, the effects of anthropogenic pressures, and the mechanisms of infectious disease transmission. The first chapter introduces an innovative methodology for incorporating historical dispersal barriers into species distribution models, improving predictive accuracy. The second chapter evaluates the impacts of deforestation, poaching, and forest fires on primate distributions in protected areas, offering insights for conservation management. Subsequent chapters investigate geographical changes in zoonotic transmission risk, incorporating the potential role of primate and sylvatic vector biogeography in the increased global risk of dengue and yellow fever transmission. The final chapter examines the effects of climate change on the future distribution of urban and sylvatic vectors, highlighting how interactions with primate reservoirs may shape transmission dynamics and identifying emerging zones critical for

proactive surveillance. In summary, my thesis demonstrates how biogeographical approaches can be applied to urgent global challenges, from species conservation to disease prevention. Its focus ranges from local ecological models to global analyses, highlighting the scalability of biogeographical methods. By integrating disease dynamics, my research reinforces the need to understand spatial transmission patterns in a rapidly changing world, offering innovative tools for biodiversity conservation and public health.

SYMPOSIUM PRESENTATIONS

Symposium: Quantitative paleoecology in the era of big data: Trends, challenges, and opportunities

Organizers: Suzette Flantua, University of Bergen, Oscar Wilson, University of Helsinki, Michelle Lawing (Texas A&M University), Leila Siciliano-Martina (Texas State U.), and Maria Alejandra Hurtado Materon (Texas A&M University)

Framework and background

Quantitative paleoecology has advanced substantially with the development of new statistical tools, computational capacities, and large datasets. This symposium focuses on how quantitative approaches reshape our ability to reconstruct past environments and biogeography, detect ecological thresholds, and understand ecological dynamics on various scales. Contributions will span methodological innovations, data handling, broad-scale syntheses, and interdisciplinary studies. The 2nd set of talks in this symposium will emphasize ecometrics, a subfield of quantitative paleoecology relating community trait distributions to the environment.

5. Estimating Vegetation Change from Fossil Pollen to Planetary Boundaries: A Global, Long-Term Synthesis Using Big Data

Ondřej Mottl, *Charles University; Suzette Flantua, University of Bergen*

Reproducible, large-scale syntheses of fossil pollen now enable a global perspective on how terrestrial vegetation has reorganised from the late Pleistocene to the present—and how these dynamics can inform today's ecological baselines and sustainability policy. Leveraging thousands of publicly available pollen time series, we outline a shift towards reproducible workflows. We introduce FOSSILPOL, which couples expert-led data governance from the Neotoma Paleoecology Database with automated quality control (cleaning and standardisation), and updated chronological modelling. The framework supports like-for-like comparisons across regions and studies, addressing challenges from heterogeneous taxonomies, variable sampling densities, and spatio-temporal uncertainty. We show how statistical advances and increased computational power enable distillation of complex palaeoecological time series into interpretable summaries of macroecological change—capturing multi-scale trends in diversity, composition, and rate-of-change. We demonstrate how fossil pollen assemblages can be integrated with complementary datasets—such as plant functional traits and climate reconstructions—to move beyond taxonomic patterns

towards holistic ecosystem properties and drivers through time. Our example—VegVault—bridges palaeo- and neo-ecology, yielding robust, scale-aware baselines against which current trajectories can be assessed. Viewed through the lens of 'planetary boundaries', long-term reconstructions help constrain historical ranges of variability for biosphere integrity and land-system change, clarifying where management might resist, accommodate, or adapt to novel states. We outline community priorities for a data-rich, macroecological palaeoecology: interoperable standards, open workflows, rigorous uncertainty handling, and tighter links to modelling and decision-making. This agenda positions quantitative palaeoecology as a cornerstone for contextualising—and governing—present climate and biodiversity crises.

6. Tracking coral reef ecosystem change over millennia in the Tropical Eastern Pacific using paleo archives

Erin Dillon, *Smithsonian Tropical Research Institute; Irene García, Smithsonian Tropical Research Institute; María Mercedes Gómez Benalcázar, Smithsonian Tropical Research Institute; Brígida de Gracia, Smithsonian Tropical Research Institute; Jonathan Cybulski, Smithsonian Tropical Research Institute; Sven Pallacks, Smithsonian Tropical Research Institute; L. Felipe Opazo, Universidad Católica de la Santísima Concepción; Kimberly García-Méndez, Smithsonian Tropical Research Institute; Aaron O'Dea, Smithsonian Tropical Research Institute*

Climate change threatens the persistence of coral reefs, which in turn may affect reef-associated organisms such as bony fish and sharks. Yet how fish and shark communities respond to such disturbances remains uncertain, owing to the long timescales of impact and lack of baseline data. This is especially true in the Tropical Eastern Pacific, where climatic variability is high and long-term records are scarce. Here, we leverage a past climate-driven reef slowdown in the Panamanian Pacific to assess how reef communities responded to a loss of coral habitat following climate stress. The reef collapse, which lasted over 2,500 years (~4.2–1.5 ka), has been well-documented through estimates of reef accretion and analyses of coral community composition in reef matrix cores collected throughout the region. We paired coral assemblage data with coeval accumulations of fossil fish ear bones (otoliths) and shark scales (dermal denticles) in cores spanning the last ~6,000 years to reconstruct coral, bony fish, and shark communities before, during, and after the reef collapse at two locations within the Gulf of Panama (Las Perlas Archipelago and Isla Iguana). Our preliminary results suggest that shark abundances decreased during the event but were able to recover once reef health improved, whereas shark community composition and relative trophic structure remained fairly stable across the event. Together, we show how insights from these different skeletal elements can be combined to track reef community structure and energetics in response to past environmental disturbances, which offer analogues for future global change.

7. From Messy to Meaningful: Integrating Big Data in Palaeoecology

Gavin Simpson, *Aarhus University*

Large community databases such as Neotoma and PANGAEA have revolutionised palaeoecology by making data available at spatial, temporal, and taxonomic scales that were unthinkable only a decade ago. This wealth of information opens the door to exciting new questions about biodiversity, biogeography, and ecological change, but it also brings a familiar problem into sharper focus: palaeoecological data are messy. Counts, percentages, concentrations, metabarcoding outputs, and presence–absence records sit side by side, often based on inconsistent taxonomies, uneven sampling in time and space, and non-random site selection. While such inconsistencies are rarely a barrier in single-site studies, they quickly become problematic when we try to combine records across proxies or regions. Traditional multivariate methods, which have served palaeoecology well, are not designed to cope with this level of heterogeneity. Fortunately, recent advances in statistical ecology offer a way forward. Integrated and joint species distribution models, model-based ordination, copula methods, and network approaches provide flexible tools for drawing together disparate data types while accounting for effort, bias, and uncertainty. Ideas such as data fusion, change of support, and borrowing strength across datasets help tackle issues around diversity estimation, rare taxa, and misaligned records. To fully unlock the potential of palaeoecological big data, however, the field will need to embrace these newer frameworks and build closer links with quantitative ecologists. Doing so will allow us to make the most of the data already in hand and to shape how we collect and curate palaeo records in the future.

8. Ecometrics: frontiers for identifying community responses to global change

Jenny McGuire, *Georgia Institute of Technology; Michelle Lawing, Texas A&M University; Melissa Kemp, University of Texas, Austin; Maria Alejandra Hurtado Materon, Texas A&M University; P. David Polly; Julia A Schap, Georgia Institute of Technology; Rachel Short, South Dakota State University, Leila Siciliano Martina, Texas State University*

Ecometric methods quantitatively relate community trait distributions to environmental factors. Traditionally, ecometrics has been used to evaluate fossil community assemblages as proxies for paleoenvironmental conditions. For example, high-crowned molars (i.e., high hypsodonty) are an adaptation that enhances durability, commonly found in animals that consume abrasive grit in grasses or other vegetation common in arid environments. As a result, the degree and variance of hypsodonty in small mammal (i.e., rodents and lagomorphs) and large mammal (i.e., ungulates) communities can be used to calculate aridity. The utility of ecometric methods has been expanding over the past several years, with applications to global change past, present, and future. Accelerating these efforts are a series of new tools and databases for analyzing community-level, trait-environment relationships. Making use of these abundant resources, rigorous studies are illuminating the

nuance that can be gleaned by exploring the relative abundances of species within communities or by integrating trait-environment relationships across different taxonomic groups. Researchers have been exploring the implications of these functional traits and their strong correlations with environmental conditions for assembly theory and the historical dynamics of community compositions. Importantly, researchers are beginning to leverage established ecometric relationships to quantify how species losses, both locally and globally, degrade mammalian community function and predict regions of trait-environment mismatch under projected global change. Community-level functional trait analyses have the potential to shift how we understand ecological responses to global change.

9. Quantitative paleoenvironmental reconstruction from mammalian ecometric traits: regression, ordination, and machine learning techniques

Abigail K. Parker, *University of Helsinki; Miikka Tallavaara, Department of Geosciences and Geography, University of Helsinki; Jeremias Glöggler, Department of Computer Science, Department of Geosciences and Geography, University of Helsinki; Liping Liu, Department of Geosciences and Geography, University of Helsinki; Swedish Museum of Natural History; Bolin Center for Climate Research, Stockholm University; Alexander Bakhia, Department of Geosciences and Geography, University of Helsinki; Sania; Zubaid, Department of Geosciences and Geography, University of Helsinki; Oscar Edward Wilson, Department of Geosciences and Geography, University of Helsinki; Juha Saarinen, Department of Geosciences and Geography, University of Helsinki; Indrė Žliobaitė, Department of Computer Science, Department of Geosciences and Geography, University of Helsinki*

Dental traits of large herbivorous mammals have a long tradition of being taken to be indicators of environmental conditions, due to the central role teeth play in mammals' acquisition and processing of plant food material. Driven by the aim of better understanding past environments, paleontologists have developed ecometric models relating dental traits in co-occurring modern herbivore communities to climate variables. These models provide quantitative reconstructions of past precipitation, temperature, productivity, or vegetation based on the traits observed in fossil mammalian assemblages. We present an updated set of ecometric models using eight dental traits that categorically describe the functional morphology of Artiodactyla, Perissodactyla, Proboscidea, and Primates. We use an ensemble of modelling techniques to relate modern community trait averages to climate variables. These models include both regression-based and decision tree-based algorithms; we discuss how different models can capture different aspects of ecometric trait-climate relationships when trained using large geospatial datasets. Some community traits change more than others when comparing extant communities to estimates of community composition if Pleistocene-Holocene extinctions had not taken place. We discuss the sensitivity of ecometric models to human impacts on the modern ecosystems from which we draw training data, and propose that spatial cross-validation techniques can be used to estimate model

error when applying models trained on modern data to fossil faunas. Finally, we discuss how ordination of data on communities' occupation of body size-diet guilds provides an alternative avenue for ecometric reconstruction based on traits comparable across a wider range of taxa.

10. Plant Traits, Canopy Structure, and Ecosystem Change Across Extinctions and Greenhouse Worlds

Regan Elizabeth Dunn, *Natural History Museum of Los Angeles County; Jessie George, Natural History Museum of Los Angeles County; Ellen D Currano, University of Wyoming*

Vegetation is the foundation of terrestrial ecosystems, shaping energy flow, biodiversity, and organization. Primary productivity and vegetation structure are tightly linked to faunal diversity and trophic complexity. In the fossil record, vegetation structure can be reconstructed using proxies from leaf epidermal traits, which capture light environment and canopy density data. Here I synthesize case studies that span critical episodes of global change. First, during the Cretaceous–Paleogene mass extinction (66 Mya), leaf epidermal morphology indicates canopy collapse under a "nuclear winter" scenario, followed by geographically heterogeneous forest recovery. Second, during the Paleocene–Eocene Thermal Maximum (56 Mya), a greenhouse gas event comparable to anthropogenic warming, epidermal and pollen data show major restructuring of forest canopies, altering both productivity and ecosystem dynamics. These deep-time events highlight how vegetation structure both responds to and shapes ecosystem resilience under climate extremes, offering analogs for understanding modern ecological vulnerability. Finally, I examine vegetation shifts following the introduction of anthropogenic fire in Southern California ~13,000 years ago. Increased fire frequency, layered onto Late Pleistocene climate warming, drove megafaunal extinction and a transition toward plant assemblages dominated by traits adapted to frequent burning. Together, these records provide natural experiments demonstrating how vegetation responds to elevated CO_2, rapid climate change, novel disturbance regimes, and biodiversity loss. Future directions include expanding paleobotanical and geochemical proxies to track primary production with high temporal and spatial resolution, and applying these data to test and refine climate models of past events that parallel the global changes now unfolding.

Symposium: Functional island biogeography

Organizers: Holger Kreft, University of Göttingen, and Tom Matthews, University of Birmingham

Framework and background

This symposium will highlight recent advances in the young and growing field of functional island biogeography, with a particular focus on the considerations related to studying the discipline in the broader context of the Anthropocene. Talks will span multiple taxa, both natural and human-altered systems, and will draw on empirical data and theoretical modeling to explore the functional dimensions of island biodiversity.

11. Functional diversity in island floras

Nathaly Guerrero Ramirez, *University of Göttingen; Thalita Ferreira-Arruda, University of Göttingen;*
Patrick Weigelt, Radboud University; Martha Paola Barajas Barbosa, iDiv; Albert Sebastien, Université de La Réunion; Dominique Strasberg, Université de La Réunion, UMR PVBMT; Baider Claudia, The Mauritius Herbarium; F. B. Vincent Florens, University of Mauritius; Isis Petrocelli, University of Göttingen; Holger Kreft, University of Göttingen

How plant ecological strategies vary among islands and how they respond to insularity may be crucial to answer central questions in island biogeography and may help elucidate the eco-evolutionary assembly of island floras. For instance, integrating plant ecological strategies, which are captured through functional traits, into biogeographical models such as the General Dynamic Model (GDM) of oceanic island biogeography can provide a deeper understanding of the emergence of island biota across biogeographical timescales. Therefore, here, we assessed the diversity of plant functional strategies, i.e., functional diversity, in oceanic island floras and determined the contributions of contrasting plant growth forms, native non-endemic species, and endemic species to functional diversity. Furthermore, we determined the extent to which the functional assembly of island floras is related to biogeographical processes through the lens of the GDM.

To this end, we collated data from ~3000 plant species from 74 oceanic volcanic islands belonging to eight oceanic archipelagos worldwide: the Azores, Canary Islands, Cook Islands, Galapagos, Hawaii, Juan Fernandez, Madeira, Mascarenes, and New Zealand. Our research contributes to the growing field of functional island biogeography, further enhancing our understanding of the assembly mechanisms of frequently taxonomically and functionally disharmonic oceanic island floras.

12. The loss of global functional diversity from island bird extinctions

Ferran Sayol, *Beta Tech Centre - UVic-UC; Søren Faurby, University of Gothenburg; Tom Matthews, University of Birmingham*

Islands are often home to species with unusual characteristics, such as many flightless birds. However, many of these unique species have disappeared following human arrival or are currently threatened. While the disproportionate loss of certain taxonomic groups and traits on islands has been widely studied, the consequences of these losses for the functional diversity of island assemblages remain poorly understood. Investigating functional diversity loss is challenging because trait data are often unavailable for many extinct species, particularly those known only from subfossil remains. This gap limits our understanding of natural community structures and constrains our ability to trace biodiversity changes across space and time. To address this, we present AVOTREX, an open-access database compiling species traits for all bird species known to have gone extinct over the past 130,000 years. Using AVOTREX, we quantified the loss of functional diversity caused by past extinctions and projected future declines. Our analysis shows that at least 610 bird species have gone globally extinct—around three times higher than the commonly cited IUCN estimate, which only counts extinctions since 1500. Island endemics—representing 80% of these extinctions—have driven particularly severe functional diversity losses, highlighting the vulnerability of insular ecosystems. These results reveal the magnitude of functional erosion already experienced and forecast alarming future losses, emphasizing the urgency of identifying and safeguarding threatened ecological functions before they vanish.

13. Islands in Transition: Functional Consequences of Bird Extinctions and Introductions in Hawai‘i

Maria Wagner Jørgensen, *University of Birmingham; Ferran Sayol, BETA Tech Centre - University of Vic, Spain; J.P. Hume; Laura Jane Graham, University of Birmingham; Jon Sadler, University of Birmingham; Tom Martin, Lancaster University; Tom Matthews, University of Birmingham*

Islands are disproportionately affected by the global biodiversity crisis, with human impacts reshaping island communities through species extinctions and introductions. These changes not only represent a turnover of species but also affect the functional composition of island communities. The Hawaiian Islands are no exception and often stand out as hotspots of both extinction and introduction, making them a good system to study these processes. We compiled information on bird communities of six Hawaiian Islands, including the traits of native extinct and native extant bird species, as well as established and non-established introduced species. With these data we are able to investigate how biodiversity has changed over time as well as what role species traits play for establishment success of non-native species. While we found that established non-native species restored multiple functional

diversity indices to pre-extinction levels, the limited trait overlap between extinct and non-native species suggests that non-native species provide a false compensation for the loss of native species: We saw a shift from forest specialists to open habitat generalist species. Additionally, we found large trait similarity between successfully and unsuccessfully established non-native species, suggesting that traits are not the primary driver for establishment success of non-native species. As we are still currently witnessing extinctions on many of the world's islands, including Hawaii, these results emphasise the importance of native species to conserve ecosystem function of pristine environments and highlight the use of functional ecology in understanding the full consequences of extinction and introduction of species on islands.

14. Island functional biogeography theory at ecological and evolutionary scales

Dominique Gravel, *Université de Sherbrooke; Alexandre Fuster-Calvo, University of Sherbrooke*

MacArthur & Wilson's theory does not account for ecological interactions in the assembly process, and predictions are limited to equilibrium species richness. Here we summarize theory solving these limitations and discuss the most promising predictions for functional biogeography. First, we describe how island assembly contributes to the dynamics and equilibrium functional diversity. A general modification to the theory is to make colonisation and extinction processes functions of functional traits of each species. These could directly influence their dynamics (e.g. dispersal mode influences the colonisation probability on remote island) or indirectly through ecological interactions (e.g. herbivores are more likely to find resources than top carnivores). Combination of these constraints on the assembly influence the equilibrium trait distribution, with alterations to mean, variance, and covariances of the multivariate functional trait space. Island area and distance to the mainland interact with selection strength and therefore generate functional area relationships with slopes that are dependent on the distance to mainland. Second, we explore how evolutionary dynamics on islands can further contribute to the emergence of ecological networks, and vice-versa. Selection arises from the effect of ecological interactions on both the establishment probability of new species and on the extinction probability. We present preliminary results on how ecological interactions influence diversification rates, and inversely how evolutionary history influence network structure. Together, our results show that the classic theory can be further expanded to include functional diversity without sacrificing much of its simplicity, offering a rich array of testable predictions at both ecological and evolutionary scales.

15. Beyond species loss: Functional diversity decline in island mammals facing extinction

Ana M.C. Santos, *Universidad Autónoma de Madrid; Sonia Llorente-Culebras, Autonoma University of Madrid; Carlos Pérez Carmona, University of Tartu; William Carvalho, Universidad Autónoma de Madrid; André Menegotto, Universidad Autónoma de Madrid; Rafael Molina-Venegas, Estación Biológica de Doñana, Consejo Superior de Investigaciones Cientificas; Richard Ladle, Universidade Federal de Alagoas*

Islands are biodiversity hotspots that host unique assemblages. However, a substantial proportion of island species are endangered and their long-term survival is uncertain, which threatens not just species diversity but also ecosystem stability and functioning. Focusing on mammals, we (i) assessed how much functional space would be lost if threatened species go extinct, (ii) determined the minimum number of extinctions that would cause a significant functional loss, (iii) identified the characteristics of the islands most vulnerable to future changes in the functional space, and (iv) quantified how much of that potential functional loss would be offset by introduced species. We analysed 1474 mammal species across 318 islands, building trait probability density functions to quantify changes in functional richness on each island if the mammals categorised by the IUCN as threatened disappeared. We found that if currently threatened mammals were lost, 63% of islands would experience a decline in functional space, though the average loss would be less than 15%. Alarmingly, even a small number of extinctions could trigger significant functional disruption, particularly on islands that are small, isolated, or species-rich. Additionally, while introduced species sometimes fill ecological gaps, they generally fail to compensate for the functional roles of native mammals. Our results show that the preservation of native species and their ecological roles remain crucial for maintaining the current functioning of island ecosystems. Therefore, conservation measures considering functional diversity are imperative to safeguard the unique functional roles of threatened mammal species on islands.

Symposium: Co-evolution of landscape and life

Organizers: Yaquan Chang, ETH Zurich, and Michael Krabbe Borregaard, Globe Institute, University of Copenhagen

Framework and background

The study of how life and landscapes co-evolve over geological time scales is benefitting from recent advances in tectonic geomorphology that allow to better reconstruct the tectonic and geomorphic history of landscapes. The field leverages the rapidly accumulating genomic and fossil data to provide a more rigorous understanding of the link between biodiversity evolution

and landscape history. This symposium brings geomorphologists into the biogeography community, thereby aiming to foster interdisciplinary discussions and collaborations.

16. Does geology shape contemporary patterns of global diversity?

Carsten Rahbek, *Center for Macroecology, Evolution and Climate, University of Copenhagen*

Traditionally, efforts to elucidate contemporary global biodiversity patterns have predominantly focused on hypotheses related to current climatic and ecological processes, evolutionary dynamics, and historical contingencies. This emphasis persists despite longstanding recognition that geological factors significantly shape global biodiversity by generating heterogeneous landscapes and influencing speciation, dispersal, species persistence, and extinction processes. Moreover, it is well established that underlying bedrock geology affects soil composition and nutrient availability, thereby directly impacting plant growth and, consequently, the animal species dependent on those plants. Although the significance of geology is acknowledged, it is frequently omitted from global biodiversity analyses or its role is inferred indirectly through statistical models of species richness that incorporate climatic, phylogenetic, and sometimes topographic variables. Or, the influence of geology is generalized from phylogenetic or phylogeographic studies focused on a limited number of species or minor clades.

This raises a critical question: to what extent does geology shape contemporary global biodiversity patterns?

In this presentation, I will examine the role of geology in relation to global mountain biodiversity, specifically focusing on amphibians, mammals, and birds. I will present preliminary analyses and reflections on the proportion of terrestrial vertebrate biodiversity attributable to the geology of mountainous regions. Furthermore, I will also explore hypothetical scenarios of global vertebrate species richness in the absence of mountains on Earth.

17. Tectonic Controls on Global Plant Biodiversity Distributions

Sean Willett, *ETH Zurich; Ao Luo, Institute of Ecology and State Key Laboratory for Vegetation Structure, Function and Construction; College of Urban and Environmental Sciences, Peking University; Yanyan Wang, Department Earth and Planetary Sciences, ETH Zurich; Zhiheng Wang, Peking University; Loïc Pellissier, Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Switzerland*

The global distribution of biodiversity exhibits patterns that suggest control by environmental and geographic factors including climate, mountainous topography, and tectonic activity. There are two main pathways by which tectonic activity drives biodiversity. First, is through surface uplift, subsidence and roughening of topography, which interacts with climate to

create new habitat, encouraging local colonization or speciation and higher regional species richness. Second is through tectonic deformation of topography which fragments habitat, separating populations, leading to vicariant speciation and higher species richness. These two pathways can be described as enhanced environmental heterogeneity and tectono-geomorphic disruption, respectively. We attempt to disentangle the relative importance of these pathways for plant species richness. By building a model for environmental heterogeneity based on modern topography and climate models, we can estimate the expected plant richness. The difference between this estimate and the observed richness is interpreted as the component due to tectono-geomorphic disruption. We find that this excess component of richness is nearly always positive and is locally a factor of up to ten above that expected by environmental gradients alone. We conduct a categorical analysis, comparing the excess richness to active tectonic and geomorphic domains and find a close correspondence between the patterns of excess richness and recent tectonic and geomorphic activity. In particular, we find that biodiversity hotspots overwhelmingly fall in areas of tectono-geomorphic activity, even after accounting for environmental heterogeneity, supporting the hypothesis that transient, tectono-geomorphic disruption is an important control on speciation rates and the distribution of biodiversity.

18. Coupled landscape and biotic evolution model reveals direct effect of mountain uplift and topography on biodiversity

Tara M Smiley, *Stony Brook University; Eyal Marder, University of Massachusetts Amherst, Department of Earth, Geographic, and Climate Sciences, Amherst, MA, USA; Katherine Kravitz, Indiana University, Department of Earth and Atmospheric Sciences, Bloomington, IN, USA; Brian Yanites, Indiana University, Department of Earth and Atmospheric Sciences, Bloomington, IN, USA*

Modern biodiversity patterns demonstrate a strong link between topographically complex mountains and biodiversity hotspots. However, our understanding of the deep-time processes governing this relationship remains uncertain and requires collaboration between (paleo)biologists and earth scientists. To probe these connections, we developed a coupled landscape-biotic evolution model. By simultaneously modeling mountain uplift, erosion and sediment deposition with biotic evolution, dispersal and speciation, our model simulates how mountain building influences biodiversity and its long-term preservation in the fossil record. We find that species richness increases with tectonic uplift and increasing topographic relief in both the high-elevation erosional mountain range and the adjacent low-elevation depositional basin. Although diversity increases across a range of uplift rate scenarios, the spatial patterns of biotic processes over time indicate distinct responses to uplift rate, with more complex and volatile dynamics unfolding under faster uplift rates. These results indicate that 1) increased speciation rates and species richness during mountain building can be recovered from the fossil record found in adjacent depositional lowlands, and

2) certain uplift histories promote stronger montane biodiversity gradients. We focus our modeling efforts on small mammals; however, the coupled modeling framework is adaptable to multiple systems, clades, and questions. Model results reflect similar spatial and temporal biodiversity patterns found across mountain ranges today and in the fossil record. Testing more complex parameter space, such as the development of climatic gradients during mountain building, will allow us to further investigate how climate-landscape-biotic interactions govern the tempo and scaling of biodiversity and fossil preservation in dynamic landscapes.

19. Geodiversity and North American freshwater biodiversity hotspot

Maya Frances Stokes, *Florida State University*

The exceptional biodiversity of mountain regions across Earth suggests that topographic deformation associated with plate tectonic processes may be causally linked to evolutionary processes. Yet, in contrast to terrestrial organisms, freshwater fishes are more biodiverse in tectonically inactive regions. Despite the tectonic quiescence of these regions, the legacy of mountain building continues to affect geomorphic dynamics. As rivers cut through ancient geologic structures, rocks with different physical and chemical properties are exposed at Earth's surface. For species whose ecology is tightly linked to lithology, this process may influence the availability and connectivity of habitat. When rock types associated with favorable habitat are exhumed, species may have the opportunity for range expansion and dispersal. Conversely, when lithology associated with unfavorable habitat is exhumed, populations may become geographically isolated, generating opportunities for vicariant speciation. The biogeographic scenario will depend on the ecology of the species and the underlying stratigraphy and structural geology. In this talk, I will present evidence from the North American freshwater biodiversity hotspot for links between erosion through heterogeneous lithology and biogeographic processes and patterns. I will first combine phylogenomic analysis, species distribution modelling, and geologic datasets to demonstrate empirical evidence of erosion-mediated allopatric speciation within two groups of endemic darters (Percidae: Etheostomatinae). Then, I will assess the importance of lithologic heterogeneity for explaining spatial patterns of riverine biodiversity across North America. The results demonstrate that long after mountain-building ends, there remain intricate links between the solid Earth, erosional dynamics, and biogeographic patterns and processes.

20. Mangroves of Asian origin in the Neogene of western Amazonia and paleobiogeographic implications

Carina Hoorn, *University of Amsterdam; Giovanni Bogotá-Angel, IBED, UvA; Universidad Distrital; Angelo Plata, Universidad de Caldas; Huasheng Huang, Sun Yat-sen University; Diana Ochoa, Universidad de Salamanca; Limi Mao, Chinese Academy of Sciences; Hanna*

van den Hil, Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam; Shweta Basnett, University of Amsterdam; Jelle Kraak, IBED, University of Amsterdam; Shirley Graham, Missouri Botanical Gardens; Fabiany Herrera, Field Museum of Natural History

Sonneratioid mangroves commonly occur in E Africa, S and SE Asia, and the northern part of Australia. The fossil record of Indonesia suggests their first occurrences are in the Early Eocene (c. 56 to 48 million years ago; Ma). Recently, sonneratioid fossil wood was reported for the Early Miocene of Panama and dated as c. 22 Ma. In this paper we explore whether the sonneratioid mangroves could have reached the Amazon Region. This is a reasonable question as the Miocene fossil record of western Amazonia holds evidence for past marine incursions that connected the Amazon and the Caribbean. To investigate this matter, we revisited the Brazilian core 1AS-4a-AM and applied light and scanning electron microscopy (LM and SEM) to selected sporomorphs. Here we report two new Early Miocene mangrove pollen species belonging to the genus Florschuetzia and compare them with other previously described taxa. We found that, although the new species resemble known fossil species from SE Asia, they also have differences. Based on an assessment of the entire palynological assemblage, we also conclude that in paleoecological sense the new Amazonian Florschuetzia species occupied a back-mangrove position, i.e. on the landward side of the Rhizophoraceae belt. We speculate that the Asian sonneratioid mangrove lineages reached the Amazon by means of marine currents across the Pacific. Moreover, it seems plausible that the Caribbean-Amazonian mangrove ecosystem was more diverse than at Present.

Symposium: Bio(cultural)geography: Exploring the spatiotemporal dynamics of species, cultures and languages

Organizers: Sietze J. Norder, Utrecht University

Framework and background

Biogeography has traditionally focused on the distribution of non-human species, but as human activities increasingly shape ecosystems worldwide, understanding the interplay between cultural diversity and biodiversity has never been more critical. Recognizing this, a growing number of biogeographers is now investigating the spatial patterns of cultural and linguistic diversity, alongside its spatial congruence with biodiversity. This diversity, however,

is disappearing at an alarming rate, and addressing this decline requires interdisciplinary collaboration. This symposium will showcase innovative interdisciplinary research focusing on the parallels and interactions between biodiversity and cultural diversity across spatial and temporal scales.

21. From the genome to biodiversity: how the supply of variation influences diversification

Lindell Bromham, *Australian National University; Xia Hua, ANU*

Many correlates of diversification rate have been identified, including biological traits and environmental features. Yet one of the consistently identified correlates of diversification rate is often ignored: rate of molecular evolution is often associated with net rate of diversification, as estimated from phylogenies across a wide range of taxa including plants, fish, birds, reptiles and amphibians. Why? I will discuss evidence from a range of studies using different methodological approaches that suggest that variation in the average mutation rate is associated with overall rate of speciation, and examine the possible causes of this relationship. The observed correlation between rates of molecular evolution and diversification potentially provide a window on evolutionary processes that drive species diversity. But this relationship also has important practical consequences because it affects our use of molecular data to reconstruct patterns and processes of macroevolution and macroecology. I will demonstrate how an association between rate of molecular evolution and diversification rate can influence phylogenetic estimates of the dynamics of diversification, potentially giving rise to misleading inference of patterns of diversification in time and space.

22. Biocultural drivers of language distribution ranges

Meeli Roose, *University of Turku; Outi Vesakoski, University of Turku*

The distribution ranges of languages are proxies for the spatial boundaries of human populations. While these boundaries often reflect a lack of contact, the reasons behind that lack can be diverse. Some are conscious, such as political borders or geographic barriers, while others are shaped by unconscious factors like social attitudes. Facilitating factors, such as shared ecological zones or trade routes, also shape contact dynamics. The interaction between these opposing forces remains poorly understood. Understanding the balance between these forces remains a key challenge in biocultural research.

This presentation introduces a series of studies that examine the formation of population boundaries using data from Finnish dialects and the broader Uralic language family. We first investigate whether linguistic similarity among Finnish dialects aligns more closely with ecological conditions, cultural landscapes, or historical administrative borders. We then

assess whether the well-known east–west division in Finland appears consistently across linguistic, genetic, and ethnographic datasets. This pattern is compared to historical boundaries, such as those between Novgorod and Sweden, as well as to reconstructed travel routes shaped by terrain and water networks.

Expanding the scope, we evaluate how the distribution of Uralic languages corresponds with ecological variation across Northern Eurasia. Using spatial modelling and 26 biogeographical predictors, we assess which environmental factors most strongly associate with linguistic range.

Together, these studies highlight how language, ecology, and cultural history intersect in shaping population structures. The work also advances spatial infrastructures that enable integrative, macroregional biocultural research.

23. Human cultural complexity drives biogeographic dynamics in island ecosystems

Sandra Nogué, *Universitat Autònoma de Barcelona; Alvaro Castilla-Beltrán, Universidad de La Laguna; Pedro M. Raposeiro, CIBIO; Xaali O'Reilly-Berkeley, Universitat Autònoma de Barcelona; Andrew Martin; Javier De la Casa, CREAF; Judit Rodrigo, Universitat Autònoma de Barcelona; Franka Gaiser, University of Bayreuth; Manuel J Steinbauer, Bayreuth University; Sergi Pla Rabes, Universitat Autònoma de Barcelona*

Island ecosystems carry the history of human cultural complexity, where successive waves of technological and economic changes have driven long-term ecological transformations marked by e.g. extinctions, exotic species introductions and establishment, ecological turnover, and biotic homogenization. Human colonisation has repeatedly altered species composition and ecosystem function, pushing many island ecosystems into novel states different from their historical baselines. Our research analyses how successive waves of human settlement and technological advances correlate with the emergence and length of ecological transitions, offering a dynamic understanding of how patterns of human migration shape, for example, ecosystem novelty and the island landscapes. Central to our approach is a systematic review of microfossils and other palaeoenvironmental indicators from multiple island and biogeographic regions, allowing us to reconstruct detailed timelines and magnitudes of these extended ecological transitions. By combining this palaeoecological data with cultural and archaeological evidence, we create a framework that helps us understand when and how strongly ecological changes occurred. This shows how cultural complexity shapes the changing patterns of biodiversity across island landscapes over time.

24. Legacy effects of European colonialism on hotspots of biocultural diversity threat

Bernd Lenzner, *University of Vienna; Andreas Baumann, University of Vienna; Sietze Norder, Copernicus Institute, Utrecht University; Franz Essl, University Vienna; Hannes A. Fellner, University of Vienna*

Patterns of biological diversity have been shaped by cultural practices in the past, while in turn, cultures and languages have evolved in close interaction with local species and ecosystems. However, in the Anthropocene, human activities are putting increasingly more and diverse pressures on ecosystems and cultures resulting in accelerating threat levels on both. Understanding where biological and cultural diversity is threatened globally, and how far current and historical anthropogenic drivers like colonialism shape their distribution is crucial for pinpointing hotspots and prioritizing efforts to counter these threats. We find that the spatial patterns of the erosion of biological diversity (using amphibians, birds, mammals and reptile diversity as a proxy) and cultural diversity (using linguistic diversity as a proxy) are only weakly congruent on a global scale and that they are driven by differential sets of mechanisms. However, our results also indicate that the European colonial expansion has left long-lasting imprints on both biological and cultural diversity. The duration of European colonialism (i.e., the time a specific region was occupied by European powers) significantly increases contemporary observed threat levels of biological and linguistic diversity.

25. Environmental influences on geographic patterns of language and cultural diversity

Michael Gavin, *Colorado State University; Marco Tulio Pacheco Coelho, Swiss Federal Institute for Forest, Snow and Landscape Research; Claire Bowern, Yale University; Simon Greenhill, University of Auckland; Carlos Botero, University of Texas at Austin*

Long-standing debates across multiple disciplines focus on the degree to which environmental conditions shape different characteristics of human societies. Despite a long history of methodological innovations driving the study of spatial patterns in diversity, biogeographers have produced relatively few studies that contribute to these debates on human diversity. Hoping to spark additional interest in human biogeography, we highlight examples of large open-access datasets. We also provide an example of a new study that draws inspiration from work on spatial patterns in biodiversity to advance our understanding of how environmental drivers contribute to global patterns of language diversity. We find that models that account for non-stationarity in the effects of environmental conditions explain substantially more of the spatial variation in language richness. We also conclude that the scale of analysis matters. Environmental variables account for >70% of the variation at coarse scales, but <30% at finer scales. We discuss how these results contribute to academic debates on environmental determinism and possibilism.

PARALLEL SESSION PRESENTATIONS

Species Area Relationships

111. The island species-area relationship for plants globally

Robert J. Whittaker, *Oxford University; Holger Kreft, University of Göttingen; Tom Matthews, University of Birmingham; François Rigal, Université de Pau et des Pays de l'Adour; Julian Schrader, Macquarie University; Kostas Triantis, National and Kapodistrian University of Athens; Patrick Weigelt, University of Goettingen.*

The form taken by ISARs across different scales has been the subject of debate for over a century. We use a dataset compiled for 1262 islands to describe the ISAR for plants across the global ocean, providing models for both native plant richness and for endemism, as well as for the archipelago species-area relationship globally. For the global plant ISAR (and the equivalent archipelagic relationship), we demonstrate that a simple power model explains a remarkable amount of variation. We also highlight contributions from island isolation and island type to variations in richness as a function of area. Increased isolation drives richness down, only partially compensated for, as area increases, by in situ speciation. Those exceptionally large, tropical, mountainous islands that were also formerly connected to continents are both rich in endemics and exceptionally species-rich overall.

112. Diverging responses of taxonomic, functional, and phylogenetic plant diversity to island parameters in arid habitat islands of southern Africa

Alexander M. Bürger, *Biogeography and Biodiversity Lab, Institute of Physical Geography, Goethe-University Frankfurt; Katharina Meyer, University of Hamburg; Pia Maria Eibes, Biogeography and Biodiversity Lab, Institute for Physical Geography, Goethe-University Frankfurt; Charlotte Lauel, Biogeography and Biodiversity Lab, Institute of Physical Geography, Goethe-University Frankfurt; Jens Oldeland, Institute for Globally Distributed Open Research and Education (IGDORE); Ute Schmiedel, Institute for Plant Science and Microbiology, University of Hamburg (Germany); Severin D.H. Irl, Institute of Physical Geography, Goethe-University Frankfurt*

Habitat islands conceptually bridge true islands and habitat patches, adding new perspectives to island biogeographical principles that shape community assembly processes. Despite growing interest, empirical studies are scarce and the drivers of biodiversity in these systems such as different aspects of island shape, isolation and habitat diversity remain unclear. Our aim was to assess how biogeographic parameters influence taxonomic, functional, and phylogenetic plant diversity on habitat islands using quartz islands in South Africa as our model system. We conducted floristic surveys on 20 quartz islands in the harsh and arid summer-rainfall region around Pofadder (Nama–Karoo, South

Africa) to quantify species richness, functional dispersion, and Faith's phylogenetic diversity. Via remote sensing, we derived island metrics and evaluated their effects on the diversity metrics, using negative binomial generalized linear models for species richness and linear models for functional and phylogenetic diversity. Island area emerged as the strongest predictor of species richness, consistent with the island biogeography theory, while isolation had no significant effect. Connectivity was a significant predictor for functional dispersion and explained most of the variation. Neither phylogenetic clustering nor overdispersion was detected when compared with the null model. Our findings highlight that different facets of diversity respond uniquely to biogeographic parameters. Integrating taxonomic, functional, and phylogenetic perspectives is therefore essential for a comprehensive understanding of biodiversity patterns on habitat islands and for providing valuable insights for conservation.

113. Multi-scale species richness estimation with deep learning

Victor Boussange, *Switzerland*

Biodiversity assessments are critically affected by the spatial scale at which species richness is measured. How species richness accumulates with sampling area depends on natural and anthropogenic processes whose effects can change depending on the spatial scale considered. These accumulation dynamics, described by the species-area relationship (SAR), are challenging to assess because most biodiversity surveys are restricted to sampling areas much smaller than the scales at which these processes operate. Here, we introduce deep SAR, a deep learning framework that combines sampling theory with deep learning to predict species richness across arbitrary spatial extents. We demonstrate the capabilities of the framework by training our model on ~490k vegetation plots from the European Vegetation Archive, to predict vascular plant species richness over Europe. We validate its performance against independent regional inventories, demonstrating a 32% improvement in coarse-grain richness predictions compared to conventional methods, while delivering finer grain estimates. Beyond prediction, the deep SAR approach reveals scale-dependent drivers of biodiversity: while mean environmental conditions dominate at fine scales, area per se and habitat heterogeneity become increasingly important at broader extents. Applied across Europe, the model uncovers the multi-scale nature of species richness patterns: for instance, mountainous regions exhibit low local diversity but high turnover, translating to regional hotspots when estimating species richness at coarser scales. The capacity of our approach to deliver comprehensive species richness estimates across the full spectrum of ecologically relevant scales is essential for robust biodiversity assessments and forecasts under global change.

114. The impact of new species discoveries on species-area relationship

Feng Lu, *Fudan University; Jiajia Liu*, *Fudan University*

The species-area relationship, widely used to predict species extinctions due to habitat loss, is based on the implicit assumption that all species are accurately described. However, with numerous new species being described annually (the Linnean shortfall), it remains unknown whether incomplete species discovery affects the species-area relationship and its prediction of biodiversity loss. To address this, we compiled species lists from 234 ocean islands and 57 archipelagos for birds, mammals, and reptiles to model the impact of incomplete species discovery on species-area relationships. We showed that the slopes of species-area relationships increased with the completeness of new species discovery. Specifically, the extent of underestimation is higher for poorly studied taxonomic groups such as reptiles and at larger spatial scales. Our findings reveal that while species-area relationship is often used as a basic tool to predict extinctions from habitat loss, it may consistently underestimate extinction baselines in less-studied islands and taxonomic groups. Our study suggests that the impact of habitat loss on biodiversity is likely to be more severe than previously thought.

Paleoecology and change through time

121. Recent advances and current directions in the Neotoma Paleoecology Database

John W. Williams, *University of Wisconsin, Jessica L. Blois, University of California, Merced; Robert Booth, Lehigh University; Donald Charles, Academy of Natural Sciences of Drexel University; Edward Byrd Davis, University of Oregon; Laura Endres, ETH Zurich; Thomas Giesecke, Utrecht University; Simon Goring, University of Wisconsin-Madison; Nicholas Hoffman, University of California-Merced; Mariena Hurley, Drexel University; Sarah J Ivory, Penn State University; Nikita Kaushal, American Museum of Natural History; Jonathan Nelson, University of Wisconsin-Madison; Suzanne Pilaar Birch, University of Georgia; Alison J Smith, Kent State University; Trisha Spanbauer, University of Kentucky; Socorro Dominguez Vidana, University of Wisconsin-Madison*

The Neotoma Paleoecology Database serves the global biogeography community by providing an open, high-quality, and living data resource for studying species and ecosystem responses to past environmental change. Much work is underway; this abstract summarizes recent advances in community and data growth and enhancements in software services. Data volumes have increased to >12M datapoints, >39,000 datasets, and >25,000 sites. The SISAL speleothem database has recently joined Neotoma, while the new PaleoOpen initiative seeks to expand the community of European Data Stewards and data contributors across a variety of proxies. Another initiative is expanding the Neotoma data schema and systems to support metabarcoding ancient environmental DNA data. The new Data Bulk Upload System

(DataBUS) provides a flexible system for uploading many datasets to Neotoma, using formats that can be customized by Constituent Databases. Neotoma is being integrated with ORCID for user identity and authentication, as a precursor to building systems to support data embargoes pre-publication or when subject to Indigenous governance. The Dataset Landing Pages, which provide DOI-linked access for individual datasets, are being complemented by landing pages for Constituent Databases, individual investigators, and taxa. The Outreach and Engagement Committee led a Spanish-language online workshop series in 2025 while also consolidating Neotoma's help resources to make them more findable. Ultimately, the goal of these activities is to continuously increase Neotoma's capacity to advance global change research by supporting an ever-growing volume and variety of paleoecological data, while growing the community of researchers who use, steward, and contribute to Neotoma.

122. Lobal abundance and distribution of grasses over the last 50,000 years

Brody Sandel, *Santa Clara University, Santa Clara, United States*

Earth's climate has been dynamic over the last 50,000 years. Over the same period, the human population has expanded rapidly, transforming from a minor ecological force to the dominant influence on many systems globally. As a result, individual species and entire vegetation types have shifted their distribution. Grasses are indicators of these changes, characterizing major biomes and thriving in human-modified environments. We ask how grass abundance has changed over this period, what climatic factors have driven this change, and whether human activity has driven a recent increase in grass abundance. We examined dynamics in the global distribution of grasses using pollen cores from more than 4000 lakes worldwide, extracted from the Neotoma database. We combined these data with paleoclimate models and estimates of human population density. Globally, cooling and drying into the Last Glacial Maximum (LGM) from 50,000 to 20,000 years ago was associated with moderate increases in grass abundance, while subsequent warming led to a sharp decline in grass pollen. This slowed and reversed in the last 10,000 years, roughly coincident with the development and expansion of agriculture and human impacts more broadly. Initially, grass pollen abundance was highest in relatively cool regions, but this pattern reversed after the LGM. Over the last 10,000 years, grasses have become increasingly associated with high human population densities. This long-term perspective on the abundance of an important plant family suggests non-stationary climate-abundance relationships and an increasing role of human activity in shaping vegetation patterns over at least several thousand years.

123. Out of equilibrium: energy, forest closure, and land use drive distinct diversity dynamics in arboreal and non-arboreal vegetation across Late Quaternary

Irena Simova, *Charles University in Prague; Petr Kuneš, Charles University; Ondřej Mottl, Charles University; David Storch, Center for Theoretical Study, Charles University*

How biodiversity responds to climate and energy change depends on whether communities track environmental shifts in real time or fall out of equilibrium. We analyzed available fossil pollen time series since the Last Glacial Maximum, distinguishing arboreal (trees) and non-arboreal (herbs and low shrubs) vegetation, to track diversity changes related to changing climate and human pressure across three continents. Diversity dynamics generally follow an out-of-equilibrium scenario: in the period of fast climate change, diversity tracks climate and energy changes with various lags, weakening the spatial diversity-energy relationship. Importantly, competition between growth forms plays a key role as non-arboreal diversity declines with forest expansion, opposite to arboreal diversity. In contrast, under climate stability, the diversity-energy relationship stabilizes as diversity approaches equilibrium. Nevertheless, agriculture in Europe disrupted this equilibrium by boosting non-arboreal and reducing arboreal diversity. Our findings illuminate divergent diversity trajectories across functional groups driven by climate change, challenge the common space-for-time substitution approach, and highlight the necessity to distinguish life form groups.

124. Cradles, museums and biodiversity disequilibria: Reconciling global diversity dynamics using equilibrium theory

David Storch, *Center for Theoretical Study, Charles University; Grace Ridder, Center for Theoretical Studies; Jordan G. Okie, Arizona State University*

Historical nonequilibrium processes are often considered the main drivers of global biodiversity patterns. However, observed patterns in fossil record and phylogenetic trees are also compatible with an equilibrium-based framework. We demonstrate how such a framework, formalized in the Equilibrium Theory of Biodiversity Dynamics (ETBD), illuminates diversity patterns in space and time, including the latitudinal diversity gradient, even if current regional species richness is out-of-equilibrium. ETBD postulates that biodiversity equilibria are driven by balance of diversity-dependent speciation and extinction rates, and addresses coupled dynamics of species richness and community abundance in both equilibrium and out-of-equilibrium situation. It implies that a classical distinction of biodiversity cradles and museums can be redefined in respect of biodiversity equilibria and out-of-equilibrium states and suggests that temperate areas may be below their equilibrium biodiversity levels, acting as current biodiversity cradles, while tropical areas could be above their biodiversity equilibrium, acting as biodiversity museums. This has profound consequences for understanding diversity dynamics during historical, current, and future climate changes, implying that extinction risk in tropical biomes may be considerably higher than expected

based only on anthropogenic pressures. We show that the equilibrium theory generates realistic phylogenetic trees, reconciles observed geographic patterns in current diversification, and illuminates biodiversity changes during the Cenozoic.

Niches and co-occurrence

131. Climatic niche similarity and spatial co-occurrence in European dragonflies and damselflies: integrating biogeographic patterns and climatic niche similarity

Mónica Gómez Vadillo, *Museo Nacional de Ciencias Naturales (MNCN-CSIC); Joaquin Hortal, MNCN-CSIC; Joaquín Calatayud, University of Umea; Fernanda Alves-Martins, CIBIO-InBIO, Research Centre in Biodiversity and Genetic Resources, University of Porto; Cristina Ronquillo, Departamento de Biogeografía y Cambio Global, MNCN-CSIC, Madrid, Spain*

Species richness patterns are shaped by both current climate and Pleistocene climatic oscillations. Additionally, habitat availability is a key driver of aquatic insect diversity, with lentic (standing water) and lotic (running water) habitats playing distinct roles. Odonates, an order of aquatic insects, show adaptive differences in response to both climate and habitat. A previous study showed that, in Europe, their overall species richness patterns are largely determined by the water–energy balance: temperature limits richness in the north, while precipitation is more limiting in the south, and past climate also influences regional richness. But lotic species richness correlates positively with their habitat availability, while lentic richness shows a negative correlation. Building on these findings, we tested whether co-occurring species also share more similar climatic niches, and whether this relationship varies across habitat types. We built n-dimensional hypervolumes using five WorldClim bioclimatic variables and estimated pairwise climatic niche similarity (Jaccard index) and co-occurrence (shared grid cells). Lentic species showed significantly higher niche similarity among themselves than lotic or intergroup species pairs. Spatial co-occurrence is strongly correlated with climatic niche similarity, especially among lentic and intergroup pairs, suggesting a stronger influence of macroclimatic filtering. Moreover, ecological differences in elevation, niche breadth, and habitat heterogeneity help explain variation in niche similarity, with lentic species exhibiting more predictable patterns. By integrating climatic history, habitat availability, and niche similarity, our work highlights how past and present environmental constraints, combined with habitat affinity, structure both species richness and spatial assemblages in European Odonata.

132. The functional diversity and trait complementarity of co-occurring plant species in patchy vegetation across two habitat types within an arid biodiversity hotspot

Pia Maria Eibes, *Biogeography and Biodiversity Lab, Institute for Physical Geography, University of Frankfurt; Julia Blumensaat, Goethe-University Frankfurt; Liesl Eichenberger, Sanbona Wildlife Department, Sanbona Wildlife Reserve (South Africa); David Kienle, University of Bayreuth*
Katharina Meyer, University of Hamburg; Ute Schmiedel, Institute for Plant Science and Microbiology, University of Hamburg (Germany)

Biotic interactions are important factors in determining the species composition and spatial configuration of vegetation communities at a local level. They play a particularly important role in arid, water-restricted ecosystems, which host highly specialised plant species that often co-occur in patches. Despite its importance as a global dryland biodiversity hotspot, the effects of biotic interactions and co-occurrence patterns in the Succulent Karoo have been investigated by few studies so far, especially at the functional level. In this study, we investigated the impact of co-occurrence on the functional diversity of vegetation patches in two areas of the Succulent Karoo in South Africa (Knersvlakte and the Little Karoo) and analysed whether the results differed between zonal and azonal habitats (quartz islands). We found that species co-occurred more frequently in zonal habitats, while patches in azonal habitats were more frequently composed of single species. When species co-occurred in patches, they tended towards complementary traits rather than similar ones. Co-occurrence preferences may be important to consider during restoration activities on disturbed sites in the Succulent Karoo.

133. From niche theory to demographic realities: the demographic niche concept for understanding range-wide population dynamic

Sean E. H. Pang, *University of Oxford; Erola Fenollosa, University of Oxford; Cory Merow, Yale University; Antoine Guisan, University of Lausanne; Jens-Christian Svenning, Center for Ecological Dynamics in a Novel Biosphere (ECONOVO), Department of Biology, Aarhus University; Roberto Salguero-Gómez, University of Oxford*

Hutchinson's ecological niche concept is central to understanding species distributions. Yet this concept often neglects the demographic processes shaping said distributions. Conversely, demographic theory rarely considers how vital rates (e.g., survival, development, reproduction) vary and covary across environments, limiting insights into range-wide population dynamics. Over 50 years ago, Maguire proposed viewing the ecological niche as composed of multiple "demographic niches" corresponding to distinct vital rates. Despite its promise, this perspective was nearly forgotten. Here, we formalise the Demographic Niche Concept (DNC), building on Maguire's vision while integrating recent advances in niche theory and demography. The DNC highlights four key principles: (i) persistence requires the

concerted effort of multiple vital rates, (ii) vital rates vary across both space and time, (iii) vital rates covary through trade-offs or synergies, and (iv) the realised niche should be understood demographically. We showcase a key innovation of the DNC: the arrangement of demographic niches, visualised in environmental or geographic space. Their degree of overlap, separation, or shift under global change elucidates population persistence, extinction debts, or intervention opportunities. We also propose the unimodal response hypothesis: vital rates generally peak at optimal conditions and decline toward margins, though deviations (density dependence, compensation, truncation) provide further ecological insight. With growing demographic databases, accessibility of process-based models, and remote sensing capabilities, the DNC is increasingly tractable. By linking demography with macroecology, this work provides a foundation for empirical research and practical applications, opening new avenues for developing ecological theory and informing conservation effects in a rapidly changing world.

134. Co-occurrence-based measures of species habitat specialisation revisited

David Zelený, *National Taiwan University, Taipei, Taiwan*

Species habitat specialisation describes how narrowly or broadly a species tolerates environmental variation. Although this concept is central to ecology, its quantification requires high-quality occurrence and environmental data, which are often unavailable. The numerical method introduced by Fridley et al. (2007) offers an interesting alternative. Their theta metric is based on the co-occurrence pattern of a target species with other species within a subset of a community dataset. It represents beta diversity, which quantifies compositional—and, by extension, environmental—heterogeneity across sites where a species occurs. I revisited the theoretical basis of this method and used a series of artificial community datasets to test the performance of individual beta diversity indices. I also reviewed the use of the theta metric in the scientific literature over the past 18 years, with a focus on the use of alternative beta diversity indices. I developed R libraries theta and simcom that introduce tools useful for index calculation and artificial data preparation. Simulations revealed that Whittaker's multiplicative beta is the most universal beta diversity index, and the review shows it is also the most frequently used one in published studies. I recommend its use and demonstrate how the metric can be calculated faster by rarefaction instead of dataset subsetting. The theta index can be straightforwardly converted into the Ecological Specialisation Index (ESI), which can be applied in a manner similar to Ellenberg-type indicator values. I provide an overview of ESI's properties and discuss the advantages and limitations of this approach.

Bird abundance change

141. Diversity regulation and local extinctions in bird communities

Eliska Bohdalkova, *Charles University; David Storch, Center for Theoretical Study, Charles University*

Equilibrium theories of biodiversity dynamics assume that diversity is regulated through diversity-dependence of processes determining species richness (extinction, speciation and/or colonization). We test this assumption at local scales by examining whether bird communities are regulated by diversity-dependent extinction. Using long-term community time-series data from 646 routes of the North American Breeding Bird Survey, we quantified extinction as both absolute extinction count and extinction probability. We assessed key predictors of community-wide extinction rates using correlation analyses, multiple regression models, Random Forest, and Structural Equation Modeling. We tested whether extinction rates are linked to population sizes, population variability, and whether they are higher at sites where species richness is higher than would correspond to resource level (productivity). We show that (i) extinction and colonization rates are balanced across sites, (ii) population size is a key predictor of extinction, with smaller populations experiencing higher extinction rates, and (iii) extinction rates are higher at sites where species richness is higher than would correspond to resource availability. All these results support the hypothesis of diversity-dependent extinction. Extinction rates are further related to population stability, with higher temporal variability increasing extinction risk. Environmental productivity has an indirect negative effect on extinction rates, mediated by population stability, as well as a direct effect. Our findings provide empirical support for diversity-dependent extinction at local scales, contributing to the growing evidence that species richness is regulated and diversity dynamics is often equilibrial. Extinction rates are additionally affected by environmental productivity that influences population persistence.

142. What drives bird abundance? – Quantifying the importance of ecological and anthropogenic drivers for Avian abundance patterns

Heléne Elisabeth Aronsson, *University of Gothenburg; Søren Faurby, University of Gothenburg; Ferran Sayol, Beta Tech Centre - UVic-UCC*

Understanding the ecological drivers of bird abundance is essential for assessing how environmental changes affect bird distributions. Gaining deeper insights into these drivers also provide opportunities to better explain global biodiversity patterns. In this study, we used bird density estimates from the “eBird Status and Trends” dataset - which estimates patterns in abundance while correcting for observer biases, to model the relative importance of abiotic, biotic and anthropogenic conditions in determining abundance patterns for over 2,600 bird species globally. The resulting dataset, containing species-specific drivers of

abundance, enabled us to identify the most important predictors. Our results show that macroclimatic variables and human population density are the most influential predictors of Avian population density across species, whereas presence of agriculture and freshwater availability are less important. We also tested the abundant centre- hypothesis but found little support for it. Overall, our study emphasizes both the importance of natural environmental conditions in determining abundance distributions and the significant role of human activity in shaping global biodiversity patterns.

143. Assessing the impact of past climate and land use change on bird occupancy dynamics in North America

Katrin Schifferle, *University of Potsdam; Natalie Briscoe, University of Melbourne; Mark Urban, University of Connecticut; Damaris Zurell, University of Potsdam*

There is growing evidence that the ranges of many species change in response to environmental change. How different global change drivers contribute to colonisation and local extinction across species is, however, poorly understood. Here, we use dynamic occupancy models that simulate simple metapopulation dynamics to assess changes in occupancy of 159 bird species across the conterminous USA over 25 years (1995-2019). We then attribute these changes to climate and land-use changes. We focus on US breeding birds as the North American Breeding Bird Survey provides a comparatively extensive data set on species occurrences across space and time. In the dynamic occupancy models, we relate site-level colonisation and extinction to climate and land use variables using a Bayesian approach. Simulated occupancy dynamics are evaluated using a spatial and temporal block cross-validation. Finally, we quantify the relative contribution of climate and land use change to the simulated occupancy dynamics based on counterfactual scenarios with detrended climate and constant land use at the levels of 1995, the first year of our observation time series. Our statistical framework allows robust attribution of multiple global change drivers on transient bird occupancy dynamics. This can provide valuable information for species management under environmental change and represents an important step towards operationalising detection and attribution in biodiversity science.

144. Where have all the grassland birds gone? 50 years of range shifts across North America

Wendy Dorman, *University of Illinois - Urbana Champaign; Mike Ward, University of Illinois Urbana Champaign*

The dramatic loss of grasslands coupled with uncertainty in their locations and extent, and the unique and understudied habitat selection behavior of grassland birds, have resulted in a conservation crisis. Grassland birds have shown the steepest, most consistent, and

widespread declines of any guild of birds in North America. While many studies expect birds in North America to shift their ranges north, often little attention is given to which species will move and the mechanism by which ranges shift. Using a Bayesian framework, we modeled shifts in breeding ranges and relative abundances for grassland birds across North America over more than ½ a century. We will discuss model outcomes and management implications for the future of migratory grassland-obligate Avian species.

Geodiversity

151. Understanding multi-scale relationships between abiotic variables, geodiversity and plant biodiversity in a semi-arid ecosystem

Brittany Pugh *Kings College London; Svenja Wanke, University of Bayreuth; Neil Brummitt, Natural History Museum; Jane Catford , King's College London; Juli Caujapé-Castells, Jardín Botánico Canario, Unidad Asociada CSIC; Felix Manuel Medina, Unidad de Medio Ambiente. Cabildo Insular de La Palma; Anke Jentsch, Disturbance Ecology, University of Bayreuth; Mark Mulligan, King's College London*

Existing research identifying plant biodiversity drivers mainly use climatic and habitat variables to define abiotic environments. However, recent studies indicate that geodiversity (variation in geology, geomorphology, hydrology and soil) and biodiversity (including species, traits and phylogenetic diversity) are correlated across spatial scales. Therefore, geodiversity variables are potentially overlooked biodiversity indicators for use in biodiversity assessment and conservation management. Importantly, biodiversity, geodiversity and their relationships do not increase linearly with spatial scale, meaning data collection and analysis scales are expected to impact geodiversity-biodiversity relationship magnitude and direction. Using field data from the Canary Islands, this study assesses whether biodiversity metrics correlate differently with mean abiotic variables compared with their spatial variation (geodiversity). Additionally, we test whether relationships between soil and hydrological abiotic variables with plant biodiversity differ when recorded across plot sizes (2m2 to 30m2). Preliminary results indicate that some biodiversity facets such as height traits may be better explained using variation in abiotic variables compared with mean values, whilst other biodiversity facets are better defined by more commonly used mean indices such as species richness. Preliminary results also indicate that the spatial scale at which abiotic and geodiversity variables are measured and correlated with biodiversity does impact relationship magnitude and direction, with high variation between measured variables. In conclusion, variation in abiotic variables, alongside mean values should be considered as potentially useful drivers of plant biodiversity, especially for plant traits. Additionally, the spatial scale of data collection should be carefully considered when interpreting geodiversity-biodiversity relationships.

152. Revisiting the Anti-Tropical Puzzle: 3D Models Through Deep Time

Hannah Lois Owens, *University of Copenhagen; Wiiliam Ludt, Natural History Museum of Los Angeles County; Corinne Myers, University of New Mexico; Carsten Rahbek, Center for Macroecology, Evolution and Climate, University of Copenhagen*

Why do some species occur in temperate regions of both hemispheres, yet are absent from the tropics in between? These “anti-tropical” distributions have fascinated biogeographers for more than a century and remain the focus of competing explanations, including dispersal across the equator during cooler climatic intervals, extinction within the tropics, or ecological constraints tied to ocean structure. Until recently, the resolution and dimensionality of available data and models limited our ability to test these ideas explicitly. Here I revisit this enigma with new tools to model species' suitable abiotic conditions in three dimensions and project them through deep time. By combining depth-explicit ecological niche models with Cenozoic paleoceanographic reconstructions, I track how suitable habitats for anti-tropical fishes have shifted across both latitude and depth. This framework allows us to ask whether equatorial corridors of suitable habitat opened and closed in step with ocean climate change, and how they may have shifted in depth. Preliminary results indicate equatorial connections were not static, but fluctuated with the changing oceans. Although not universal for all the species studies, these shifts may have provided rare opportunities for some fishes to disperse across the tropics. More broadly, this work demonstrates how integrating 3D ecological modeling with paleoenvironmental data can reveal the dynamic processes underlying disjunct distributions and yield new insights into one of biogeography's enduring puzzles.

153. How can geology and biology help each other? The history of the cave fauna of the Mecsek Mountains, Hungary

Gergely Balázs, *Eötvös Loránd University; Krisztina Sebe, HUN-REN–MTM–ELTE Research Group for Paleontology, Budapest, Hungary; Zsófia Ruszkiczay-Rüdiger*

Caves as habitats are considered isolated and stable environments that respond differently to surface changes than epigean ecosystems. While some geological changes pass almost unnoticed, others have fundamental effects. The dispersion ability of troglobionts is limited. This makes caves evolutionary traps, therefore cave communities should reflect the geological history of an area. The cave fauna of the Mecsek Mountains (SE Hungary) contains representatives of ancient lineages and many troglobionts show extremely high levels of endemism which requires long persisting habitats to evolve. While the karstification of the Mecsek Mountains possibly started as early as 30 mya, recent geological research showed that the recently active caves are only approximately 2.5 million years old. Karstification was interrupted several times by sediment coverage, fill-up, and high marine or brackish water which raises questions about our knowledge on the history of the local cave fauna. Over the

last decades results sometimes contradicted, sometimes reassured the ancient origin of the cave fauna. We evaluated the available literature and concluded that the contradiction only seemingly exists. Most of the aquatic troglobionts show high levels of endemism and are from ancient lineages while this is not true for terrestrial fauna, therefore the biological patterns and the geological results are concordant. Moreover, most of the aquatic species are from taxa with members known to live in interstitial habitats, therefore they could survive in the water and sediment filled caves during high water levels and sediment coverage when classic cave habitats were temporally absent in the area.

154. Methods for measuring geodiversity at local and continental scales in biodiversity research

Helena Tukiainen, *Geography Research, University of Oulu, Finland*

There is a long tradition in biogeographical research of acknowledging the importance of abiotic nature, such as climate and topography, for biodiversity patterns. Recently, there has been growing interest in studying the relationship between biodiversity and the holistic diversity of abiotic nature, known as geodiversity. Geodiversity includes the diversity of soils, rocks, topography, geomorphology, and hydrology on the Earth's surface and subsurface, and it can be measured in a variety of ways at different spatial scales – from simple measures of georichness (the number of geodiversity elements in a site, comparable to species richness) to more complex indices.

In this presentation, I will scrutinize two methods that our research group has developed for measuring geodiversity in a biodiversity context. First, I will introduce a local-scale field methodology for observing geodiversity, which can be applied alongside biodiversity field investigations. Second, I will present a GIS-based methodology by using openly available European-wide geodiversity data as an example. The data is at resolutions of 1 km and 10 km and is specifically designed to be used in conjunction with various types of landscape-scale biodiversity data.

In addition to examining the characteristics of geodiversity measurement methods, this presentation demonstrates their applicability in biodiversity analysis through a range of empirical examples. These examples highlight the various ways in which geodiversity can be integrated into biodiversity research in local and continental scales, offering new perspectives for future studies and further applications, particularly in nature conservation management.

211. Loss of dispersibility in the flora of the Andean Sky Islands

Diana Libeth Aparicio Vasquez, *University of Bergen; Suzette Flantua, University of Bergen Carolina Tovar, Royal Botanic Gardens, Kew; Roswitha Schmickl, Department of Botany, Faculty of Science, Charles University*

Over decades, islands have inspired scientists to develop ideas that have revolutionized our understanding of the origin of species on Earth. Islands often host high levels of diversity and endemism but, despite their endemicity, similar functional traits can be found across different insular biotas. Island syndromes provide fascinating examples of convergent evolution, but their understanding is limited by the lack of fundamental knowledge of species-specific traits and their evolutionary pathways. We introduce a pioneering research project that combines macroecology and phylogenomics to study seed dispersal evolution in insular systems and its contribution to the assembly of the unique insular floras. As our model system, we choose the “sky islands” from the Northern Andes, which bear one of the most spectacular mountain floras worldwide in terms of species richness and explosive evolution. With the aim to assess the link between current species distribution, adaptation and the evolution of seed dispersal, we build a complete database of Andean plant dispersal traits, and we leverage on existing state-of-the-art phylogenies for representative plant groups to achieve ancestral state reconstructions. We hypothesize that adaptation to the extreme environmental conditions that characterize the Andean sky islands resulted in reduced seed dispersal of the high-elevation Andean plants, implying a shift from traits supporting long-distance dispersal, necessary to colonize isolated mountain peaks. We discuss the implications of the presumed loss of dispersibility in the assembly of the Andean hyperdiverse flora and whether theories built upon sky islands can also apply to oceanic islands.

212. Homogenization of plant communities on islands globally

Anna Johanne Walentowitz, *University of Bayreuth; Sandra Nogué, Universitat Autònoma de Barcelona; Manuel J Steinbauer, Bayreuth University*

Floristic homogenization is a widespread characteristic of the Anthropocene and has been extensively studied in recent decades. However, its long-term dynamics over millennia remain poorly understood. We study floristic homogenization over the past 5,000 years by applying pairwise similarity metrics to pollen records from 57 oceanic islands globally. By integrating human history and environmental characteristics of the study islands, we quantify the trajectories of floristic homogenization at global, oceanic and archipelagic scale. Globally, floras have become increasingly similar over the past 5,000 years, although absolute similarity values remain low. Notably, the trajectories of floristic similarity vary

considerably across oceanic basins and archipelagoes, with homogenization partly being displaced by differentiation processes. The similarity of island floras can be explained by a combination of anthropogenic influences and environmental contexts, which jointly shape homogenization and differentiation. As anthropogenic forces continue to reshape plant dispersal pathways and environmental filters, floristic communities increasingly reflect predictable patterns of assembly, highlighting the long-term and directional nature of floristic homogenization in the Anthropocene.

213. Renaturalisation dynamics on Mediterranean small islands detected by plant community resurvey

Alessandro Chiarucci, *BIGEA - University of Bologna, Bologna, Italy*

The biodiversity hotspot of the Mediterranean Basin is home to thousands of islands, with 2217 of them larger than 0.01 km2. The flora and vegetation of these islands have been widely studied in the last century, with a great amount of data collected by many European research centers. This makes the Mediterranean islands an ideal system to study the plant communities' responses to environmental drivers. We set an experimental approach to test the equilibrium theory in island plant communities in face of climate and global changes. To do this we selected a subset of small islands (0.01-1 km2) to relocate and resurvey vegetation plots recorded at least 25 years ago. In the period 2021-2024 we re-surveyed a total of 237 plots on 55 islands belonging to Croatia, France, Greece, Italy and Spain. We assessed consistent compositional changes in small island plant communities, with a general decrease of species richness, coupled with an increase in abundance of woody species. We also detected evidences of secondary successional processes caused by the land uses changes. In some cases, we observed the relevant role of seagull population dynamics, which drove nitrophilic and ruderal species to dominate local plant communities. Our study provides the first insights on the recent changes of plant diversity on small Mediterranean islands, highlighting how land use change appeared to be the major driver affecting this process. These findings suggest renaturalisation dynamics ongoing on these small islands, which deserves to be properly considered to plan effective conservation plans.

214. Island biogeography in the Anthropocene

Tom Matthews, *University of Birmingham; Holger Kreft, University of Göttingen; Ferran Sayol, Beta Tech Centre - UVic-UCC; Filipa Coutinho Soares, Faculdade de Ciências da Universidade de Lisboa, Portugal; Julia Helena Heinen, Center for Macroecology, Evolution and Climate; Søren Faurby, University of Gothenburg*

Islands have long been foundational to the development of ecological and evolutionary theory, serving as model systems for studying patterns of biodiversity. However, pervasive

anthropogenic impacts – particularly species extinctions and introductions – have significantly altered island ecosystems, complicating inferences drawn from contemporary data. Here, we review how these human-driven changes have reshaped key biodiversity patterns on islands, including patterns of species richness, community composition, evolutionary dynamics, and species interaction networks. We show that many current ecological and evolutionary patterns observed on islands reflect not just natural processes but also a legacy of human-induced change spanning millennia. Extinction and introduction processes – often non-random and trait-dependent – have altered classic island biodiversity patterns such as the species–area and species–isolation relationships, driven biotic homogenisation across islands, obscured the prevalence of certain island syndromes and modified the structure of island species interaction networks. Approaches that incorporate palaeoecological and molecular evidence, along with improved databases and modelling techniques, can help better reconstruct pre-human biodiversity baselines on islands.

Faunal Paleontology

221. Temporal uncertainty can mischaracterize ecological niches during periods of climatic instability

Jessica L. Blois, University of California, Merced; André Michael Bellvé, Ohio State University; Val Syverson, University of California, Merced; Marta A Jarzyna, The Ohio State University

Reliable models of species niches and distributions rely on an accurate match between occurrences and environments, which is typically made through associating occurrences to environments via spatial and temporal coordinates. Fossil occurrences, however, can be uncertain in space and time, and temporal uncertainty is particularly acute for vertebrate fossils due to assemblage time-averaging. Time-averaging may create mismatches between fossils and associated environments, distorting models of inferred niche and distribution. We sought to determine how temporal uncertainty affects the reconstruction of species niches and distributions. We used a virtual ecology approach, examining how varying degrees of temporal uncertainty (±200 years - the entire late Quaternary) affected niche and distribution estimation, for four virtual species centered on three different periods (Holocene, 6ka; deglacial, 13.5ka; Last Glacial Maximum, 18 ka). For each level of temporal uncertainty, we compared the “true” niche/distribution with the “uncertain” niche/distribution, by matching occurrences from the focal period with environmental layers drawn from different times within the temporal uncertainty window. We then examined whether mismatch varied with time period, temporal uncertainty, or environmental variability. Overall, during periods of environmental stability, niches/distributions were robust to temporal uncertainty; while individual species or reconstructions within some periods were influenced by uncertainty, significant mismatch didn’t occur until ±1500 years uncertainty. However, the magnitude of

environmental variability influenced accurate estimation of niches and distributions - mismatch was highest during the environmentally-variable deglacial period. These results highlight potential for accurate paleodistribution reconstruction, as well as indicate conditions in which reconstructions may be limited.

222. Biotic interactions are more important than climate for shaping animal niches

Inger Greve Alsos, *The Arctic University Museum of Norway; (UiT) Dorothee Ehrich; Dilli Rijal; Marie Merkel, UiT; Anne Karin Hufthammer, University of Bergen; Youri Lammers, UiT; Antony Brown, UiT; Jan Magne Gjerde, Norwegian Institute for Cultural Heritage Research; Nigel Yoccoz, UiT; Jostein Bakke, University of Bergen; Kari Anne Bråthen, UiT; Chris Clark, University of Sheffield; Helen Dulfer; Lucas Elliott, UiT; Christer Erséus, University of Gothenburg; Peter Heintzman, Stockholm University; Karin Helmens, Swedish Museum of Natural History; Dirk Nikolaus Karger, Swiss Federal Institute for Forest, Snow and Landscape Research WSL; Sylvain Monteux, UiT; Loïc Pellissier, WSL; Sakari Salonen, University of Helsinki*

The response of ecosystems to ongoing rapid climate change is dependent on individualistic species response and biotic interactions. It is therefore critical to know how realised niches shift with changing climate and changing biotic interactions among species. At present, empirical niche investigations rarely include biotic niche dimensions and are limited to short time spans. Sedimentary ancient DNA (sedaDNA) is revolutionising our ability to study the development and dynamics of ecosystems by enabling the simultaneous identification of plants and animals from their past living environments. Here, we develop this method by combining sedaDNA from ten lakes with a novel compilation of regional rock-art and bone records, as well as palaeo-topography, to reconstruct animal arrival times, changes in plant–herbivore-carnivore networks, and estimate shifts in the biotic and climatic niches for key animal species over the last 16 ka. Marine fauna and tundra plants appeared soon after deglaciation, and birds and freshwater species arrived at approximately 13 ka. However, reindeer did not appear until 5 millennia later at 11 ka, and most terrestrial mammals arrived only in the last 8 ka after vegetation had stabilised. Realised climatic and biotic niches shifted with increased herbivore niche-filling, and niche-overlap increased with ecosystem complexity build-up, implying increasing herbivore interactions. Our study provides the first long-term empirical evidence that shifts in biotic interactions are more important than climate for shaping ecosystems, and must be considered when attempting to mitigating effect of climate change.

223. Mammalian carnivore guilds respond differently to the terminal Pleistocene extinction

Felisa A. Smith, *University of New Mexico; Emma Elliott Smith, University of New Mexico; Catalina P. Tomé, Indiana State Museum; S. Kathleen Lyons, Unviversity of Nebraska - Lincoln*

At the terminal Pleistocene human activities began a strikingly size-biased extinction of large-bodied mammals, which continued through the Holocene and has accelerated in modern times. This trophic and body size downgrading is leading to changes in the structure and function of modern ecological communities because the role of large-bodied animals is not always replicated by smaller-bodied congeners. Here, we use the fossil record of the terminal Pleistocene megafauna extinction in the Americas as a proxy for characterizing the consequences of modern biodiversity loss, with particular emphasis on the carnivore guild. We examine four families, the Felidae, Canidae, Mephitidae and Mustelidae, who experienced very different levels of biodiversity loss. Using fossils from the Edward's Plateau of Texas, we quantify both the isotopic (δ13C and δ15N) and body-size niche at 7 time intervals from the late Pleistocene to modern (~20 to 0 ka) biodiversity loss to assess shifts in the ecology and ecological interactions of survivors. We find in the Pleistocene, there was a strikingly regular partitioning of dietary isotopic niche with body size within each carnivore family that was largely non-overlapping. Moreover, the largest carnivores were highly specialized. Post-extinction, shifted their dietary isotopic niche and considerable body size and isotopic niche space were lost; most carnivores became more generalized. We find evidence of prey-tracking among Felidae, but not for other carnivores. Our work highlights the importance of integrating a paleontological perspective into modern conservation efforts to develop a more synoptic understanding of ecosystems.

224. Carrying capacity of the Pleistocene mammoth steppe

Wolfgang Traylor, *Independent researcher; Matthew Forrest, Senckenberg Biodiversity and Climate Research Centre (BiK-F); Thomas Hickler, Senckenberg Biodiversity and Climate Research Centre (BiK-F)*

During the last glacial, large grazers inhabited Eurasia's mammoth steppe. This cold steppe was productive enough to sustain a diverse assemblage of large mammals, but it remains controversial which population densities it could support. Whether large herbivores created or sustained the mammoth steppe depends on carrying capacity. We developed a process-based grazer model, dynamically coupled with a dynamic global vegetation model, in order to simulate a range of plausible glacial grazer densities. We simulated the woolly mammoth (Mammuthus primigenius) as a proxy for estimating an upper bound of per-area carrying capacity for the large-herbivore guild. Based on informative prior distributions for all grazer parameters we performed Bayesian sampling that maximizes mammoth survival over its climatic niche. This approach let densities emerge bottom up from the mechanistic model.

The resulting posterior densities for mammoth steppe carrying capacity lie in between lower and higher estimates from earlier studies. Even though our approach could only capture part of the predictive uncertainty, our results prompt caution to extrapolate very high potential megafauna densities as a natural baseline.

Human impacts and conservation

231. What species are used by restoration projects and what does that mean for the Sahel: a north Nigerian case study

Joao de Deus Vidal, *University of Leipzig; Abubakar Bello, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; Enrico Ille, University of Leipzig; Kimberly Thompson, iDiv; Janina Kleemann, Martin-Luther-University Halle-Wittenberg, Institute for Geosciences and Geography, Dept. Sustainable Landscape Development; Alexandra N. Muellner-Riehl, Leipzig University*

Ecosystem restoration is a key strategy for mitigating biodiversity loss and climate change. These efforts often involve the introduction or re-establishment of plant species, but the selection of species and restoration practices varies widely across interventions. Although such projects are increasingly widespread and play a major role in national environmental goals, little is known about how species selection affects restoration outcomes. Here, we document different aspects of the species used across regreening projects in Nigeria to understand the rationale and impacts on local restoration. We combine field surveys, stakeholder interviews, project documentation, and time series of satellite-derived greenness data to provide a comprehensive database with commonly used species by projects in Kano, Katsina, and Jigawa during the past 50 years. Our results show that while most projects still rely on Eucalyptus and Azadirachta indica, native species such as Acacia senegal, Balanites aegyptiaca, and Khaya senegalensis are becoming more frequently utilised, with objectives shifting from landscape management to climate change mitigation. Our study also shows that species selection influences the effectiveness of restoration in achieving different goals, and that the policy-to-practice translation is driven mostly by the interaction between farmers, nurseries, and project offices. We provide examples of long-term change, demonstrating how local economic, political and ecological contexts reflect methodological approaches to restoration. These insights can inform future regreening efforts across the Sahel and other drylands, where scaling up successful models depends on aligning explicit goals with ecological knowledge and local practices.

232. Urban fungal diversity shaped by legacy effects of historical meadows

Oscar Zarate Martinez, *University of Tartu; Meelis Pärtel, University of Tartu; Petr Kohout, Institute of Microbiology of the Czech Academy of Sciences*

Historic land use is an important predictor of current species diversity and distribution across various organism groups. While some evidence links modern landscape configuration to soil biodiversity, the scale at which historical landscape legacies affect soil microbial communities remains unclear. We investigated the response of arbuscular mycorrhizal (AM) fungal diversity to long-term habitat loss and fragmentation due to urbanisation. Soil samples were collected from 764 urban green areas in the city of Tartu, Estonia, where land use has been recorded since the early 20th century. AM fungal diversity was assessed using DNA metabarcoding. Historical proximity to meadows, forests, urban areas, and croplands was derived from historical topographic maps. We found a significant association between AM fungal diversity and historical proximity to meadows: current AM fungal diversity was higher in areas that were within 200 meters of meadows in the early 1900s. These results demonstrate that past land use continues to shape urban soil microbial communities. Recognising historical landscape legacies is important for understanding present-day biodiversity patterns and should be considered in future urban green space planning and soil conservation strategies.

233. CamtrapReport: An R Package for Automating Camera-Trap Data Reporting for Wildlife Monitoring

Elham Ebrahimi, *Wageningen University and Research; Patrick A. Jansen, Utrecht University*

Camera traps are vital for wildlife monitoring and biodiversity research, enabling continuous data collection across diverse ecosystems. However, processing, standardizing, and analyzing these datasets can be challenging, as existing methods for data validation, interpretation, and visualization are often too complex for many end users. Beyond simplifying workflows, there is a critical need to establish reproducible computational pipelines that ensure transparency, comparability, and reliability in ecological research, ultimately strengthening biodiversity conservation efforts. To address these challenges, we developed camtrapReport, an object-oriented, extensible, and mutable R package that delivers reproducible camera-trap data processing workflows and automates the generation of informative ecological reports. The package accepts datasets formatted in the widely used Camtrap DP standard and is organized into three main components: (i) Data Status Check, which performs automated diagnostics of data quality; (ii) Report Generation, which produces standardized outputs with a comprehensive suite of ecological analyses and visualizations, including sampling effort, species richness, species co-occurrence, abundance distributions, community composition, habitat use, activity patterns, population density, and spatial mapping; and (iii) a Graphical User Interface, a Shiny-based environment

for interactive filtering and exploration of results. By transforming raw camera-trap data into structured ecological insights, camtrapReport standardizes data collection and analysis, thereby enhancing comparability, scalability, and reproducibility across sites and time. Its automated workflow reduces technical barriers, supports users across programming skill levels, and accelerates biodiversity trend detection and wildlife status assessment. In doing so, the package enables transparent, efficient, and timely ecological reporting, providing a powerful tool for evidence-based conservation decision-making.

234. Spatial biodiversity indicators and a composite index for conservation prioritization in Switzerland

Antoine Adde, *Eawag - Swiss Federal Institute of Aquatic Science and Technology; Victor Boussange, WSL; Yohann Chauvier, Eawag; Marie-Ange Dahito, WSL; Johan Früh, WSL; Antoine Guisan, University of Lausanne; Catherine Graham, Swiss Federal Research Institute WSL; Loïc Pellissier, WSL; Niklaus E. Zimmermann, Swiss Federal Research Institute WSL; Florian Altermatt, EAWAG*

Spatially explicit indicators that quantify to which extent landscapes support biodiversity are essential for guiding evidence-based conservation planning, yet they are often limited to only one or a few biodiversity dimensions as input. Here, we present a high-resolution (25 meters) dataset for Switzerland that supports conservation prioritization at the national scale. It includes three key biodiversity indicators—Complementarity, Extinction Risk, and Ecological Connectivity—developed from habitat suitability maps of about 7,500 species, which together can serve as a composite index. The Complementarity Indicator (CI) measures the conservation importance of a pixel based on its contribution to taxonomic, functional, and phylogenetic diversity, as well as its distinct community species composition; the Extinction Risk Indicator reflects the importance of a pixel for maintaining species, with emphasis on rare and at-risk species; and the Ecological Connectivity Indicator captures the role of a pixel for maintaining group-specific habitat connectivity across the landscape. Each indicator was generated independently and then rescaled to a common dimensionless 0 to 1 scale. All indicators are provided both individually and as part of a composite index, and are available separately for individual species groups. Layers are delivered in raw form as well as in versions adjusted for species richness, acknowledging that all three indicators are influenced by richness levels. Relationships among the three indicators were analyzed to assess their distinct contributions to the composite index. This dataset and underlying methods provides a robust multidimensional foundation for spatial conservation planning and can serve as a blueprint for developing similar indicators in other regions.

Macroecological Drivers of Avian Community Assembly and Change

241. Large-scale co-occurrence dynamics in bird assemblages

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Studies of biodiversity dynamics in recent decades have shown stronger changes in community composition than in species richness. Yet the exact nature of how species assemblages change remains unclear. Focusing on birds, we analyzed spatial associations (co-occurrences) among species pairs using four independent, large-scale, long-term datasets covering the Czech Republic, Europe, New York State, and New Zealand. Each dataset spans an average duration of 30 years, offering a unique temporal view on co-occurrence patterns. Given the environmental changes and the generally observed temporal community composition turnover, we also expected to see changes in the spatial associations among species. Surprisingly, we found that large-scale bird co-occurrence patterns remained remarkably stable through time. Changes in spatial associations lacked any directional trend and did not correspond with species' phylogenetic or functional distances, nor with shifts in their range sizes. There was mild evidence for changes towards more aggregation in aquatic species. In addition to small quantitative changes in co-occurrence of species pairs, the per-species composition of associated species showed little change over time as well. Overall, our data show that most species maintain their spatial associations over decades, suggesting that co-occurring species show comparable reactions to environmental changes. Exploring how this surprising stability in co-occurrence patterns aligns with previously observed temporal community composition turnover could be an exciting direction for future work.

242. Replacing extinct birds with similar extant birds using a functional trait-based method

David Pereira, *University of Birmingham; Tom Matthews, University of Birmingham; Jon Sadler, University of Birmingham; Joe Wayman, University of Birmingham; Tom Martin, Lancaster University*

Oceanic islands harbour high species diversity and endemism. But since human colonisation of islands, their endemic species have become threatened by anthropogenic drivers such as habitat loss, overexploitation and the introduction of invasive non-native species. As such, many endemics were driven to extinction, with birds being particularly hard hit. A consequence of these extinctions has been the loss of unique species traits responsible for the performance of ecological roles, such as seed dispersal and pollination, which help maintain island ecosystem function. The introduction of ecological substitutes – extant species capable of performing similar functions once performed by extinct species – has been trialled as a means to restoring missing island ecosystem functions. Yet approaches for selecting substitutes have varied by case, and so far, there is no unified evidence-based method to identify them and assess their suitability as replacements. To address this research gap, we use a novel application of trait-based approaches to identify and compare extant island birds who could theoretically replace functional traits lost due to extinction at a global scale. We use global Avian trait databases, including both extant and extinct birds, focusing on traits linked to ecological roles. Results will highlight candidate species which best approximate the traits of extinct island endemic birds. By providing an analysis-based method from which to select and evaluate replacements, this study aims to improve island conservation strategies concerning the evaluation of ecological replacement suitability to restore missing ecosystem functions.

243. Unpacking species richness anomalies: The interplay of regional history and local abundance in Nearctic and Palearctic temperate forest birds

Vladimir Remes, *Palacky University; Tereza Hladka, Palacky University*

Species diversity varies significantly across space and time due to current ecological conditions and historical factors. Diversity anomalies, where areas with similar climates exhibit strong differences in species diversity, are ideal for disentangling drivers of this variation. Previous research indicated larger bird species pools in temperate forests of North America (Nearctic) than Europe (Palearctic). However, these studies focused on broad continental or regional scales, with limited examination of local scales or abundances. To fill this gap, this study provides a detailed insight into this diversity anomaly in temperate forest birds, examining both regional and local scales using comprehensive territory mapping data from 202 sites in eastern North America and Europe. Regionally, we confirmed a larger species pool of forest specialists in eastern North America, with 94 species detected

compared to 71 in Europe. In contrast, on a local scale, European sites exhibited slightly higher species density and total individual density. Abundance-based rarefaction also showed higher local species richness in Europe, with the difference increasing at higher total abundances. We propose that the higher local diversity in European forests is driven by greater bird abundances and increased recruitment from species pools. Our findings highlight that regional biodiversity does not necessarily predict local species richness, emphasizing the importance of multi-scale biodiversity studies.

244. Contrasting mechanisms of African raptor colonization in Europe via climatic favourability and assisted vagrancy

Antonio Román Muñoz Gallego, *Universidad de Málaga; Sandro López Ramírez, Universidad de Málaga; José María García-Carrasco, Universidad de Washintong; Raimundo Real, University of Malaga*

We investigated the mechanisms underlying the recent colonization of Europe by African raptors, a process that entails overcoming not only geographical barriers but also the biogeographic boundary between the Afrotropical and Palaearctic realms. Focusing on the Atlas Long-legged Buzzard (*Buteo rufinus cirtensis*), Rüppell's Vulture (*Gyps rueppelli*), and White-backed Vulture (Gyps africanus), we modelled breeding favourability across 6,203 operational geographic units in the Afro-Palearctic region. We then compared model outputs with known breeding records, recent sightings, and species-specific traits, including evidence of interspecific interactions and hybridisation. The Buzzard displayed broad favourability across North Africa and parts of southern Europe, consistent with recent breeding and a likely climate-driven expansion. In contrast, the African vultures showed minimal climatic favourability in Europe. Yet, Rüppell's Vultures have bred in the region, always as hybrids with Griffon Vultures (Gyps fulvus), and White-backed Vultures are increasingly observed as immatures. These patterns suggest a distinct, behaviourally-mediated colonization process involving socially assisted vagrancy, whereby immature African vultures accompany Griffon Vultures across the Strait of Gibraltar and integrate into their social and spatial networks. Our findings reveal contrasting mechanisms of biogeographic transgression: climate-driven expansion in the case of the Buzzard, and socially facilitated dispersal among vultures. These results underscore the importance of integrating behavioural ecology and interspecific interactions into species distribution models, especially when forecasting range shifts in response to global change. Vagrancy, particularly when socially assisted, emerges as a key and underappreciated mechanism shaping contemporary species redistribution.

Impacts of Hunting

251. Translating ecological models into genomic simulations: a spatially-explicit reconstruction of muskox genomic data responding to climate change and human hunting

Elisabetta Canteri, *University of Copenhagen; Martin Petr, University of Copenhagen; Fernando Racimo, University of Copenhagen*

Investigating the effects of environmental changes on species distributions has been a central focus of biogeography studies. This has been usually done by employing ecological niche models (ENMs), but recently, advancements in modelling techniques allow to explicitly simulate population dynamics responding to global change drivers, incorporating ENMs into spatially-explicit population models (SEPMs). Given that the ecological processes that shape species distributions also determine patterns of genomic diversity, translating these spatially- and process-explicit ecological models into genomic simulations might provide new opportunities to better understand evolutionary processes in space and time, determine the genomic signatures of extinction and resilience, and directly evaluate the effects of environmental changes on the genome. In this study, we have developed a pipeline for translating process-explicit ecological models into spatio-temporal genomic simulations. Using muskox as a case-study, we used the 'paleopop' R package to simulate 21,000 years of population growth, extirpation, and dispersal responding to changes in environmentally suitable conditions and hunting by humans. Model outputs are gridded maps of simulated population abundances, which were used as input in the 'slendr' R toolkit to simulate muskox genomic data. This will allow us to determine how well process-explicit ecological models match (ancient or present-day) genetic data from a target organism, and potentially refine SEPM model fitting by matching real genomic data to simulated genomic data, in combination with ecological data matching. Our framework provides a way forwards towards genomically-informed process-explicit analyses of species distributions, to ultimately unveil the impacts of environmental changes at multiple biodiversity levels.

252. Uncovering the cryptic vulnerability of tropical birds and mammals to hunting

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Unsustainable hunting is a major yet underrepresented driver of biodiversity loss in tropical ecosystems. Most global assessments rely on the IUCN Red List, which fails to adequately incorporate the spatial dimension of threats. Here, we present a trait-based vulnerability assessment of tropical birds and mammals to hunting, applying a framework of exposure, sensitivity, and adaptive capacity across their tropical ranges. Exposure was mapped using

spatial predictions of hunting pressure, while species-specific sensitivity and adaptive capacity were inferred from ecological, morphological, and life-history traits. We observed strong geographic variability in vulnerability. The Indomalayan realm had the largest extent of highly vulnerable areas, in Southeast China and the Sunda Islands, with refugia in New Guinea, central Borneo, and Sichuan. In the Afrotropics, vulnerability peaked in the Gulf of Guinea and Southeast Africa, whereas the Congo Basin had areas that were not particularly vulnerable. The Neotropics showed mostly low-risk zones, with persistent hotspots in the Gulf of Mexico and the Atlantic Forest. Patterns were consistent between taxa but varied by hunting purposes. Species-level analyses showed: first, the identification of highly vulnerable species, *Melursus ursinus, Elephas maximus, Axis axis,* and *Macaca nigra* among mammals, and *Amazona barbadensis, Pavo muticus,* and *Ardeotis nigriceps* among birds; second, the presence of strong phylogenetic biases in vulnerability. We also confirmed that several species currently listed as not threatened displayed high vulnerability. By proposing the first spatially explicit assessment of species' vulnerability to hunting, we provide outputs that can inform conservation planning, complement IUCN assessments, and support global biodiversity targets.

253. Size-biased defaunation reshapes biomass and body mass distributions of wild mammals across tropical forests

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Human activities have caused profound defaunation of tropical mammal communities since the Late Pleistocene, with habitat loss and overhunting disproportionately impacting large-bodied vertebrates. Despite local- and regional-scale assessments, pantropical estimates of human impacts on biomass and body mass distributions across trophic guilds remain lacking. We assessed shifts in biomass and body mass distributions of tropical mammals between a baseline scenario based on historical unimpacted ranges, and a present-day scenario where communities have been affected by hunting and habitat loss. Hunting-induced changes in abundance were projected based on Bayesian regression models, while habitat loss was assessed by comparing historical and current suitable habitat availability.

Total biomass has collapsed by 64.5% (265.0 to 94.0 Mt wet weight), driven particularly by losses of megafauna such as proboscideans (-94%). These losses have driven Afrotropical and Indomalayan biomass levels to converge toward historically lower Neotropical values, leaving only 2.5 million km^2 of tropical forests (7.6%) with near-baseline biomass levels. Additionally, mammal communities shifted from 2.04 kg to 0.8 kg in average body mass (48% of reduction), with herbivores and carnivores showing the most severe declines. Defaunation of large-bodied species affected trophic guilds differently, yet community-weighted means showed consistent distributions across biogeographic realms and scenarios. Our study provides the first pantropical quantification of how synergistic human pressures have reduced mammalian biomass and homogenized body mass distributions across the tropics, highlighting the importance of baseline conditions for understanding the extent of human-driven changes in modern tropical mammal assemblages.

254. What's on the menu and what's good? Understanding spatiotemporal variation in zooarchaeological assemblages using ecological niche models

Peter Yaworsky, *Aarhus University & Copenhagen University, Denmark*

Models, methods, and theory developed by ecologists are often adopted and adapted by archaeologists. In recent decades, archaeologists interested in understanding how aspects of the environment influences and structures human dispersal and land use patterns have incorporated models used by ecologists understanding species' distributions. Here I will focus on models collectively referred to as ecological niche models (ENMs) and how they can be used in concert with anthropological archaeology to address important questions relating to human-environment interactions, subsistence variation, and species extinctions during the Middle Pleistocene to early Holocene. At the core of these questions is understanding local hunting ecologies and human hunting decisions, or what's on the menu and what's good on the menu. Using ENMs, we can estimate species compositions of specific hunting ecologies in the past to understand what's on the menu. Then, using Prey Choice Model, we can estimate what's good on the menu based on subsistence payoffs, like calorie, fat, and other macronutrients. In combination we can a). derive expectations about human-animal interactions and the composition of specific zooarchaeological assemblages to better understand spatial and temporal variations in the archaeological record, b). identify the hunting ecologies in which specific species are more likely to be hunted, and c). better define the role humans and climate played in specific extinction events.

Rewilding, Herbivores, and the Future of Ecosystem Function

311. Northwest Shift in Suitable Climate Expected for North American Bison by the Year 2100

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In response to changing climate, numerous species are beginning to shift their geographic ranges. However, dispersal limitations for wildlife continue to increase in prevalence and severity due to habitat loss and land fragmentation, complicating the management and conservation of species. Addressing this challenge in North American bison (Bison bison) is exceptionally challenging, due to their dual identity as wildlife and livestock. Although bison are a species of high ecological, cultural, and economic importance, the size of the bison population remains at risk since their near extinction in the 1800s. We compiled 21,000 years of paleontological, archaeological, and historical records prior to 1700 CE of bison to develop a comprehensive climate envelope model that avoids the bias of heavily human-modified distributions. We used a variation inflation factor and LASSO model to determine that warmest temperature of the warmest month, temperature seasonality, and precipitation of the coldest quarter predicted bison occurrences, resulting in an AUCROC score of 0.7853. Moreover, it identified an optimum threshold of 8.5%. To assess changes in climate suitability with predicted increases in aridity and temperature, we projected the model onto the present climate and four future time intervals extending to 2100. By 2100, the centroid of suitable climate is expected to shift northwest from the U.S-Canadian border toward the northern border of Canada. The rapid northwest movement of suitable bison climate demonstrates the need for anticipatory studies to help guide conservation strategies to mitigate the hindered ability of modern species to track suitable climate.

312. Plants and large mammals have historically tracked climate with high fidelity in North America, then diverged after the arrival of Europeans

Corentin Gibert Bret, *Université de Lille - EEP Lab; Julia A Schap, Georgia Institute of Technology; Jenny McGuire, Georgia Institute of Technology; Benjamin Ranier Shipley, Georgia Institute of Technology; Yue Wang, Sun Yat-sen University*

The relationship between climate and species distributions is highly complex as illustrated by the fact that, today, half of observed species are not tracking climate in directions predicted by niche models. However, this apparent complexity could be link to the fact that large-scale

dispersal is a long-term process, difficult to detect with modern data and that could be hindered by anthropogenic pressure. In consequence, we have reconstructed the climatic niches of 16 genus of plants and 45 species of mammals in North America from the last deglaciation to modern days. Measuring the temporal stability of climatic niches at multiples scales, we demonstrate that plants have tracked climate better than mammals. Some large mammals have depicted comparable capacity than plants, but most small mammals were struggling to keep-up with last climate change. When looking at the effect of the growing anthropogenic impact, mammals were more strongly impacted than plants. Plants climatic niches were weakly impacted by the exploitation of the land, when large mammals have been strongly extirpated from areas that would become settlers' cities and crops. These large mammals have been pushed toward cold and arid area mal-adapted to industrialization. On the opposite, small mammals were facilitated to cities and crops. At continental scale, plants communities constantly depicted a latitudinal gradient of climate fidelity since deglaciation. The same latitudinal gradient in mammalian communities started to fade under the pressure of natives and totally disappear after the arrival of European, replaced by a pattern corresponding to land-use intensity.

313. Parallels between hemiparasitic plants and large herbivores: implications for rewilding of European landscapes

Jakub Těšitel, *Masaryk University, Brno, Czech Republic*

The importance of large herbivores for ecosystem functioning and biodiversity maintenance is recognised worldwide. This gave rise to the trophic rewilding framework currently used in a series of projects aiming at fostering ecosystem functioning and supporting biodiversity. Based on evidence from field experiments and large-scale biogeographic research, I argue that hemiparasitic plants have ecosystem effects which are very similar to those of large herbivores. Hemiparasites suppress the growth of their hosts and impact on the competitive balance in the community. Thus, they decrease the dominance in plant communities, including also preventing or even reversing encroachment by competitive grasses and shrubs. Recent research has demonstrated their ability to strongly suppress some noxious invasive plants. Beyond direct parasitism, they accelerate nutrient cycling through litter effects and create gaps in communities, thereby facilitating seedling establishment. The nutrient cycling and availability may be further supported by a special, partly mutualistic interaction between hemiparasites and nitrogen-fixing legumes. Besides vegetation, hemiparasitic plants affect higher trophic levels through cascading effects. Reduction of grasses and supporting forbs also supports forb-feeding insects and pollinators. Reduction of sward density and the resulting gaps create habitats for heliophilous arthropods. Hemiparasitic plants are an ubiquitous component of European biota, albeit decreasing due to land-use change. On the large scale, their occurrence is associated with high species

richness of the vegetation, reflecting their multifaceted ecological roles. Integrating hemiparasites into rewilding strategies could enhance biodiversity and ecosystem resilience.

314. Food web similarity increases with productivity similarity at a continental scale

Lydia Beaudrot, *Michigan State University; Ann Finneran, Rice University; Cesar Uribe, Rice University; Kai Hung, MIT; Chia Hsieh, Department of Integrative Biology, Michigan State University; Matthew Wuensch, University of North Dakota; Matthew McCary, Rice University*

Primary productivity and trophic interactions are fundamentally linked. However, it remains largely unknown how food web structure varies along primary productivity gradients at large spatial scales. Furthermore, anthropogenic pressure threatens the integrity of food webs globally. Here, we test how plant productivity and anthropogenic fragmentation predict the pairwise similarity of food web networks within and among regions for 127 protected areas that span deserts to tropical rainforests. We measured food web structural equivalence independent of species identities and accounted for the inherent scale dependency of food web structure with species richness and connectance. Food webs were significantly more similar where plant productivity was similar at the continental scale and within some regions, but did not vary significantly with anthropogenic fragmentation. These empirical results inform how food web structure mediates biodiversity and ecosystem function.

315. The walking forest: how palatable trees regenerate in the presence of large herbivores

Liesbeth Bakker, *Netherlands Institute of Ecology; Nacho Villar, Netherlands Institute of Ecology NIOO-KNAW; Céline Sijlmans, Netherlands Institute of Ecology*

Contemporary west-European landscapes are often devoid of most wild large herbivores, or these occur in very low densities. Therefore, if large herbivores are present at higher densities, they often are considered 'too abundant' to let natural processes, such as tree regeneration, take place. Especially the regeneration of palatable tree species becomes limited in forest stands, in the presence of herbivores. However, paleo-evidence shows that palatable trees and high densities of wild herbivores have co-occurred, suggesting that there are mechanisms that allow palatable trees to regenerate in the presence of herbivores. Here, we test the walking forest concept, which predicts regeneration of palatable, light-demanding trees, such as oak, to occur in open fields, away from the dense forest. Furthermore, oak regeneration is particularly successful by association with thorny shrubs in the presence of herbivores. We demonstrate in two rewilding areas in The Netherlands that these evolutionary species-interactions drive regeneration of palatable trees in grazed and browsed landscapes, creating forest landscapes rather than forests and open grasslands. Over time, this will result in spatio-temporal mosaics of grassland, shrubs and trees, as also described

from paleo-evidence. Therefore, the patterns found in paleo ecology inform current landscape restoration, whereas current tests of species interactions provide mechanisms that can explain the development of forest landscapes in the present and past.

316. Trophic Rewilding as a Biogeographic Strategy for the Anthropocene

Jens-Christian Svenning, *Aarhus University, Denmark*

Biogeography in the Anthropocene demands restoration approaches that align with rising ecological novelty. Trophic rewilding—in practice, restoration of trophic complexity via diverse, wild-living megafauna while reducing human control—offers a principled pathway. Synthesizing paleo- to present evidence, current knowledge indicates that megafauna re-establish core processes underpinning biodiversity and ecosystem functioning: vegetation and soil heterogeneity, seed dispersal, nutrient redistribution, and creation of biotic microhabitats; these effects interact with geodiversity to structure fine- to landscape-scale mosaics. An integrative framework is articulated linking trophic rewilding to biogeographic dynamics under accelerating global change: (i) facilitation of plant range shifts via body-size–dependent dispersal; (ii) enhancement of microclimatic variability and functional redundancy that buffers ecosystem collapse; (iii) moderation of invasive plant dominance via herbivory; and (iv) scalability through autonomous population dynamics and, where appropriate, functional replacements, including carefully screened non-native megafauna. Climate relevance is evaluated, emphasizing that rewilding can aid adaptation and may contribute to mitigation (e.g., reduced catastrophic fires, potential soil-carbon gains, altered albedo), while acknowledging uncertainties and the primacy of rapid emissions reductions. Implementation requires attention to social-ecological context, governance, equity, and coexistence in human-dominated landscapes. Priority tests are outlined—from trait-based predictions of faunal functional completeness to spatial mapping of where restoring extant species to near-natural ranges most increases community biomass and process rates—to embed trophic rewilding within biogeography's modeling, monitoring, and planning agendas. Properly designed, trophic rewilding has potential to convert novel assemblages from risk into opportunity for biodiversity and people, with adaptive management at scale globally.

Linking Evolution, Traits, and Ecosystem Function in Birds

321. From Core to Periphery: Mapping Evolutionary Potential Across Species Ranges

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of Aarhus University; Leiting Yang, Center for Evolutionary Hologenomics, Globe Institute, University of Copenhagen; Goujie Zhang, Evolutionary & Organismal Biology Research Center Zhejiang University, China; Hernán E Morales, University of Copenhagen; Shaohong Feng, Evolutionary & Organismal Biology Research Center Zhejiang University, China; Carsten Rahbek, Center for Macroecology, Evolution and Climate, University of Copenhagen; David Nogues-Bravo, Center for Macroecology and Evolution

Peripheral populations are often thought to exhibit reduced genetic diversity and increased genetic differentiation due to smaller effective population sizes and greater isolation, yet this widely accepted idea—central to the center-periphery hypothesis—has rarely been tested using whole-genome data. Understanding how genomic diversity, inbreeding, and mutational load are distributed across species' ranges is critical for evaluating the evolutionary potential of populations under environmental change. Here, we integrate whole-genome sequencing data from 88 Avian species with geographic range data to investigate how spatial position within a range affects key genomic metrics. By combining estimates of heterozygosity, inbreeding (runs of homozygosity), and genomic load with spatial measures of peripherality, we aim to disentangle the effects of demography, drift, and selection across biogeographic gradients. This work provides a foundation for understanding how evolutionary processes shape genetic variation within species and informs conservation strategies focused on range-edge populations.

322. Contrasting Evolutionary and Environmental Drivers of Avian Niche Diversification Worldwide

Chia Hsieh, *Department of Integrative Biology, Michigan State University; Peter Wiliams, Department of Integrative Biology, Michigan State University; Fredric Janzen, W. K. Kellogg Biological Station, Michigan State University; Elise Zipkin, Michigan State University*

Ecological niches emerge from evolutionary processes shaping trait adaptations to environmental dynamics across deep timescales. While previous studies often isolate single traits or latitudinal gradients, such approaches insufficiently incorporate the multidimensional strategies species use to survive and reproduce. Consequently, we lack a comprehensive understanding of how niche evolution along multiple dimensions, such as physiology, resource-use, and reproduction, has responded to environmental dynamics at regional scales. This limits our ability to assess vulnerabilities under future environmental change. Using native, resident birds as a global model, we integrated multi-trait diversity and phylogenetic information to quantify evolutionary signals along three major niche dimensions - overall ecological strategies, environmental envelope-resource use, and life history-breeding - across 604 terrestrial biogeographic regions. We then applied regression models to test how speciation rate and long-term environmental variability in climate and productivity shape patterns of niche evolution. We found that higher speciation rates were consistently associated with slower evolutionary signals, reflecting accumulation of similar ecological

niches along species diversification. In contrast, environmental variability over geological timescales had dimension-specific effects: temperature variability primarily drove diversification in life history and breeding traits, whereas productivity variability promoted diversification in environmental envelope-resource use traits. These findings highlight the importance of disentangling both evolutionary and environmental drivers of niche diversification. By revealing how different ecological dimensions respond differently to long-term environmental fluctuations, our study provides a framework for understanding the assembly of regional bird niches, with implications extending to broader taxonomic groups, and the variable vulnerability of functional diversity under ongoing global change.

323. Global patterns of trait divergence and speciation rates in birds

Melina Forgiarini Maxwell, *Institute of Microbiology of the Czech Academy of Sciences; Antonin Machac, IMIC Prague*

Evolution of species and their life histories has fascinated biologists ever since Darwin. While species diversification is inherently linked to trait evolution, the link itself remains controversial. Classic studies suggest that diversification and trait divergence correlate positively, being faster in species-rich tropical regions where functional diversity is high. However, recent studies suggest the opposite, faster divergence in extra-tropical, recently colonized regions, with limited diversity and presumably empty niches. Using birds as our model system (7,413 species), we test these two alternatives, integrating geographic, trait, and phylogenetic data. Our diversification analyses, null models, and GIS reveal that diversification rates are positively related to the rates of body mass evolution but negatively related to beak evolution. Moreover, diversification is faster in extra-tropical regions, whereas trait divergence lacks a consistent geographic pattern. These findings clarify when diversification and trait evolution are correlated versus decoupled, shedding new light on the processes governing global biodiversity.

324. Functional distinctiveness of the world's Avian resident and migratory avifauna

Reymond Miyajima, *The Ohio State University; Marta A Jarzyna, The Ohio State University*

Functionally distinct species are crucial to ecological communities, as their unique characteristics contribute to important ecosystem functions. Despite their importance, assessments of how functional distinctiveness is distributed spatially and, crucially, how it changes throughout the year are lacking. Roughly 20% of all Avian species exploit seasonally abundant resources during favorable times of year, causing assemblages to experience shifts in both composition and trait structure as migrants arrive. However, the spatiotemporal variation in functional distinctiveness —both at the species and assemblage-level—has not been previously explored. To investigate this, we addressed three key questions (1) Does

spatial variation in local and global functional distinctiveness differ between breeding and non-breeding seasons for both species and assemblages? (2) Do these seasonal patterns differ between migrants and residents? and (3) Are resident and migratory birds distinct when compared to the global pool or locally? We compiled traits from publicly available databases and used expert range maps reflecting breeding and non-breeding distributions to derive local assemblages at a 110 × 110 km resolution. We then used a corrected Gower's distance matrix to quantify species dissimilarity in trait space. We found that seasonal differences were greatest in boreal and Arctic regions for both assemblage-level local and global distinctiveness, where assemblages became less distinct upon migrant arrival. At the species level, both migrant and resident distinctiveness varied little between seasons. However, migratory species were more functionally distinct globally than in their local assemblages. Our results indicate that resident and migratory birds contribute differently to an assemblage's functional diversity.

325. Loss of morphologically unique Avian frugivores diminishes seed dispersal function and natural restoration potential pan-tropically

Jun Ying Lim, *National University of Singapore*

Seed-dispersing, frugivorous bird species play critical roles in maintaining the diversity of ecosystems but many are threatened by habitat loss and overexploitation, with unknown consequences for seed-dispersal functioning at the global scale. By combining data on the ecology, morphology, geographical distribution, and threats of frugivorous birds, we show that extinctions of at-risk species will drive worldwide declines in functional richness, and shifts in the functional composition, of Avian frugivore assemblages. These impacts will be strongest in the Neotropics and the tropical Indo-Pacific where species threatened by rapid habitat loss and degradation are concentrated, with the contribution of hunting to these patterns especially high in many parts of mainland and insular Southeast Asia. Furthermore, a substantial proportion of tropical areas with medium or high natural forest restoration potential coincide with areas where the functional diversity of Avian frugivore assemblages are at greatest risk. Our results suggest that the defaunation of frugivorous birds will substantially diminish the ability of many tropical ecosystems to recover fully after disturbance, highlighting the need to enhance efforts to halt or reverse losses in this important functional group.

326. Disentangling the Evolutionary and Ecological Determinants of Avian Specialization

Axel Arango, *CCTB; Ana Berenice Garcia-Andrade, CASUS/HZDR*

The adaptation of species to narrow ecological niches -or ecological specializaiton- shapes biodiversity patterns and species persistence across scales. While specialization is

inherently multidimensional, involving traits such as diet, habitat, and foraging behavior, its global drivers remain poorly understood. Evolutionary history, environmental stability, topographic complexity, and biotic interactions have all been proposed as mechanisms fostering specialization, yet their relative contributions remain unresolved. Here, we propose a synthetic framework to disentangle the ecological and evolutionary processes underlying avian specialization worldwide. We compile a comprehensive dataset integrating species distributions, phylogenetic relationships, climatic history, and ecological traits. Using structural equation modeling (SEM), we will test how colonization time, climate stability, topographic heterogeneity, and competition directly and indirectly shape specialization across global and regional scales. By linking historical, ecological, and evolutionary perspectives, this study aims to provide a unified understanding of the drivers of ecological specialization.

Mapping and Remote Sensing

331. Bugs from Space: Linking Remote Sensing to High Throughput Sequencing of Arthropod Communities to Assess Signatures of Ecosystem Integrity in Hawaiian Forests

Rosemary Gillespie, *University of California Berkeley; Jonathan Price, Dept. of Geography and Environmental Studies; Natalie Graham, University of Hawaii at Hilo; Ryan Perroy, University of Hawaii Hilo; Isaac Overcast, Columbia University; Daniel Gruner, University of Maryland; Iryna Dronova, University of California Berkeley*

What are the processes that shape community assembly through extended time and how are they affected by recent and ongoing anthropogenic modifications? Using the model system of the Hawaiian Islands, we couple high-throughput arthropod biodiversity sequencing and remote sensing imagery to examine correlated shifts across two orthogonal gradients set within the same forest type. The first is a geological chronosequence, across which arthropods increase in diversity and become more ecologically specialized. The second, intersecting gradient is composed of a landscape matrix that runs from native to heavily invaded forest habitats on each island. At plot scales, we sample whole arthropod communities, using genetic signatures from the high-throughput sequencing to test models of community assembly over extended ecological-to-evolutionary time, and the changing roles of key processes of filtering, competition, and neutrality; the models allow us to construct trajectories of disassembly in the face of rapid biotic change. We couple arthropod community analyses with remote sensing imagery at scales ranging from regional (archipelago; satellites), to area (leeward slope of one mountain; helicopter), to plots within heterogeneous landscapes (drone imagery and lidar). We combine the remote indicators of change (spectral properties, leaf and water content, nitrogen content, plant stress) using structural equation models (SEMs) to identify candidate parameters that reflect arthropod

community dynamics in rapidly changing island forest systems. Results to date show the spatial extent at which patterns can be detected, and identify the signatures that reflect change across scales, from satellite imagery to arthropod diversity patterns.

332. Clustering biomes from space

Elena Plekhanova, *Swiss Federal Research Institute, WSL; Philipp Brun, WSL; Haozhi Ma, WSL; Niklaus E. Zimmermann, WSL*

In biogeography, a biome is a critical concept, but its traditional definitions, which often rely on subjective criteria or fixed climate thresholds, are becoming outdated due to rapid climate change. As climate zones shift, so do biomes, although vegetation's slower adaptation means these shifts lag behind. To accurately track these shifts, we need reliable data from direct observations, but in-vivo sampling often lacks the necessary temporal and spatial coverage. Remote sensing provides spatially uniform (global) observations updated regularly and captures both plant functional traits and canopy structure, enabling a more reproducible and easily updatable way to monitor biome shifts.

In this study, we leverage remote sensing data to cluster biomes and compare these clusters against existing biome maps. We used two methods: a per-pixel approach and advanced computer vision models that capture spatial structure. Our results show that the per-pixel method effectively distinguishes seasonal vegetation and low-biomass areas but struggles with temporal vs. tropical regions and temperate grassland vs. tundra. In contrast, the computer vision model improves spatial consistency and distinguishes temperate from tundra regions but at the cost of losing information on seasonality. Both methods consistently identified evergreen tropical forests as a distinct, robust cluster, though with a smaller extent than current maps. We conclude by discussing the benefits and drawbacks of using modern computer vision for ecological research, highlighting its potential for more accurate, dynamic biome mapping in a changing environment.

333. Investigating 4-D microclimate change across African biodiversity hotspots

Brittany Trew, *Harvard University Topsham, United States*

Global biodiversity is under threat from ongoing climate change. Ecological studies investigating this threat naturally require climate data, yet readily available datasets typically represent conditions measured by weather stations. These stations are deliberately placed in open areas, shaded from direct solar radiation and located 1–2m above the ground, meaning measurements can be substantially decoupled from the microclimatic conditions actually experienced by organisms. Mechanistic microclimate models, which estimate conditions based on underlying climate-forcing processes, offer a powerful alternative. However, their scope is often limited by the availability of vegetation structure data, which influences

microclimatic variability in both horizontal and vertical space. Increasingly accessible remote sensing technologies such as LiDAR are transforming this field, allowing the quantification of three-dimensional vegetation structure, including vertical strata, directly from point clouds. This enables microclimate models to explicitly capture vertical gradients. To understand how natural habitats are threatened by climate change, we derive four-dimensional maps of projected microclimate change — by capturing spatiotemporal microclimatic variation — across sites in several African biodiversity hotspots. High-resolution, multi-strata canopy maps derived from UAV LiDAR imagery are used to generate hourly near-ground and within-canopy climate conditions at each site. We will present analyses illustrating how projected microclimate novelty varies across vertical strata and between biomes. Our findings demonstrate how coupling remote sensing with mechanistic microclimate models can transform our understanding of where biodiversity is most exposed to climate change, and thus provide more realistic projections of climate impacts on species and ecosystems; a critical step for biogeography and conservation planning.

334. In the Shade or in the Sun? Unveiling European Forest Light Regimes

Wanben Wu, *Department of Biology - Aarhus University; Jens Christian Svenning, Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University; Sean E. H. Pang, University of Oxford; Robert Buitenwerf, Aarhus University*

Light regime is a fundamental ecological factor shaping forest ecosystem functioning, influencing productivity, nutrient cycling, and biodiversity. However, its spatial patterns and environmental controls remain poorly quantified at continental scales due to the lack of broad-scale monitoring. Here, we leverage multi-source Earth observations, including optical and SAR imagery, together with over 250,000 European vegetation survey plots and Ellenberg light ecological indicator values from 14,054 taxa, to provide the first spatially explicit assessment of the European forest light regime and its drivers. Using state-of-the-art remote sensing and machine learning, we produced a 10 m resolution, wall-to-wall map of forest light regimes across Europe, achieving robust predictive performance (R^2 = 0.70, RMSE = 0.54). Our results also reveal pronounced gradients across forest management regimes, with close-to-nature forestry being ~10% darker than unmanaged forests. Forest structure and climate emerged as primary determinants of light regime, while disturbance and human modification played stronger roles at local scales. Our study advances a pan-European understanding of forest light environments and highlights the influence of management and disturbance on forest microclimate conditions.

335. Mapping functional and response diversity can reveal the geographic distributions of ecosystem services

Jamie M. Kass, *Tohoku University, Sendai, Japan*

Understanding the geographic distributions of ecosystem services that people depend on is crucial in this era of global change. Ecosystem services such as crop pollination, seed dispersal, nutrient cycling, and carbon sequestration are typically mapped at regional scales using land-use data as proxies for biodiversity. However, as species are responsible for maintaining these services, biodiversity model predictions should be more directly informative and accurate, especially when making projections for future scenarios. Using workflows that employ species distribution models to make grid-cell level community composition predictions, then calculate diversity indices per predicted community, we can map varied indices of biodiversity that have strong links to ecosystem services. In particular, diversity of function (e.g., traits) and environmental response (e.g., relationships with environmental variables) are two indices that can theoretically contribute more proximal information about ecosystem services than species richness alone. In this talk, I will discuss new methods we can use to calculate and map functional and response diversity based on species distribution modeling predictions, some preliminary results for pollinators and plankton in Japan, and what future research we should pursue to improve the quality and accuracy of ecosystem service maps.

Biodiversity, Dark Diversity, and Anthropogenic effects

341. Dark diversity reveals hidden and lagged species loss from regional and local human disturbance

Meelis Pärtel, *University of Tartu; Diego Pires Ferraz Trindade, University of Tartu, DarkDivNet Consortium, University of Tartu*

Species loss from natural habitats is an urgent global issue, often obscured by high natural variation in biodiversity. Using the DarkDivNet global network, we recently demonstrated that regional human influence reduces plant diversity in natural areas across the world, detectable only through comparisons between observed (alpha) diversity and dark diversity—species ecologically suitable but absent. Community completeness, defined as the proportion of suitable species present at a site, declined with increasing regional human impact. Here, we extend this approach by comparing paired natural and anthropogenically disturbed sites across 116 regions worldwide. Species suitability was estimated from >5000 consistently sampled 100 m2 sites using co-occurrence-based models. Despite similar alpha and beta diversity and species pool sizes between natural and disturbed sites, dark diversity was significantly higher in locally disturbed sites (paired t-test, $p = 0.015$), indicating more absent ecologically suitable species. Community completeness was correspondingly lower

(p = 0.008), revealing biodiversity erosion not captured by traditional metrics. Additionally, species observed in disturbed sites had lower ecological suitability (p = 0.007), suggesting a time-lag in species loss and an elevated risk of future extinctions. Crucially, the differences between paired natural and anthropogenic sites were not modified by the level of regional human impact, demonstrating their independent negative effects on biodiversity. The dark diversity framework thus provides a powerful tool to uncover masked anthropogenic impacts on vegetation. Our results underscore the need to integrate dark diversity metrics into conservation assessments to better detect and mitigate biodiversity loss.

342. Filling the blank space in indicators to track (and understand) biodiversity change from local to biogeographical scales

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Reaching the 2030 targets of the Global Biodiversity Framework (GBF) is an urgent and major challenge. We need to monitor and report indicators reflecting ongoing biodiversity changes so that every nation evaluates progress at least once within the next five years. These indicators need to capture complex biodiversity trends at biogeographical scales, alongside fast-paced, on-the-ground changes at the local scale of conservation action. Ultimately, they must be grounded in theory so we can understand and address the ecological processes underlying biodiversity changes across scales. We asked experts to delineate the spatiotemporal scales at which they expect indicators to reflect biodiversity changes and synthesized their answers to reveal how our leading indicators practically work together across space and time. Our synthesis shows that the focus on monitoring global and national biodiversity changes has left a gap in our ability to capture changes at local and short-term scales, which are key for a bottom-up and mechanistic understanding of biodiversity change. To fill this gap, we recommend complementing monitoring programs with locally-sourced data, testing the performance of indicators at their relevant spatiotemporal scale with hypothetical scenarios of biodiversity change, and developing strategic monitoring and indicators to detect fine-scale biodiversity changes. Going forward, a strong theoretical basis is needed to understand the processes driving the biodiversity changes detected by indicators from biogeographical to local scales. Strengthening this link between theory and indicators is critical to ensure that decisions taken across management levels maintain the ecological processes that shape biodiversity from local to global scales.

343. Dark diversity affinity in plants: Global consistency and variability in drivers of suitable yet absent species

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Recent estimates show that, globally, 75% of ecologically suitable and regionally present vascular plant species are absent, forming dark diversity of local sites. Understanding biodiversity patterns therefore requires focused attention on the mechanisms underlying dark diversity. Here, we analyzed global patterns of species- and site-level drivers that increase the probability of species belonging to dark diversity. We applied the dark diversity affinity (DDA) framework to a global vegetation dataset from the DarkDivNet, covering 5543 sites (10 × 10 m) across 113 regions. Within each region, we partitioned species and site contributions to each species absence from their suitable sites by attributing them to a hypothetical affinity, DDA, estimated using a Bayesian model. Separate sub-models linked DDA to three relevant variables for species and three for sites. Globally, species with short height, large leaves, or limited dispersal capacity tended to have high DDA, indicating a greater chance of being absent from suitable sites. Similarly, sites with taller canopies exhibited higher DDA, placing species into the dark diversity disregarding species identity, while human footprint and habitat availability showed no consistent patterns. Further, a post hoc analysis identified environmental conditions that explained regional deviations from global DDA trends. Notably, regions under high climate velocity tended to keep species in dark diversity if species had low dispersal capability or at sites with low accessibility, while in low-velocity regions these filters were weaker. Overall, this study provides mechanistic insights into how species traits, site conditions, and regional contexts interact to determine dark diversity patterns worldwide.

344. The velocity of biodiversity change: Applying the climate velocity framework to biodiversity metrics

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Species distributions are dynamic, constantly shifting in response to external factors, such as climate and land-use change, as well as intrinsic ecological processes, including dispersal. Quantifying these shifts is a central question in ecology, with direct implications for biodiversity conservation and management. Velocity informs on the speed and direction of

change for a given variable. In biodiversity research, it has been primarily applied in the form of climate velocity, indicating how fast and where species would need to move to maintain constant climatic conditions, allowing the identification of climate refugia as well as novel and disappearing climates. Here, we extend this framework to biodiversity data, applying it to metrics including species presence, probability of occurrence, richness, nestedness, and turnover. Using temporally replicated breeding bird atlases from multiple temperate regions, we calculated biodiversity velocities by dividing the temporal gradient of each metric by its spatial gradient across a gridded landscape. These velocities capture different facets of biodiversity change, including observed range shifts (probability of occurrence), the location of diversity hotspots (richness), and community changes (turnover and nestedness).

We found that biodiversity velocities varied across metrics, species, regions, and periods. Many velocities are low, indicating local stability, while others show rapid shifts. Extending the velocity framework to biodiversity metrics allows us to quantify how fast and in which direction different aspects of biodiversity are shifting, complementing the insights provided by climate velocity and potentially helping biodiversity conservation.

345. The global disruption of plant biogeography

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Human activities have altered the composition of biotas worldwide by introducing non-native species, breaking down biogeographical boundaries. Using global distribution data of 279,441 native and 10,067 naturalized seed plant species across 549 regions, we analyzed the impact of species introductions on natural biogeographic patterns. We found that plant invasions disrupted natural biogeographical patterns, leading to the loss of formerly distinct floristic realms and subrealms. Geographical proximity and dispersal barriers lost importance when including naturalized species, while trade facilitated species exchange. However, environmental factors continued to constrain species establishment and distribution. Our findings reveal the profound influence of plant invasion and underscore the urgent need for coordinated scientific, industrial, and policy action to manage invasions and protect native biotas.

346. Illuminating Africa's plant diversity dark spots: Addressing Linnean and Wallacean shortfalls through NaijaFLO and herbarium resources

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Although Africa harbours extraordinary biodiversity, our understanding of its plant diversity is limited by the Linnean shortfall (species yet to be described or properly documented) and the Wallacean shortfall (incomplete knowledge of species distributions). These "dark spots" limit our capacity to conduct robust biogeographical analyses, assess extinction risks, and design effective conservation strategies. We present the Database of Vascular Plants of Nigeria (NaijaFLO) as a best-practice example for overcoming such shortfalls. NaijaFLO is a comprehensive, expert-verified, and curated checklist of all vascular plants reported from Nigeria, developed at the German Centre for Integrative Biodiversity Research (iDiv) in collaboration with an international team of editors. It integrates multiple taxonomic sources (IPNI, POWO, WFO, LCVP, WP, APD) and herbarium vouchers to validate occurrences and classifications. Covering 7,770 taxa across 232 families and 1,859 genera (including 6,753 species, of which 5,396 are native and 41 endemic), NaijaFLO provides authoritative information on taxonomy, nomenclature, distribution status, and growth form. Importantly, all data are openly available under a CC BY 4.0 license via the iDiv PlantHub and GBIF. We argue that curated national and regional plant databases, grounded in herbarium specimens, are critical tools to close biodiversity knowledge gaps in Africa. By standardising names, verifying distributions, and linking data to global infrastructures, projects like NaijaFLO demonstrate the potential to illuminate biodiversity dark spots, support conservation planning, and strengthen Africa's role in global biogeography. Building stronger herbaria, training young scientists, and fostering transnational collaboration are essential steps to ensure that such efforts scale across the continent.

Invasive Species

351. Ancient invaders, Modern Warnings: Assessing environmental forces shaping biogeography of last Interglacial southern California molluscan fauna.

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Shaped by dynamic oceanographic and environmental conditions, the southern California coast sustains high biodiversity, yet this very complexity leaves it vulnerable to climate-induced changes such as species shifts and extinctions. The geological records of southern California enriched with fossil records, snapshots of effects of warming events and sea level high stands during Interglacial cycles. Thermally anomalous occurrences in the fossil records

can indicate pre-anthropogenic species invasion in response to warming and cooling cycles. Understanding the patterns of invasion during the last interglacial (LIG) period—driven by natural climate variations—can provide valuable insights for monitoring these species under future warming conditions.

Our results indicate that nearly 20% of the ~800 species of mollusks known from the last Interglacial of southern California are represented by thermally anomalous occurrences, and can therefore be considered potential invaders. The spatial distribution of these migrators is notably patchy, reflecting the influence of a range of environmental conditions (e.g., temperature gradients, shelf exposure, substrate type). Our results include map-based depictions of habitat availability on both LIG and modern coastlines. Warm-water southern species are concentrated within these sheltered (soft-bottom) regions, while cold-water northern species are more frequent in exposed (rocky) habitats. Collectively, these factors offer insight into why certain regions may have served as refugia for invaders in the past. These findings enhance our ability to identify and predict those taxa that will migrate, and preferred geographic areas that will be impacted, under ongoing and future climate change.

352. Combining the anthropogenic road transport network with landscape resistance maps allows to forecast spread of invasive species on the European scale

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Invasive species pose significant ecological and economic threats, and the identification of pathways and spread dynamics is crucial to install effective mitigation measures. The two distinct modes of dispersal, i.e. long-distance anthropogenic transport and natural dispersal across short distances, challenge modelling efforts and only few relatively complex and species-specific models have so far considered both transport modes in parallel. Here, we present a novel open data-based model approach combining both dispersal mechanisms: Our method integrates (1) a gravity model of the terrestrial road transport network, using economic and social variables of urban areas and their distances to predict traffic volumes between city-pairs, with (2) landscape resistance maps for the dispersal of species derived from species distribution models. This combination of information layers allows us to simultaneously simulate long-distance transport via anthropogenic transport routes and unaided dispersal based on habitat preferences. We validated our approach using temporally and geographically resolved data of well-documented invasions in Europe, including *Senecio inaequidens* (plant), *Tapinoma magnum* (insect), and *Myocastor coypus* (mammal). Despite its simplicity and sole reliance on open data, our model effectively identifies connections and vulnerable areas across large distances and biogeographic barriers. Here, we present preliminary results from these case studies to demonstrate the effectiveness of our integrated approach, highlighting its potential to model the spread of invasive species across various taxa and support their management.

353. Empirical invasion biogeography European Database of Alien Flora: Towards a Harmonised Resource for Plant Invasion Research

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Despite decades of research, data on alien plants have remained fragmented, often inconsistent in taxonomy, categories and completeness. To address this, we developed the European Database of Alien Plants (EuDAP), a harmonised and comprehensive resource essential for understanding plant invasions across Europe. EuDAP focuses on three main aspects of alien status: (1) residence status (archaeophytes vs. neophytes), (2) invasion status (casual, naturalised, invasive), and (3) region of origin, broadly following the TDWG continental scheme with biome-specific refinements. Countries serve as core units, with selected islands and regions assessed separately. In contrast to previous datasets, we consider geographical context and distribution in neighbouring countries when assigning status, while also analysing native species patterns to reveal data gaps and biases. EuDAP is based on data from 134 sources, including checklists, scientific literature, and major databases such as Euro+Med PlantBase, GloNAF and POWO. In addition, nearly 50 local experts critically reviewed the taxon–region assignments (acknowledged in our presentation). EuDAP will be continuously updated and made publicly accessible through the FloraVeg.EU platform. Here, we present the contents of EuDAP and comparisons with other major databases. In particular, we highlight maps of absolute and relative (to native flora) alien species numbers, hot- and coldspots, spatial patterns across different alien categories, and influencing factors. We believe EuDAP will significantly advance research in biogeography and ecology, and serve as an important tool for biodiversity conservation and restoration efforts.

354. Life history traits and functional trade-offs as predictors of invasion in plants

María Ángeles Pérez-Navarro, *Centre for Ecological Research and Forestry Applications; Roberto Salguero-Gómez, University of Oxford; Jane Catford, King's College London*

Humans are introducing species beyond their native ranges at an ever-increasing rate with the consequent impact on biodiversity, ecosystem function, human health, and economy. Disentangling if invasive species already possess functional and life-history traits that allow them to spread and outcompete resident species in non-native ranges or whether invasive species shift their behaviour and function during the invasion process is key to predict invasiveness. Here, we use global datasets of plant functional traits and demography (as TRY and COMPADRE) to explore differences in main functional trade-offs and life-history traits between native, exotic non-invasive and invasive species in their native and non-native range.

To do that, we followed two alternative approaches: 1) including all plant species with coordinates present in the datasets and 2) considering only species with paired population data both at native and non-native ranges. Overall, we found that invasive species showed faster life-history traits than exotic non-invasive and natives, respectively, including larger growth rate, shorter generation times and higher amplification in transient dynamics. Furthermore, exotic populations showed higher survival in the non-native range compared with the native one, highlighting the relevance of processes enhancing species performance during invasion. Respect to functional traits, exotic species did not show inherent superior trade-off curve than natives, but rather their primacy depends on the functional range. For example, exotic species showed more resistant leaves than natives only in case of larger ones (LDMC-SLA trade-off). Our results highlight the relevance of plant function and evolutionary history to disentangle and predict invasiveness.

355. Plant invasions reduce the degree of nestedness on warm temperate islands

Fabio Mologni, *University of Vienna, Austria*

Island floras are often nested, with species-poor assemblages being subsets of species-rich ones. However, the circumstances of this are often unclear. To understand the processes shaping island floras, we incorporated taxonomic and trait categories to investigate the relationships between the degree of nestedness of 1,543 native and non-native plant species and the island characteristics (e.g., area) on 264 islands offshore northern Aotearoa New Zealand. We hypothesised that nestedness declines with island area (non-random extinctions), increases with isolation (non-random colonisation), declines with exposure to ocean-borne disturbances (non-random local extinction of specialists with their habitat), and is higher on volcanic compared to sedimentary islands (assembly rules). Additionally, plant invasions will reduce overall nestedness and trends will vary depending on plant traits. We compiled information about species' taxonomy at the fine (species) and coarse level (e.g., monocots), growth form (e.g. graminoids) and dispersal mode (e.g. animal-dispersed). We quantified nestedness by organising species matrices using the NODF (i.e. nestedness metric based on overlap and decreasing fill) and fixed-fixed null models. We related island nestedness ranks with island characteristics. Most plant categories were nested: however, non-native species reduced the overall degree of nestedness, modifying the species composition of island floras. Nestedness ranks were related to island area and to exposure to ocean-borne disturbances, but rarely to isolation and geological origin. These results strongly support selective extinction and habitat nestedness hypotheses. The overarching effect of island area in shaping insular plant composition underscores the key role of large islands for conserving plant diversity.

356. Effects of modelling choices on early invasive risk assessments: lessons from the psyllid vectors of *Citrus* Huanglongbing

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Species distribution models (SDMs) are widely used in early invasion risk assessments and are increasingly critical for anticipating biological threats under global change. Yet, SDM outcomes can vary substantially depending on modelling choices, many of which remain poorly standardized. These variations have tangible consequences when model outputs guide regulatory and management decisions. Here, we systematically evaluated how five key modelling decisions affect the performance and spatial projections of early-stage invasion risk models: (i) quality and curation of occurrence data, (ii) use of native-only versus native and invasion occurrence data in model calibration, (iii) background point selection, (iv) environmental variable selection, and (v) ensemble versus single-model approaches. In addition to conventional whole-range evaluation metrics (AUC, TSS, Boyce index), we applied a complementary index focused on the invaded range: the invasive False Negative Rate (iFNR). Finally, differences in projected areas at risk were estimated using the Jaccard index of overlap. As a case study, we modelled two invasive insects with contrasting invasion histories and current distributions —*Diaphorina citri* and *Trioza erytreae*— vectors of the bacteria responsible for Huanglongbing (HLB), the most devastating citrus disease worldwide. Our results demonstrate that expert-curated occurrence data and inclusion of validated invaded-range records consistently improved model performance in novel environments. Moreover, conventional classification metrics alone failed to distinguish between models producing widely divergent invasion forecasts. Incorporating invasion-focused metrics and comparing spatial projections was essential to discriminate between models and to support more robust, policy-relevant decisions in invasion risk assessments.

Extinction

411. Pleistocene sea-level change as a driver of island extinction and trait selection: a novel research framework in biogeography

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Greece; Sietze Norder, Copernicus Institute, Utrecht University; Stylianos Michail Simaiakis, Natural History Museum of Crete; E. Emiel van Loon, University of Amsterdam; Alexandra Anna Enrica van der Geer, Naturalis Biodiversity Center Johannes Erwin De Groeve, University of Amsterdam

Pleistocene sea-level fluctuations have dramatically altered the area and connectivity of continental islands, yet the effects of these spatio-temporal dynamics on extinction and trait selection remain poorly understood. Over the last decade, we have developed a novel research framework to quantify these spatio-temporal changes and assess their influence on contemporary biodiversity. Central to this work is *tabs*, *Temporal Altitudinal Biogeographic Shifts*, a recently developed R package that facilitates spatio-temporal coastline reconstructions. Since the Last Glacial Maximum (21 Kya), a 135 m rise in sea level inundated continental shelves, submerging land bridges and leading to the contraction and fragmentation of terrestrial (eco)systems. We constructed a robust model of these geospatial changes for the Aegean Archipelago, accounting for local geological uplift and subsidence, thereby determining accurate island fragmentation timings. *Tabs* allows for the introduction of new metrics that help to explain patterns in present-day biodiversity. For instance, the time elapsed since land-bridge submergence serves as a proxy for the isolation duration of populations on the resulting islands. This can be used to assess how isolation time predicts modern extinction debts and affects the genetic diversity of stranded populations. *Tabs* can also generate island fragmentation dendrograms, “nesogenetic” trees showing the sequence of island fragmentation over time. This may help to identify which traits are preferentially selected over time on islands. Quantifying the geospatial dynamics of Pleistocene islands provides a new basis for investigating how the rate of environmental change affects biota and has shaped modern insular biodiversity.

412. Assessing extinction risks of island trees using process-informed neural networks

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Over one-third of tree species are at risk of extinction worldwide. Oceanic islands harbor a major portion of global tree diversity, including many endemic species found nowhere else in the world. This is likely due to both island isolation and volcanic processes (i.e., tephra deposition) providing a strong selective mechanism that drives the speciation of upright woody species in herbaceous lineages. Due to their long lifespans and high exposure, trees are especially vulnerable to changes in environmental conditions. On islands, where habitat area is limited by human settlements and agriculture, these problems are amplified. Here, we provide a global assessment of the extinction risks to island trees under ongoing climate change and land-use intensification. We address two main challenges faced by species distribution models (SDM) of island trees: 1) island trees are poorly represented in species

occurrence databases and 2) islands are small geographic areas with high topographic and climatic variability. Therefore, we develop a novel approach using process-informed neural networks (PINN) for predicting future habitat suitability of island trees. By incorporating prior knowledge of physical and ecological processes that drive the distribution of tree species, we attempt to overcome challenges with data availability and small study areas. We test if PINNs could improve predictions beyond conventional SDMs to inform conservation efforts of global tree diversity on islands.

413. Quantifying the unrecorded loss of Avian phylogenetic diversity

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Humans have drastically reduced Avian diversity, with the majority of extinctions occurring on islands. Previous studies have quantified various aspects of this decline, including both taxonomic and phylogenetic diversity loss due to recorded extinctions. Other studies have estimated that unrecorded island bird extinctions – those that left no known fossil evidence – may represent hundreds of additional losses. However, these analyses have only focused on species diversity. In this study, we bridge these two research efforts by estimating the phylogenetic diversity lost due to unrecorded island bird extinctions. Our findings suggest that the loss of phylogenetic diversity may be substantially smaller than expected, given the number of extinctions. Our results suggest that, while the unrecorded extinctions represented around 60% of all species extinctions, most of the phylogenetic diversity loss was caused by recorded extinctions. This pattern arises because – while extant island endemics are on average slightly more phylogenetically distinct than expected by chance – most unrecorded extinctions are predicted to have been from the same region: the islands in the eastern Pacific. Birds from this region generally have lower phylogenetic distinctiveness than elsewhere and hence the extinct species, therefore, likely did as well. Our results suggest that future studies should not only account for the number of extinctions but also their evolutionary histories, as losses of phylogenetic diversity may not always scale directly with losses in species counts.

414. Hotspots of diversity at continental scales: predicting evolutionary Hotspots following the next mass extinction

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At the end of the Cenomanian epoch, an era referred to as the Cenomanian Turonian Boundary period, the Earth experienced dramatic global warming and climate shifts, triggering the 5th great extinction. During this period upwards of 90% of extant genera went extinct. However, research showed that there were some biodiversity HotSpots that remained, and it is hypothesized that these hotspots seeded the biodiversity of today. We recently combined the United States Breeding Bird Survey data (N= 4,067 survey points measured from 2006 – 2021) with a detailed literature review of bird genetic diversity (N = 207 species x locations published from the same time period) to identify areas of the continental United States that exhibit both high bird species richness, diversity, and rarity as well as high within bird species genetic diversity. At a continental scale the correlation between bird species richness and within species genetic diversity was weak ($r = 0.09$; $P > 0.14$). However, by using a combination of emerging Hotspot analysis, Geographically Weighted Regression, and Multiple Response Permutational clustering analysis, we were able to identify specific regions where species richness and within species genetic diversity co-occurred (GWR $R2(GD|SR)=0.32$; $MRPP\Delta=1136$; $P<0.00$). We suggest that these areas of both high species richness and high within species genetic diversity might be critically important centers of future Avian diversification and evolution following the current 6th mass extinction event.

415. Adapting land use to climate change mitigates global biodiversity decline

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Future biodiversity outcomes under climate change depend not only on the magnitude of warming but also on whether land use and the habitats species depend on adapt to shifting conditions. To assess this, we combined an ensemble of species distribution models for more than 20,000 terrestrial vertebrates with harmonized climate inputs and contrasting land-use scenarios: one adaptive to climate change and one non-adaptive within the Intersectoral Impact Model Intercomparison Project (ISIMIP3). Under a sustainability scenario (SSP1-2.6), global differences in land use between adaptive and non-adaptive pathways remain modest by mid-century, though regional shifts in cropland, pasture, and secondary non-forest already alter habitat availability. In higher-emission scenarios (SSP3-7.0 and SSP5-8.5), divergences intensify: adaptive pathways reduce cropland expansion in South America, Africa, and the U.S., while non-adaptive pathways maintain higher cropland

pressure, often at the expense of primary forest and non-forest systems, with direct effect on biodiversity. In adaptive scenarios, mid-century losses in tropical hotspots such as the Amazon, Central Africa, and Southeast Asia are moderated (–5 to –25%), while temperate regions gain richness, reflecting poleward shifts. In non-adaptive scenarios, tropical declines reach –50% and remain severe by century's end, while temperate gains are weaker and spatially constrained. Adaptive pathways instead sustain a more balanced redistribution of richness, with partly offsetting gains and losses of species across latitudes. Our results demonstrate that when land-use and habitats adapt to climate change, it reduces the projected global biodiversity losses of terrestrial vertebrates and highlights opportunities for climate-resilient conservation planning.

416. Dark extinctions in a rapidly changing world

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We are currently witnessing a mass extinction crisis due to increasingly overwhelming human impacts on the biosphere. While the documented extinctions from the last few hundred years included in the global Red List of the IUCN are well-known at least for some taxonomic groups, these represent the tip of the iceberg. While there is accumulating evidence that the number of historic human-induced extinctions is far higher than documented in the 'gold standard' for assessing extinction risks - the IUCN Red List - the extent and characteristics of poorly documented or 'dark extinctions' remain insufficiently known. Dark extinctions span a gradient from events that left no direct trace, where only indirect inferences and extrapolations from comparable and better documented cases can be made, to well-documented losses supported by substantial evidence (e.g., subfossil remains, ancient DNA, historic descriptions, specimens in herbaria or museums, observation records). These latter cases are amenable to a suite of emerging analytical methods for shedding new light on dark extinctions. Here, we synthesize the state of knowledge on the discrepancy between documented and actual anthropogenic extinctions. We examine key aspects that define their extent and characteristics in the Anthropocene. Finally, we discuss the implications of dark extinctions on the likely true scale of the unfolding extinction crisis.

Climate change and boreal regions

421. The global geography of snowbed habitats and their microclimatic change

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Snow is a fundamental driver of ecosystem processes and species distributions at high latitudes and altitudes. Snowbed habitats, areas with extended snow cover, serve as biodiversity hotspots in mountain and tundra regions, but they are also among the most vulnerable to climate change. Despite their ecological significance, a global assessment of their distribution and dynamics has been lacking. In this study, I present a novel workflow to map and monitor snowbed habitats globally. I derived multi-decadal Snow Cover Duration (SCD) and vegetation greenness from Landsat satellite imagery at a 30-meter resolution across 600 forest-free study sites in the Arctic, Antarctic, and alpine regions. Additionally, I utilized multi-year microclimate logger timeseries from nearly 800 measurement locations and downscaled ERA5-Land climate data to retrospectively model snow dynamics and their influence on local microclimates. My results reveal substantial spatial heterogeneity in snow cover duration and a drastic decrease in late snow occurrence across nearly all study sites. This heterogeneity suggests that microclimatic change likely varies across landscapes and between contrasting snow habitats. The local relationship between SCD, elevation, and vegetation greenness also varied widely across sites. These findings suggest that altered local snow conditions may complicate and mediate the effects of climate change, leading to heterogeneous microclimatic and biogeographical responses that are difficult to predict. This research demonstrates the power of combining remote sensing with in-situ and reanalysis data to unravel the complexities of how snow-driven microclimates shape biodiversity and productivity in a warming world.

422. The asynchronous rise of alpine floras reveals general responses of biotic assembly to orogeny and climate change

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Understanding how biotic assembly processes responded to past geo-climatic changes is key to explaining the origins of mountain biodiversity and the causes of regional disparities in species richness. Here, we jointly reconstructed geographic ranges and biome-niche evolution for 34 diverse plant clades across five major Northern Hemisphere mountain systems and quantified how late Neogene cooling increased arctic-alpine habitat

connections across regions. We reveal that, while alpine floras originated asynchronously and were assembled through distinct evolutionary processes over the past 30 Ma, general biological responses to orogeny and environmental change are apparent. Across regions, in situ diversification was consistently elevated during heightened phases of tectonic activity. Over the past 5 Ma, enhanced arctic–alpine connectivity facilitated biotic interchange and positioned the boreal–arctic region as a major biogeographic crossroads linking Eurasia and North America.

423. Expedition to the past: historical resurveys to understand 70 years of Arctic vegetation change

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Responses of species communities in regions of the world exposed to a single main global change driver should, in principle, be easy to predict. The Arctic has warmed faster than the rest of the world, but has had low exposure to non-climatic drivers. As expected, plant communities in the tundra are experiencing shrubification and thermophilization. But why does the direction and speed of richness changes and community reshuffling vary so much across space, often lagging behind theoretical expectations? To answer this question, my team and I went in the footsteps of two pioneers of vegetation mapping in Greenland: Tyge W. Böcher (1909-1983) and Bent Fredskild (1929-2022). We located and repeated the original surveys from the 1940s and 1950s, giving us a unique opportunity to study temporal processes over >70 years across a 1,000 km gradient. Our first findings change our understanding of the role of local microenvironment in mediating vegetation responses to regional warming, and the scale-dependency of biotic homogenization.

424. Impacts of borealization on biodiversity and carbon balance

Heidi Kristiina Mod, *University of Helsinki; Anna-Maria Virkkala, University of Helsinki*
Lea Opitz, University of Helsinki; Gangotri Chattopadhyay, University of Helsinki; Miska Luoto, University of Helsinki

In the climate change-driven process called borealization, trees and shrubs are expanding northward and upward to previously treeless high-latitude and -elevation areas. For example, in northern Finland, the occurrence of pine seedlings on treeless fell tops and the replacement of lichen-rich habitats by shrub-dominated vegetation provide clear evidence of this phenomenon. Borealization reshapes tundra ecosystems, for example, by introducing new and shuffling existing species and functional traits, and by enhancing carbon uptake.

However, the impacts and outcomes of borealization are not yet comprehensively understood. In this presentation, I will address the impacts of borealization on two critical and topical ecosystem characteristics – biodiversity and carbon sequestration – by building upon our research where we have demonstrated that, depending on environmental conditions, shrub and tree expansion may lead to either increases or declines in plant biodiversity, and that shrub-dominated communities can also act as net carbon sources to the atmosphere. I will also present preliminary results from a newly launched research project that assess the context-dependent impacts of borealization on biodiversity and CO2 fluxes. This project is based on comprehensive field surveys in northern Finland, focusing on both taxonomic and functional biodiversity as well as CO2 fluxes along gradients from forest to treeline to tundra. Based on this work, preliminary future scenarios of borealization and its impacts on northern ecosystems are presented. Importantly, the impacts of borealization are context-dependent and outcomes differ between biodiversity and carbon balance, making borealization a double-edged sword at the intersection of nature conservation and global change.

425. Impacts of climate change on bryophyte distribution: a comprehensive assessment at fine spatial resolution across Europe

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Bryophytes, the second most diversified lineage of land plants, have long been identified as the canaries in the coal mine of climate change, but a comprehensive assessment of future climate-change impacts on their distribution and diversity is still missing. We compiled an expert database of >2,900,000 occurrences for 1476 (82%) species across Europe to

calibrate species distribution models at 100 m resolution and project them to 2071–2100 climate under several scenarios of global warming. Despite large differences among climate change scenarios, all models point to substantially higher median loss (12–91%) than gain (8–18%) of future suitable habitats and median northern shifts of the centroid of species habitat suitability of 65-255 km. These general patterns hide contrasting impacts depending on biogeographic regions, with a median loss of 25–100% vs 2–26% of future suitable habitats in Boreo-montane vs Mediterranean regions, respectively. The regions predicted to experience the lowest (<10% of variation in habitat suitability) impact of future climate change are distributed along the Atlantic coast, identifying these areas as potential climatic refugia for the bryophyte flora in a warming world. Areas with the highest predicted loss of habitat suitability are concentrated in the mountain regions (Pyrenees, Alps, Tatras) and northern Scandinavia. In turn, the pixels predicted to exhibit the highest increase (>50%) in habitat suitability are distributed in mid-western Europe, largely corresponding to the northern shift of climatically suitable areas for Mediterranean species. The cascading effects of a future impoverishment of the bryophyte flora on ecosystem functioning in Europe will be discussed.

426. Six decades of biodiversity and composition changes in European plant communities

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University of Agriculture in Kraków; Sabine Rumpf, University of Basel; Irati Sanz-Zubizarreta, Department of Plant Biology and Ecology, Faculty of Science and Technology, University of the Basque Country UPV/EHU, Bilbao, Spain; Vasco Silva, Egas Moniz Center for Interdisciplinary Research (CiiEM), Egas Moniz School of Health and Science, Caparica, Portugal; Jens Christian Svenning, Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University; Grzegorz Swacha, Botanical Garden, University of Wrocław, Wrocław, Poland; Irina Tatarenko, School of Environment, Earth and Ecosystem Sciences, Open University, Milton Keynes, UK; Martin Večeřa, Masaryk University; Denys Vynokurov, M.G. Kholodny Institute of Botany, National Academy of Sciences of Ukraine; Petr Keil, Department of Spatial Sciences, Czech University of Life Sciences Prague, Czech Republic

Quantifying long-term biodiversity change is key to conservation and management, yet comprehensive time series data are often limited. We developed spatiotemporal interpolation methods based on machine learning to overcome the lack of temporal replication in survey data, enabling continent-wide assessments of vascular plant diversity and community dynamics. Using nearly more than 600k one-time surveyed vegetation plots and validating against more than 20k time series, we quantified changes in species richness and community-mean ecological indicator values (light, temperature, soil moisture, nitrogen, and soil reaction) across Europe between 1960 and 2020. We found near-zero net change in species richness over six decades. Nonetheless, species richness declined from 1960 to 1980 and increased after 2000, with declines strongest in forests and gains more common at higher latitudes and elevations. In parallel, community composition shifted towards species demanding higher nitrogen across most habitats, reflecting eutrophication and reduced management intensity. Other changes in environmental conditions were more habitat-specific: forests became associated with lower soil acidity, grasslands with more shade-tolerant species, and wetlands with less moisture-dependent species. Temperature-related shifts were limited overall, except for alpine and arctic habitats where warming-tolerant species increased. While species richness trends are highly context-dependent overall, ecological indicator values point to a gradual cross-habitat homogenization, with communities increasingly dominated by species adapted to intermediate conditions, and a decline in those specialized to the extreme ends of environmental gradients. Our approach demonstrates how large datasets without temporal replication at individual sites can be used to reconstruct biodiversity and environmental dynamics across broad geographic extents.

Spatio-temporal modelling

431. Spatiotemporal dynamics of diebacks in the world's largest bamboo forest

Kalle Ruokolainen, *Aarhus University; Niko Kulha, University of Eastern Finland; Evandro Ferreira, Universidade Federal do Acre; Hanna Tuomisto, Aarhus University and University of*

Turku; Natalia Reategui, Universidad Nacional Agraria la Molina; Julio Nauán, Universidade Federal do Acre; Jurandir Gomes, Universidade Federal do Acre; Risto Kalliola, Geography section, Department of Geography and Geology, University of Turku

The largest bamboo-dominated forests in the world are in southwestern Amazonia covering ca. 160,000 km2. There are at least two species of bamboo involved, both having a gregariously semelparous life cycle of 28 years in which individuals flower and produce fruits simultaneously with thousands or millions of other individuals in the same neighborhood. After the reproductive event, all fruiting individuals die and new generation sprouts from the seeds. There is a published map of bamboo dieback year at the resolution of 30 m by 30 m over the whole area and the length of the full life circle. We use this map together with our own and published field observations of the timing of bamboo reproduction to ask how long a single event of mass reproduction can last, does the timing of reproduction show a spatial trend (flowering wave) and is the timing related to high-resolution topographical variation or to regional variation in geology or precipitation. The answers to these questions are not easily compatible with the hypothesis of seed predator satiation, a widely assumed evolutionary explanation for gregarious semelparity. Also, our results suggest that the timing of the start of reproduction is at least partly controlled by exceptionally wet dry seasons and some undefined mechanism of communication among bamboo individuals.

432. Direct integration of population genetic diversity into dynamic species distribution modeling to reconstruct the postglacial history of *Piper nigrum*

Michael P. Nobis, *Swiss Federal Research Institute WSL; Sandeep Sen, University of Amsterdam; Yoshiaki Tsuda, Sugadaira Research Station, Mountain Science Center, University of Tsukuba*

Climate change significantly affects species ranges and genetic structures, yet these climate impacts are often associated with large uncertainties when analyzed separately. In this talk we present a novel framework that integrates population genetic diversity into dynamic species distribution models (DSDMs) for the reconstruction of the postglacial history of wild black pepper (*Piper nigrum*), a perennial woody vine endemic to India's Western Ghats. DSDMs were applied from the Last Glacial Maximum (LGM, 21,000 years BP) based on high-resolution paleo-climatic suitability and the KISSMig model, evaluating various combinations of migration rates and the width of the species' climate niche. In addition, we analyzed genetic data of 243 individuals from 14 populations across the entire native species range using six chloroplast and five nuclear DNA simple sequence repeats (SSRs). This genetic data revealed higher genetic diversity at lower latitudes, with two major phylogeographic groups, splitting around the LGM. The integration of population genetics into the DSDMs resulted in a genetically informed DSDM, optimizing the model parameters to maximize the correlation between genetic diversity and the simulated colonization history since the LGM. This genetically informed DSDM showed a northward expansion from low-latitude refugia followed

by a recent fragmentation of the species range. Our integrated method clearly reduced uncertainties in the estimated DSDM parameters and enhanced the interpretation of population genetic structure. This added value is not achievable when population genetics and species distribution modeling are applied independently and merely compared.

433. Forecasting future disequilibrium through species distribution models in a quasi-permanent non-equilibrium state

Etienne Lalechère, *Center for Ecological and Evolutionary Synthesis, Department of Biosciences, University of Oslo; Jonathan Lenoir, CNRS; Ronan Marrec, UMR CNRS 7058 EDYSAN, Université de Picardie Jules Verne, France; Franz Essl, Division of Bioinvasions, Global Change & Macroecology, Department of Botany and Biodiversity Research, University of Vienna, Vienna 1030, Austria; Ingolf Kühn, Helmholtz-Centre for Environmental Research UFZ; Torbjørn Ergon, Center for Ecological and Evolutionary Synthesis, Department of Biosciences, University of Oslo, Norway*

Shifts in species distribution are known to lag behind their natural and anthropogenic drivers. However, future projections are still based on the unchallenged quest for an existing baseline, sometime in the past, during which biodiversity is considered to be in an equilibrium state with its environment. This assumption prevents us from accounting for the long-term effects of past dynamics in many biodiversity drivers. Existing frameworks aiming to tackle this issue still rely on the equilibrium assumption because non-equilibrium dynamics are only considered as transient phases between successive equilibrium states. Here, we propose a paradigm shift considering multiple trajectories of long-term environmental changes and disturbance events that push biodiversity into a quasi-permanent non-equilibrium state. Based on this conceptual framework, we developed a non-equilibrium species distribution modelling (SDM) approach in order to evaluate the current and future lagging dynamics in species redistribution. This approach was applied on the distribution of 92 European forest birds in response to past trajectories of change in forest cover and climate. Non-equilibrium SDMs suggested unprecedented long-lasting effects of past global changes (average time lag extents ranging from 9 to 231 years). Accounting for these time-lagged effects, future projections of species distribution indicated that the disequilibrium will increase until the end of the century, impacting different biodiversity facets (species richness, phylogenetic and functional diversity).

434. Formalizing and expanding the Constraint-based model of Dynamic Island Biogeography via a Markov chain, trait-space plots, and simulations

Robert P. Anderson, *City College of CUNY; Cecina Babich Morrow, University of Bristol; Trevor Fristoe, University of Puerto Rico - Río Piedras; Robbie R Burger, University of Kentucky*

Directional and cyclical environmental changes affect islands and habitat patches, as well as their communities. Predicting such turnover remains limited by difficulties integrating species traits and past environments. The recently proposed Constraint-based model of Dynamic Island Biogeography (C-DIB) invokes hysteresis (dependency on both the present and past) by alternating consideration of traits related to colonization vs. extinction. We formalize the C-DIB mathematically, expand it via trait-space plots, and conduct simulations. First, we define a time-inhomogeneous discrete-time Markov chain that uses a transition matrix (probabilities of colonization, non-colonization, extinction, and persistence) to predict a species' presence and absence, and then extend to a multi-species model. Second, we introduce trait-space plots of presence or absence of each species based on traits related to colonization and extinction. Current environmental conditions lead to deterministic predictions for species falling in much of the trait-space, but expectations for those corresponding to current isolation yet sufficient area are contingent on the history of the system. Third, we simulate occupancy of that space. The simulations yielded expected gradual patterns of occupancy for species falling in parts of trait-space dominated by determinism. In contrast, a stark gradient occurred in the rest of the space (particularly subject to contingency): high occupancy for species with medium connectivity and low areal requirements, to low occupancy for those needing high connectivity and medium area. These advances set the stage for empirical tests under the C-DIB, which we and collaborators are implementing in various montane "sky island" systems in the Western Hemisphere.

435. Temporal change and drivers of multiple facets of biodiversity at mesoscales

Florencia Grattarola, *Czech University of Life Sciences Prague (CZU), Prague, Czech Republic; Gabriel Ortega, CZU Praha; François Leroy, Czech University of Life Sciences; Carmen Diana Soria, Czech University of Life Sciences; Kateřina Tschernosterová, Czech University of Life Sciences Prague; Friederike Johanna Rosa Wölke, Stockholm University; Vladimír Bejček, Czech University of Life Sciences Prague; Richard Fox, Butterfly Conservation; Julie Hart, New York Natural Heritage Program; Sergi Herrando, European Bird Census Council; Lisbeth Hordley, Butterfly Conservation; Verena Keller, Swiss Ornithological Institute; Ivan Mikulas, Czech Society for Ornithology; Adrian Monks, Landcare Research; Karel Šťastný, Czech University of Life Sciences Prague; Petr Voříšek, European Bird Census Council; Mutsuyuki Ueta, Japan Bird Research Association; Susan Walker, Landcare Research; Petr Keil, Department of Spatial Sciences, Czech University of Life Sciences, Prague, Czech Republic*

We expect declines, but reported trends and drivers of global biodiversity change vary across taxa, regions, and scales. Most studies focus on a single metric, typically species richness or temporal turnover. They also assess change at either local or global scale, rarely at the intermediate grain, and with limited analyses of the drivers of these changes. Here, we present a near-global study (9 regions across 4 continents) at a novel meso-scale (100–2500 km^2 contiguous grids), measuring multiple facets of contemporary biodiversity change (species richness, occupancy, temporal and spatial turnover during the past 50 years). We also examine their potential drivers, including temperature, precipitation, human footprint, tree coverage, and cropland area. We account for variation in sampling effort (using Frescalo and Bayesian occupancy models) and we identify both static and dynamic drivers of the change (via Random Forests). We show that 8 out of 9 regions exhibit an increase in mean occupancy per species over time. Most regions are gaining species on average and these changes seem to be driven by temperature, change in temperature and change in precipitation. At smaller grains, we see a weak taxonomic homogenization which vanishes at larger scales. Temporal turnover patterns vary by region and are driven again mostly by changes in temperature and precipitation. Overall, we present the most up-to-date synthesis of temporal biodiversity change and its underlying drivers at a previously underexplored mesoscale.

436. Is exclusive competition a realistic expectation at macroecological scales?

Armand Rausell-Moreno, *National Museum of Natural Sciences, Madrid; Nuria Galiana, Museo Nacional de Ciencias Naturales (CSIC); Miguel Bastos Araújo, CSIC*

Understanding the determinants of species distributions is a central question in ecology. While abiotic constraints have traditionally dominated explanations, species exist within a web of interactions that may modulate or reshape their geographic ranges. The role of

competition is well documented at local scales, yet its influence at macroecological scales remains largely unresolved. Here, we introduce a framework to test whether and how exclusive competition shapes species distributions across broad spatial extents, using a European trophic database applied to the Iberian Peninsula. Potential competitors are identified through a relative competition index that integrates diet overlap, body mass, and trophic position similarity. For each species pair with high competitive potential, we compare their spatial distributions to detect cases of potential exclusive competition —defined as high competition indices but low spatial overlap. To account for alternative explanations, given that species distributions also result from abiotic constraints and dispersal limitations, we further assess the proportion of each species' realised range relative to its potential environmental space and identify anthropogenic and environmental barriers that may constrain distributions independently of competition. With this framework, we aim to expand our knowledge about how we approach exclusive competitive interactions and understand under which conditions these negative interactions could be shaping species distributions at macroecological scales.

Biomes, Mapping and Macroecology

441. A concept of biome biogeography

Niklaus E. Zimmermann, *Swiss Federal Research Institute WSL; Philipp Brun, WSL; Dirk Nikolaus Karger, WSL; Michael P. Nobis, WSL; Wen-Na Ding, WSL; Elena Plekhanova, WSL; Haozhi Ma, WSL*

Biome biogeography explores the global distribution of the Earth's major biological communities, known as biomes, how they have formed through evolution, how they have evolved traits and trait syndromes to adapt to prevailing environmental conditions, and how their patterns have shifted over time. The field investigates the ecological and historical forces shaping where specific biomes, such as deserts, tropical forests, or temperate grasslands, occur. It further explores why and where biome-dominant species have evolved traits that enable them to thrive in these environments.

Yet, the topic has not been well defined nor conceptualized to date. With this presentation, we aim to explore, to what degree we can define the field of biome biogeography. We will discuss the degree to which island biogeography concepts can be applied to, or require adaptation for, biome biogeography. Finally, we will assess opportunities to develop novel theoretical aspects that extend beyond island biogeographic principles. Special focus will be given to the validity of biomes representing "islands", and the possible consequences of richness differences between patches of the same biome, if biome conservatism is a prevailing evolutionary mechanism. Yet, we will also discuss the influence of evolutionary

idiosyncrasies, which may have resulted in regionally differing biomes or dominant traits or life forms under similar or identical environmental conditions in different regions.

442. A hierarchical framework for mapping ecosystem extent using Earth Observation data

Borja Jimenez-Alfaro, *Oviedo University; Jose Manuel Alvarez Martinez, Biodiversity Research Institute, University of Oviedo, Spain*

Mapping the extent of natural and semi-natural ecosystems is a key target for biodiversity conservation, supporting global initiatives such as the IUCN Red List of Ecosystems and the United Nations' ecosystem accounting framework. A powerful foundation for high-resolution Ecosystem mapping can benefit from the combination of ground-truth observations with Earth observation data. Yet, operational frameworks capable of integrating diverse data sources and classification systems remain underdeveloped. Here, we present a hierarchical framework that incorporates multiple ecosystem typologies, field-based sampling, and distribution modeling to produce large-scale, high-resolution maps of natural ecosystems. We applied this approach in Central Anatolia (Turkey), a biogeographically distinctive region facing urgent conservation challenges and lacking comprehensive ecosystem maps. Using standard land-cover datasets, we developed a systematic field sampling strategy to collect calibration data across multiple hierarchical levels of natural ecosystems – from IUCN-defined functional ecosystems to ecological types classified under the European EUNIS classification. Models trained with ground truth observations and Earth Observation-derived predictors achieved strong performance in both spatial precision and typological detail, generating actionable outputs for conservation planning. We identify the key conceptual components required to adapt this framework to regions that are either data-poor or structurally complex, as well as to areas where biodiversity knowledge is available and the use of Earth Observation technologies remains limited.

443. Climate contiguity, niche breadth and their roles in shaping global patterns of species richness

Pascal Title, *Stony Brook University*

Which universal factors influence global patterns of species richness has been a long-standing question in ecology and evolution. Biotic factors, such as ecological and phenotypic attributes of species, are known to shape how many taxa can co-occur in a community by enabling (or hindering) the expansion and sub-partitioning of niche space. However, the relative importance of abiotic factors, such as climate and topography, is less well understood. Solar energy and temperature have long been proposed as potential drivers of increased species richness, be it via increased mutation rates and speciation, or by enabling

high productivity environments that support more niches. Where species can occur on the globe is partially defined not only by their climatic tolerances, but by the breadth of tolerance. Therefore, the contiguity of climatically suitable conditions is dependent on an interaction between abiotic factors such as topography and geography, and also biotic factors such as climatic breadth. These interactions have been less explored in the context of macroecology. Here, I explore the interaction between climatic variables and geographic and topographic constraints on a global scale. I then project climate niche breadths of squamates within these constraints and consider how these factors play a role in shaping global species richness and range size patterns, both in the present and in a time-integrated manner. Aside from confirming previously appreciated influences of topography and temperature on global patterns of diversity, I find that the way in which climate manifests itself geographically holds additional explanatory power.

444. Global vulnerability of seed dispersers to human modification of habitats

Emma-Liina Marjakangas, *Aarhus University; Camille Magneville, Center for Ecological Dynamics in a Novel Biosphere (ECONOVO), Department of Biology, Aarhus University; Eva Moracho Martinez, Aarhus University; Alejandro Ordonez, Aarhus University*

Seed dispersal interactions are crucial for maintaining the regeneration of plant species and their ability to shift ranges under global change. While animals play a pivotal role in ensuring this function, global assessments of the vulnerability of seed-dispersing animals remain scarce. The vulnerability of these communities to human modification of habitats consists of three components: their exposure to the modification, their sensitivity to the modification, and their capacity to adapt and cope with the modification by altering their fruit consumption. Together, these components indicate which seed disperser communities are most vulnerable and require intensive conservation interventions. In this global study, we quantified the vulnerability components of seed disperser communities in 1° by 1° grid cell localities. We assessed how vulnerability components (co)vary spatially and summed standardized exposure, sensitivity, and adaptability into a measure of total vulnerability. We identified the vulnerability hotspots worldwide and evaluated which component contributed most to the overall vulnerability of the seed disperser communities. The average seed disperser community exhibited relatively low vulnerability, with few communities classified as highly vulnerable across all three components. Instead, vulnerability was most commonly driven by high exposure rather than high sensitivity or limited adaptability. Our results highlight spatial interlinkages among the vulnerability components and localities that would benefit from intensive conservation interventions to maintain the composition of seed disperser communities and the seed dispersal functions they provide in the future.

445. Geographic range shapes influence species richness in global hotspots

Jesper Sonne, *University of Copenhagen, Denmark*

Despite centuries of investigation, we are still struggling to understand the fundamental processes determining global patterns of species diversity. Why certain areas become extraordinarily species-rich (so-called 'biodiversity hotspots') is considered one of the grand enigmas in biology. It is well documented that global biodiversity hotspots are associated with aggregations of small-ranged species, especially within tropical mountain regions. However, size is only one of several fundamental attributes of species ranges that determine species richness within a given area. However, the ranges of mountain species are also distinctly more patchy and elongated than those found in adjacent lowlands. Our global analysis of mainland birds demonstrates that these range shapes profoundly augment the geographic pattern of species richness, above and beyond the climate regime and the processes that affect species richness through range sizes. Both the elongated and patchy range shapes are most pronounced in a-seasonal and topographically complex regions, most notably in the tropical Andes, where these range shapes contribute more to the pattern of species richness than broad-scale variations in range size. These findings have implications for our understanding of the factors that determine global patterns of biodiversity and open the door to new analytical approaches to gaining better insight into what determines the global pattern of life on Earth. Notably, our results change the established view that global hotspots of species richness in mountain regions derive solely from the aggregation of small-ranged species.

446. Body mass-abundance relationships reveal uneven global energy distribution across size classes

Luis Camacho, *Museo Nacional de Ciencias Naturales; Miguel Bastos Araújo, Museo Nacional de Ciencias Naturales, CSIC*

The relationship between species body mass and abundance (MAR-SPP) is a fundamental characteristic of ecosystems, shaping whether energy is accumulated in few large or many smaller organisms. While larger species are generally less abundant than smaller ones, the universality of this pattern and its underlying mechanisms remain uncertain. Here, we present a global assessment of MAR-SPP by modelling the abundance of 11,807 bird and mammal species, analysing community assemblages at a 1-degree spatial resolution. We show that increases in ecosystem productivity and human activity are associated with a relative decline in the abundance of small species. This shift is primarily driven by a pattern in which small organisms become more speciose but not correspondingly more abundant, resulting in a dilution of individuals across an increasing number of species. Given that basal metabolic rate scales with body mass to the power of 0.75, our findings suggest that larger species, on average, capture more energy than smaller ones—particularly in productive

ecosystems. However, greater species richness among smaller organisms implies that they collectively account for most of energy available within ecosystems. This study underscores the complex interaction of body mass, energy distribution, and ecological opportunity in structuring global biodiversity patterns.

Aquatic Distributions

451. Lessons from recent advances in marine biogeography

Mark John Costello, *Nord University, Bodo, Norway*

Recent advances in marine biogeography include (1) the first data-driven classification of biogeographic realms by endemicity, (2) an environmental explanation for why species richness declines with depth, (3) that the latitudinal gradient in marine species richness is bimodal, symmetrical and shifting as predicted due to global warming since the last ice age, (4) but species turnover (betadiversity) peaks at the equator, and (5) the mechanism behind why species richness declines above an annual average temperature of 20oC. These findings are summarised, and new results on global patterns in terrestrial biogeography are presented.

452. Incorporating coral genus distributions as predictors in modelling distributions of coral reef fishes

Yi-Shiuan Horng, *National Taiwan University, Taiwan*

Climate change and human disturbances have accelerated coral bleaching and mortality, additionally forcing distributions of reef-dependent fish and altering marine ecosystems. Most reef fish studies focus on regional scales and overlook the effects of coral habitats. By categorizing reef fishes into tropical and non-tropical groups, this study compared predictive performance of two models considering only environmental variables or both environmental and coral-distribution variables using the Ensemble Species Distribution Models (eSDMs). The best models were then used to predict global distributions of reef fishes under future climate scenarios (including SSP1-2.6 and SSP5-8.5 scenarios for the periods 2050–2060 and 2090–2100, respectively). Currently, this study analyzed 53 coral genera, 11 non-tropical, and 10 tropical reef fish species. The results showed that the ensemble models showed better performance than individual models for both coral and fish distributions. For reef fishes, the models including coral predictors slightly increased model performance. Bottom temperature was the most important variable for both coral and reef fish distributions when using only environmental variables. On the other hand, the coral distributions became the most important variable when including coral-distribution variables. From 2090 to 2100, under the high-emission scenario (SSP5-8.5), both coral and fish distributions would expect

to shift more toward higher latitudes than under the low-emission scenario (SSP1-2.6). Coral and non-tropical fishes would show the largest range shifts, whereas tropical fishes would show limited range changes. These findings improve our understandings of global coral and fish distributions and can support future conservation and management strategies.

453. Oceanic Islands as Seasonal Aggregation Sites: Partial Migration and Restricted Home Ranges Short-Finned Pilot Whale

Marc Fernandez, *ARDITI/MARE-Madeira; Mieke Weyn, ARDITI/MARE Madeira; University of Madeira; University of Évora; Rita Ferreira, ARDITI/MARE Madeira; Massimiliano Rosso, CIMA Research Foundation; NBFC Mafalda Correia, CIIMAR/CIMAR LA; Karin Hartman, Risso's Dolphin Research Center; Nova Atlantis Foundation; Pieter van der Harst, Risso's Dolphin Research Center; Nova Atlantis Foundation; Ana Dinis, ARDITI/MARE Madeira; Filipe Alves, ARDITI/MARE Madeira*

Understanding habitat use and residency patterns in cetaceans is essential for developing effective conservation strategies. We used data from 16 satellite tags deployed on short-finned pilot whales (*Globicephala macrorhynchus*) around Madeira Island from 2018 to 2024 to characterize movement patterns and habitat use, focusing on residency behaviour. A two-step analysis investigated (1) spatiotemporal behavioral states using Hidden Markov Models with covariate dependence and (2) key residency areas using continuous-time movement models and autocorrelated kernel density estimators. The tags transmitted a maximum of 180 days, with a mean of 85 days, moving across a study area of 1,170,790 km^2, spanning from 33°N (north of Madeira) to 23.5°N (south of the Canary Islands) and extending from offshore regions to the African coastline. Results indicated a higher prevalence of residency-type behavior near oceanic islands from June to December, likely associated with seasonal changes in temperature and water column structure, while traveling/ exploring behavior dominated during the remaining months. However, some individuals showed residency during the first half of the year, indicating variable individual strategies within the population. A total of 12 animals showed residency behavior around Madeira Island, with eight remaining for over 20 days and one for up to 120 consecutive days. Home ranges were highly restricted (95%: 1,823 km^2; 50%: 350 km^2), concentrated in waters southeast of Madeira. These results indicate a partially migratory population with varying residency strategies. This behavioral flexibility in response to environmental variability emphasizes the need for adaptive management approaches that account for seasonal patterns and individual diversity.

454. Beyond land: a framework for modelling aquatic species distributions

Georgios Vagenas, *National Museum of Natural Sciences, Spanish National Research Council; Miguel Matias and Miguel Bastos Araújo, both at Museo Nacional de Ciencias Naturales, CSIC*

Species Distribution Models (SDMs) in aquatic ecosystems present unique conceptual and methodological challenges, from dealing with spatially constrained river networks to capturing the interplay of hydroclimatic drivers. These challenges have so far limited the establishment of generalized modeling protocols for freshwater taxa. In this study, we advance a multi-stage framework that explicitly addresses these challenges by combining

novel spatial strategies, hierarchical model structures, and flexible predictor sets. Using presence-only records of freshwater fish from the Iberian Peninsula, we tested: (i) two hierarchical strategies — global-to-regional models, trained globally and projected regionally for widespread species, and strictly regional models, developed within the region for endemic species; (ii) two spatial strategies — unconstrained models, covering the full freshwater range of each species, and constrained models, restricted to watersheds with known occurrences; and (iii) multiple predictor combinations, from single-variable to hierarchical sets that integrate climatic, hydrological, and interactive factors. By systematically cross-comparing these methodological dimensions, we show that spatially constrained models deliver markedly higher predictive accuracy, and that climate-based predictors consistently outperform purely hydrological ones. Our results highlight that no single modelling step suffices in isolation: only through the proposed integrative protocol can aquatic SDMs achieve robust predictive power. This framework provides a methodological advance towards standardizing SDMs in freshwater systems, ensuring more reliable inference under the intrinsic complexity of aquatic environments.

455. Resolving tuna–prey overlap with trophic species distribution models

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Species distribution models (SDMs) have extensively acknowledged species' direct physiological and ecological responses to habitat conditions and climate, but they have rarely included direct representations of trophic effects on species' presence mediated via other interacting community members. For Atlantic bluefin tuna, however, prey availability may dictate presence. To test this possibility, we develop trophic SDMs that include prey fields based on known tuna diet. By resolving climatological sea temperature at fine spatial scales (down to ~1 km grid resolution), we expect to reach higher precision in estimating ecological niches and trophic interactions. The enhanced SDMs will allow us to quantify gains in predictive accuracy for large and mobile predators when prey availability is included, and to assess how this alters projections under ocean warming scenarios.

Evolution, Diversification, and Historical Biogeography

511. The evolution of ecosystem and Earth system engineering

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Over the last ~3.5 billion years, life has increasingly modified our planet with successive waves of evolutionary innovation leading to stronger controls over the distribution and flow of resources and influencing the character and distribution of ecological niches. The recognition that some taxa have oversized effects on other species and the environment led to the concept of ‘ecosystem engineers’ (EE). Extending this concept into a deep-time and evolutionary context poses conceptual challenges. To accommodate uncertainty in the fossil record, we focus on the resultant processes rather than on specific taxa as ecosystem engineers. We also propose a new concept – ‘Earth system engineering’ (ESE) – to describe biologic processes whose influence is particularly extensive, altering the structure and function of planetary spheres and impacting the habitability of the planet as a whole. Using this framework, we quantify the richness and functional diversity of ecosystem and Earth system engineering processes over the last 4 billion years encompassing six broad organismal groups (microbes, fungi, vertebrates, invertebrates, plants, and humans). We find that ecosystem and Earth system engineering processes appear as soon as life evolves, and once they appear they rarely go extinct. Ecosystem engineering processes are much more common than Earth system engineering processes, but the diversity of both increases with the evolution of multicellular life, with the acquisition of new areas of the planet or with new morphologies. Humans, a single species, perform almost as many ecosystem or earth system engineering processes as entire divisions of the tree of life.

512. Climate, rather than geography, governs global patterns of speciation in vertebrates

Antonin Machac, *IMIC Prague; Felipe Osmari Cerezer, Center for Theoretical Study, Charles University*

Why some regions and climates accumulate species faster than others remains largely unresolved. Here, we study the patterns of present-day speciation in vertebrates. We reconstruct the speciation patterns, both in geographic and climatic space, and test their three hypothesized causes: (1) the geographic area covered by the climate, (2) the geographic isolation of the climate, (3) the climate itself. We compare the relative effects of these causes and study their interactions, using diversification analyses, path models, and GIS (across 30,000+ species). Our results reject the geography of climate, namely climate area and isolation, as the main driver of present-day speciation. Instead, we find consistent support for the effects of climate itself. Path models revealed the underlying mechanism, whereby climatic niche divergence accelerates present-day speciation, especially outside the tropics. These findings held, independently, across four vertebrate classes (amphibians, reptiles, birds, and mammals) and multiple diversification methods. We conclude that faster speciation in temperate regions and climates is driven mainly by climate-mediated niche divergence. These effects surpass those of niche conservatism, as well as those of climate area or isolation. Knowledge of the patterns of species origination and their causes is essential not only for biodiversity theory, but also to anticipate how biodiversity will respond to changing climates.

513. Global prevalence and evolution of animal-mediated seed dispersal

Francisco Rodriguez-Sanchez, *Universidad de Sevilla; Elena Quintero, Universidad de Sevilla; Ignacio Ramos-Gutiérrez, Universidad de Sevilla*

Along Earth history, plants have long relied on animals to spread their seeds and colonize new habitats. Yet many important aspects of such a crucial interaction remain largely unknown. We have assembled a large database (+60,000 species) on plant dispersal modes to tackle three basic questions: (1) How many plants have their seeds dispersed by animals worldwide? What is the prevalence of animal dispersal across plant families and genera? (2) Where do these plants occur? Are there geographical patterns in the importance of biotic dispersal across regional floras (i.e. biotic dispersal hotspots)? (3) How has this interaction between plants and animals evolved since the origin of seed plants (angiosperms and gymnosperms) more than 300 million years ago? Using hierarchical Bayesian and phylogenetic comparative analyses, we found that over half seed plants can be dispersed by animals worldwide, with large variation existing across plant families. Likewise, biotic seed dispersal is particularly important in many tropical regions, being relevant in some extra-tropical regions too. Finally, biotic dispersal evolved soon after the origin of seed plants (e.g. cycads and magnoliids), with many evolutionary switches to and from biotic dispersal

occurring since then, associated to the diversification of angiosperms through the Cenozoic. Current defaunation trends in large parts of the world threaten the functioning of such a crucial mutualistic interactions/service.

514. Evolutionary time and climatic stability as underlying drivers for floristic hyperdiversity across global biodiversity hotspots

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Biodiversity hotspots contain high species richness and endemism, but whether shared eco-evolutionary dynamics underlie this diversity remains unknown. We synthesized species richness, diversification rate, and age for 1,928 plant lineages across 21 hotspots, and applied phylogenetic comparative methods to disentangle shared and idiosyncratic drivers of diversity across hotspots. Hotspots differed substantially in their evolutionary dynamics: the highest diversification rates were found in island-like hotspots (Páramo and the Hawaiian Islands), and the oldest lineages in Southeast Asia and the Himalayan-Hengduan hotspots. Furthermore, older lineages had more species, and lineages that evolved in hotspots that have been climatically stable over time had higher diversity and diversification rates. Regions that shared a common environment (e.g., Mediterranean climate) were often similar in lineage ages and diversification rates, suggesting shared ecological opportunities. Our results indicate that the most diverse biodiversity hotspots contain old lineages that have accumulated diversity over time, but the highest diversification rates are found in young, island-like hotspots. Furthermore, lineages within biodiversity hotspots share similar ages and rates, suggesting that region-specific drivers have shaped lineages in similar ways. Our

synthesis sets the stage for further investigation on whether hotspot lineages also respond in concert to ongoing threats of extinction.

515. Latitudinal gradient of species diversification - decoding the enigma of different methods, definitions and datasets

Jan Smycka, *Center for Theoretical Studies, Charles University; Grace Ridder, Center for Theoretical Studies; Arne O Mooers, Simon Fraser University; Sarah P Otto, University of British Columbia; David Storch, Center for Theoretical Study, Charles University*

Several recent influential papers suggest that large groups of organisms such as marine fish, mammals or angiosperm plants might have higher speciation rates in high latitudes. This is in stark contrast with the traditional explanation of the latitudinal gradient of diversity by higher speciation rates in the tropics. Moreover, the results of these papers are often contradicted by other studies using different methods of diversification inference and different definitions of latitudinal categories, even on the same underlying data. Here we reanalyze a collection of macroecological datasets recently published in relationship with latitudinal gradient of diversification. For each dataset, we use an exhaustive combination of methodological choices, including tip-rate metrics and state-dependent diversification models. We also explore the effect of different definitions of latitudinal categories. Our results show that certain groups of organisms, such as marine fish or mammals, have consistently higher speciation rates in high latitudes, irrespectively of diversification metric or model used. The models estimating both speciation and extinction also suggest that the faster speciation might be overcompensated by fast extinction, resulting in lower diversity in high latitude biotas. Interestingly, this fast turnover only concerns biotas above c. 40° of latitude, which explains why it could not be captured by the studies comparing tropics with the extra-tropics, and why it is not detectable in reptiles and amphibians. The latitudinal diversification gradient, while decoupled from diversity, might thus reflect the colonisation dynamics of the cold biomes emerging since the late Miocene.

516. Global biogeographic disjunctions in seed plants

Jan Hackel, *Stockholm University; Alexander Zizka, Philipps University Marburg*

Disjunctions in the geographic ranges of taxa have provided important evidence for reconstructions of the past. Yet their study has mostly concentrated on particular geographic areas of interest. We produced a global overview of biogeographic disjunctions in seed plants by combining phylogenetic and distribution data. We identified 7,440 clades and 84,411 species whose distribution is disjunct between botanical countries worldwide. The oldest disjunct clade was found in the ANA grade at c. 122 Ma divergence, but old disjunct clades also occur in other angiosperm groups while the oldest disjunct gymnosperm clades are less

than 40 Ma old. Disjunct clades are, on average, older and more tip-balanced than non-disjunct clades. Geographically, hotspots of clade disjunction were found between Madagascar and mainland Africa, and New Guinea and Northwestern Australia. On a continental scale, North America–South America has the highest shares of both disjunct clades and species, while a proportionally high number of clades, but not species, are disjunct between South America–Africa and North America–Temperate Asia, respectively. Taken together, our results are consistent with a highly dynamic assembly of global biodiversity, where dispersal even between distant areas must have occurred frequently.

Island diversity and trophic structures

521. Towards a Synthesis of Island Floras – New Insights and Resources for Island Biogeography

Holger Kreft, *University of Göttingen, Göttingen, Germany*

Islands contribute disproportionately to global plant biodiversity and are hotspots of both historical and ongoing species extinctions. At the same time, they serve as classic model systems for studying the biogeographical processes underlying the assembly of floras. However, global-scale analyses of island floras have long been constrained by the fragmented nature of island systems and limited data availability across the thousands of islands worldwide. In this talk, I present how the Global Inventory of Floras and Traits (GIFT; https://gift.uni-goettingen.de/) has enabled island biogeography research at an unprecedented scale and resolution. Recent studies using GIFT reveal that 31% of all vascular plant species are native to islands, and 21% of global plant diversity is endemic to islands. These analyses provide new insights into the nature of endemism—particularly the distinction between neo- and paleoendemism—and illuminate patterns of taxonomic and phylogenetic turnover between island and continental floras. Despite these advances, major knowledge gaps remain—especially at the community level and in the availability of plant functional trait data and highly resolved phylogenies. To address this, I will introduce BioMonI-Plot, a new community-driven initiative aimed at mobilizing and sharing local vegetation data. This effort has the potential to significantly advance basic research, biodiversity monitoring, and ecosystem restoration in island environments.

522. Cradles and Graveyards of Biodiversity

Carl Beierkuhnlein, *University of Bayreuth, Bayreuth, Germany*

The contribution of volcanic oceanic islands to global biodiversity is immense. These islands are a traditional arena of biogeography. Analyzing patterns of their natural biodiversity and endemism was mostly focused on isolation, size, elevation, and climate. The bedrock and

soils of oceanic islands are comparable, but species assemblages are individualistic which cannot be explained by climate or isolation only. Also, the life cycle of such islands and the duration of volcanic activity is highly relevant. Speciation is highest not towards the mature end, but during the early phase of island ontogeny with ongoing impacts such as lava flows, gas emission, and pyroclastic ejections. However, the fundamental aspect of their existence, volcanic processes themselves were either seen as destructive or were ignored. Here, I present research on the effects of gas emissions and tephra deposition on ecosystem dynamics and speciation at the example of Canary Island ecosystems. Deterministic processes in the development of vegetation structures are linked to idiosyncratic processes in speciation. The 2021 eruption of Tajogaite volcano on La Palma Island enabled us to study the role of repeated volcanic activity on biodiversity, with implications for the relevance of oceanic islands as cradles and graveyards of global biodiversity.

523. From land to ocean: unraveling global patterns of beta diversity in archipelagos

Luiza Waechter, University of Miami; Chancey MacDonald, Newcastle University; Juan Pablo Quimbayo, University of Miami

Global biodiversity is unevenly distributed, shaped by distinct mechanisms in terrestrial and marine systems. Archipelagos are particularly relevant since represents natural laboratories to understand ecological, historical and evolutionary processes. However, despite its importance, studies simultaneously assessing multiple archipelagos and taxa remain scarce. We evaluated across taxa taxonomic and functional beta diversity in 19 archipelagos worldwide. Species richness data were compiled at the island level for birds, plants, reef fish, and corals, along with taxa specific functional traits related to food acquisition, reproduction, and mobility. Diversity was measured using Sørensen's dissimilarity index, partitioned into turnover and nestedness components. Species richness varied widely among the 137 islands, whereas mobility capabilities appeared to influence distribution patterns. For plants, Hawaii showed the highest richness (n = 3,084), while for birds it was the Maluku Islands (n = 917). In reef environments, coral richness peaked in the Andaman and Nicobar Islands (n = 483), whereas reef fish richness was highest in Fiji (n = 1,493). Plant assemblages were mostly characterized by high taxonomic turnover, whereas bird communities showed greater nestedness. Corals and reef fish also exhibited high nestedness, likely reflecting similar richness among islands. Functional beta diversity was comparable among the four groups, predominantly shaped by nestedness patterns. By integrating terrestrial and marine taxa across multiple archipelagos, our study reveals consistent functional patterns but contrasting taxonomic results across taxa. These findings highlight the importance of incorporating cross ecosystem perspectives to guide global biodiversity conservation both terrestrial and marine island ecosystems.

524. Humans simplified trophic structures in island lake ecosystems

Miguel Matias, *Museo Nacional de Ciencias Naturales; Vitor Gonçalves, CIBIO; Sergi Pla-Rabes, CREAF; Armand Hernández, Universidade da Coruña, GRICA-BIOpast Group, Centro Interdisciplinar de Química e Bioloxía (CICA), Spain; Manuel Mendoza, Museo Nacional de Ciencias Naturales (CSIC); Miguel Bastos Araújo, CSIC; Sandra Nogué, Universitat Autònoma de Barcelona; Nora Richter, Department of Surface Waters - Research and Management, Swiss Federal Institute of Aquatic Science and Technology (EAWAG), Dübendorf, Switzerland; Martín Souto, CIBIO; Universidade dos Açores; Ricardo Trigo, Instituto Dom Luiz, Faculdade de Ciências, Universidade de Lisboa, Portugal; Roberto Bao Casal, Universidade da Coruña, GRICA-BIOpast Group, Centro Interdisciplinar de Química e Bioloxía (CICA), Spain; Alberto Saez, UB-Geomodels Research Institute. Departament de Dinàmica de la Terra i de l'Oceà, Facultat de Ciències de la Terra, Universitat de Barcelona, Barcelona, Spain; Santiago Giralt, Geosciences Barcelona; Pedro M. Raposeiro, CIBIO*

Lakes on oceanic islands are exceptionally vulnerable ecosystems and serve as unique natural archives of past environmental change. Yet long-term, ecosystem-level reconstructions from these systems remain rare, particularly those spanning multiple lakes and trophic levels. Here, we reconstruct 2,000 years of ecological change across nine lakes in the Azores by analyzing shifts in trophic guild composition and richness in lake sediments. We document an archipelago-wide shift toward plankton-dominated lake trophic structures, accompanied by declining species richness and increasing homogenization. Consumer guilds declined steadily in richness after ~1050 CE, whereas primary producers showed divergent, lake-specific trends, revealing a decoupling of trophic responses. The timing and sequence of change suggest that land use was the primary driver of lake ecosystem restructuring between 1050 and 1450 CE. After vegetation change stabilized around 1600 CE, climate became the predominant factor—a role likely to intensify in the future. By identifying when, how, and why lakes reorganized, our findings highlight that ecological baselines are not fixed states but dynamic outcomes of long-term interactions among humans, climate, and ecosystem resilience.

525. Functional macroecology and island biogeography of Caribbean birds

Trevor Fristoe, *University of Puerto Rico, Río Piedras*

The study of islands as natural laboratories has provided critical insights into the processes that maintain and structure biodiversity. A pillar of island biogeography theory is the well-established link between the size of an island and its species richness – an idea that has been influential in applied conservation. However, species losses may be non-random, with certain traits or functional roles more likely to be missing from low-diversity systems. Here, I perform a macroecological assessment of functional biogeography in Caribbean birds. Combining data on traits, diet, and distributions for over 200 species across 177 islands

(ranging from < 1 to > 100,000km2), I test the idea that persistence on smaller islands is constrained by traits linked to space use through their influence on energetics, trophic level, or ecological specialization. Consistent with macroecological theory, species on the smallest islands tend to converge towards a relatively small 'ideal' body size between 30-100g. Across species, we found that extreme bill morphologies were associated with specialized diets (e.g. pure carnivores or herbivores), with mixed diets occurring at intermediate trait combinations. As diversity decreases, carnivores and their associated traits were lost first - consistent with higher space requirements at higher trophic levels. Herbivores, and associated extreme bill morphologies, were the most likely species to occur on the smallest islands. Despite predictions favoring generalists on smaller islands, species with mixed diets and intermediate trait values were under-represented. Together, these results indicate predictable links between traits, ecology, and extinction risk, with important implications for predicting biodiversity change.

526. Plant-bird frugivore mutualistic networks on subtropical forested islands

Xingfeng Si, *East China Normal University; Wande Li, East China Normal University; Yao Shen, East China Normal University; Xiaotao Zhou, East China Normal University; Chen Zhu, Princeton University; Ping Ding, Zhejiang University*

Species interaction is a key component of biodiversity. However, monitoring species interactions is challenging, especially for plant-bird frugivore mutualistic interactions because frugivore foraging behavior generally occurs in the trees. We developed a camera-trap sampling method to monitor plant-bird frugivore interactions simultaneously and continuously during the whole mature fruiting periods on 22 subtropical forested islands and six nearly mainland sites in the region of Thousand Island Lake, China. Since June 2019, we have obtained ca. seven million photos and videos of frugivore events. We systematically reviewed the first three-year data and identified a total of 17572 independent interaction events, including 39 bird species and 31 fleshy-fruited plant species. We analyzed this high-resolution data of plant-frugivore networks, and found large islands supported higher species richness of plants and birds and their interaction richness. Small islands had more connected, less modular, and more nested networks that consisted mainly of small-bodied birds and abundant plants. Common bird species with small body size and high mobility dominate frugivory interactions, potentially serving as crucial mobile links between fragments via seed transfer. From the temporal scale, migratory birds accounted for 14% of all interactions. Small islands hosted 43% of migratory interactions, highlighting the importance as stopover sites for migratory birds, while large islands supported more frugivore richness but lower migratory proportions, acting as refugia for residents. These findings challenge area-centric conservation priorities by revealing the complementary roles of small and large islands, and advocate enhancing habitat connectivity to sustain seed dispersal and ecosystem resilience in fragmented landscapes.

Species distribution modelling

531. Variation across species distribution models of the same species modeled by independent teams: Are we converging as a field?

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Developing a workflow for a species distribution model (SDM) requires making multiple decisions about data sourcing and cleaning; delineation of the study region; modeling algorithm, parameterization, evaluation; and managing extrapolation; among many others. While guidance for each of these aspects exists in the literature, conflicting results, differing methodological options, and context can make identifying optimal decisions challenging. The degree to which methodological differences arise from SDM "culture"—i.e., practices applied by different teams of analysts—has been little explored. Here, independent teams of modelers "blinded" from one another constructed SDMs for the same two species, for which only instructions including species' names and general requested outputs were provided. Across 24 participating teams, predictions of suitable habitat only generally agreed. Depending on the time period of projections (present vs. future), teams' predictions clustered into two to four groups. No single workflow decision (e.g., spatial resolution of the analysis, number of predictors, accounting for intraspecific variation) was associated with the clusters, and clusters did not differ by the degree to which they met SDM quality standards. Multivariate analysis revealed clusters were associated with simple decision pathways related to the size of the calibration region and its method of delineation, sample size, number of climate predictors, and, for future projections, choice of global circulation model. Fully capturing the range of uncertainty in SDM predictions requires employing independent analysts and considering the sum effect of multiple decisions on predictions. The field has yet to converge on methodological frameworks, reporting, and predictive capacity.

532. Can Species Traits Predict Changes in Abundance and Area of Occupation?

Arthur Rodrigues, *University of Helsinki, Finland*

Environmental changes, including shifts in climate and land use, are affecting species distributions and population sizes. These changes may lead to population growth, decline, or redistribution, depending on how species respond. Responses can involve tracking suitable environments, adapting locally, or failing to cope, which may result in reduced abundance or extinction. Species traits, reflecting ecological strategies such as life-history, dispersal, and resource-use, may help explain and predict these responses. Here we assess whether species traits can predict temporal trends in distribution area and abundance across Finland. Using 20 years of monitoring data on birds, mammals, butterflies, and moths, we quantify changes in population size and distribution using joint species distribution models informed by climate and land-use variables. From the spatial predictions, we estimate annual area of occupation and abundance at national and biogeographical levels. Temporal trends are derived using generalized linear models. Uncertainty from species distribution modeling is propagated throughout the analysis, including in the estimation of trends and trait-based predictions. We then test whether traits grouped into three axes (life-history, dispersal ability, and resource-use) can predict these trends. Models include main effects and interactions among axes. We also examine trait space structure using hypervolume analysis to assess

whether species with similar trends cluster in trait space. We expect that interactions among traits, particularly between life-history and resource-use, will be informative for predicting abundance trends, while dispersal ability may be more relevant for changes in area of occupation. This work assesses how species traits explain biodiversity trends under environmental change.

533. Triple threats to tropical biodiversity: scenario-based assessments disentangling the impact of future climate change, disease and deforestation on vulnerable species range dynamics with RangeShiftR

Emma L. Underwood, *Kingston University London; Jette Wolff, University of Potsdam; Rebekka Allgayer, University of Aberdeen; Nigel Walford, Kingston University London; Mark Mulligan, King's College London; Kerry Brown, Kingston University London*

Climate change is causing plants to alter their known ranges to track newly suitable habitats. Species extinction risk is highest on geographically isolated islands with high endemism such as Madagascar. For plants like *Calophyllum*, they face a triple threat, after high mortality rates were discovered within Ranomafana National Park, linked to a newly identified vascular wilt like pathogen. Anthropogenic change, including deforestation, degradation and habitat fragmentation is impacting frugivores that are often the sole dispersers of seeds. We develop our understanding of these abiotic and biotic drivers by generating multi-scenario mechanistic models to identify their impact on population abundance and occupancy. These scenarios include (i) climate and deforestation, (ii) biological invasion and (iii) loss of dispersal function via defaunation. We use RangeShiftR, a spatially explicit individual-based modelling platform using stage-structured population demographics and dispersal processes of the focal species in a virtual version of the landscape. Results highlight the interplay between change-drivers, including the most threatening combination of scenarios affecting *Calophyllum* in Madagascar. Predicting potential outcomes for this vulnerable, endemic tropical tree allows us to predict extinction risk, disentangle the multiple threats, and emphasise the highest at-risk populations to conserve. Conservationists require an improved understanding of how different organisms may respond to environmental change drivers, and how those threats combine to exacerbate existing vulnerabilities. The results from mechanistic studies like this can in turn, inform management strategies that require evidence-based decisions to progress interventions to the species and locations that need it most.

534. A trait-informed deep learning model to map species distributions and assemblages of Swiss flora

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Biodiversity models extend predictions of species assemblages beyond direct observations, supporting applications such as informing conservation efforts. Yet, predicting the spatial distribution of species assemblages remains a persistent challenge in biogeography, as both abiotic and biotic processes shape community composition through complex interactions. Multi-species distribution models are promising because they integrate information about species co-occurrence, but they are typically limited to environmental filters. Functional trait data, such as morphological, physiological, or phenological characteristics, have considerable yet underutilized potential to inform models about species responses to the environment and ecological assembly rules. Here, we propose a two-step deep learning approach to integrate traits into assemblage predictions. First, we model trait-informed habitat suitability by training a deep learning species distribution model using opportunistic occurrence records, high-resolution environmental predictors, and species trait data. Second, we use plot data to train a transformer model to predict assemblages from predicted habitat suitability scores and learned trait representations, by learning relationships between species through attention mechanisms. We evaluate the model on over 1000 plant species across Switzerland, combining large-scale presence-only observational data with a smaller, but high-quality set of vegetation plots. Our results show that trait-informed, attention-based modeling improves assemblage predictions and demonstrate how the flexibility of deep learning enables application-driven integration of diverse data sources. Our approach aims to bridge species distributions modelling and trait-based community ecology, offering scalable and ecologically grounded predictions of biodiversity patterns.

535. Spatially-nested hierarchical Species Distribution Models with sabinaNSDM

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Species distribution models (SDMs) are central to biodiversity assessments and global change ecology, but they face a persistent challenge: identifying the optimal scale. Models calibrated only within part of a species' range risk niche truncation (i.e., underestimating the breadth of environmental conditions a species can occupy), while full-range models often rely on coarse-resolution data that fail to capture fine-scale species–environment

relationships. Spatially nested hierarchical SDMs (N-SDMs) resolve this trade-off by combining global-scale models, which describe broad patterns of the ecological niche, with regional-scale models that integrate high-resolution covariates, resulting in a powerful multiscale framework. In this work, we review existing methods and tools for fitting N-SDMs and present sabinaNSDM, an R package that enables their implementation in a user-friendly and reproducible way. The package offers two alternative nesting strategies and streamlines the entire workflow from data preparation and model calibration to projection. It further incorporates tools for background data generation, spatial thinning, and covariate selection. By simplifying the modelling steps, sabinaNSDM makes advanced N-SDM workflows accessible to a broad community of ecologists and conservation practitioners.

We demonstrate its potential with a case study of 200 woody plant species in Spain under current and future climate scenarios. Results confirm that N-SDMs outperform traditional approaches by reducing niche truncation and delivering fine-resolution, policy-relevant forecasts. Our contribution highlights the value of N-SDMs for robust biodiversity projections and positions sabinaNSDM as a practical tool for their wider adoption in conservation planning and climate change research.

536. Illusion of pseudo-absences: a call for non-informative backgrounds in species distribution modelling

Babak Naimi, *University of Utrecht; Miguel Bastos Araújo, Museo Nacional de Ciencias Naturales, CSIC; Edwin Pos, University of Utrecht*

Species distribution models (SDMs) learn from two data channels: presences and a reference of non-presence locations—variously called pseudo-absences or background. Although often defined differently (“absence” vs. “availability”), these points play the same functional role: they provide the contrast that allows the learner to detect species–environment structure. Because learners are sensitive to the frequency and distribution of these reference points, any structure embedded in them becomes informational, steering model parameters, variable importance, and apparent accuracy. We highlight five pervasive illusions: (1) “background isn’t absence”—yet presence-only methods still contrast presences against background and are affected by how it is sampled; (2) “random pseudo-absences are neutral”—geographically random sampling encodes environmental prevalence and sampling bias, inflating discrimination; (3) “more pseudo-absences are always better”—sheer quantity or overly broad extents distort prevalence and metrics; (4) “spatial or environmental constraints guarantee realism”—poorly chosen buffers/envelopes create over-optimistic or over-restricted niches; and (5) “presence-only avoids absence problems”—background choice remains a dominant driver. We argue for reference-agnostic training: (i) generate or re-weight non-presence points to be (as far as possible) uniform in environmental space and monitor residual multivariate dependence; (ii) adjust learners to neutralise the active covariate when fitting each term (sequential/additive “term-wise” de-informing or ensembles

of small models); and (iii) where feasible, model presences with bias-explicit point-process/likelihood formulations or integrate presence–absence with presence-only data. We call for reporting standards that include reference-sample diagnostics and sensitivity analyses. The key message: distinguishing "pseudo-absence" from "background" obscures the real task—making the reference non-informative so biology, not sampling artefacts, drives inference.

The Neotropics and Asia

541. On the evolutionary assembly of the tree flora in the Cerrado biodiversity hotspot

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The Cerrado of South America houses the most diverse tree flora of any savanna region worldwide, yet only 10% of its territory is protected. Determining conservation priorities in such biodiverse regions, however, is no easy task. Recent studies have documented the diversity and dominance of Cerrado tree species at large spatial scales, showing that almost half are rare or microendemic. Here, we explore the evolutionary assembly of the Cerrado tree flora to advance our understanding of the origins of ecological dominance in this biodiversity hotspot. We compiled a comprehensive dataset describing the abundance, distribution, taxonomy and phylogenetic relationships of 220 angiosperm lineages, representing 58% of all tree genera known from the Cerrado savannas. We find no phylogenetic signal for species richness, range size, and ecological dominance in the Cerrado tree flora. These results hold when analysed for each Cerrado ecoregion separately. Although two-thirds of the lineages in our analyses have low abundance and incidence (i.e. occurring at few sites), they cover large spatial extents (2,320 km on average). We also show that rare tree lineages in the Cerrado stem from relatively shorter branch lengths in the phylogeny, which results in a higher contribution of dominant lineages to the phylogenetic diversity of Cerrado savannas. Efforts aiming to protect the full spectrum of evolutionary diversity in the Cerrado biodiversity hotspot must go beyond traditional metrics, accounting for the intricate patterns of lineage dominance, rarity, and phylogenetic structure.

542. Unraveling diversity and vulnerability in Brazilian montane systems: insights from functional, phylogenetic, and spatial dimensions of Velloziaceae

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The unique environmental conditions of the Brazilian Campos Rupestres (CR), such as shallow nutrient-poor soils, high temperatures, intense solar radiation, water scarcity, and natural fire regimes, have likely driven the evolution of distinctive functional strategies, e.g., desiccation and fire tolerance in Velloziaceae species. Although the effects of climate change on mountain biodiversity remain debated, the CR already faces serious threats from ecotourism, mining, increased fire frequency, and exotic species. In this context, integrative studies combining distribution data, functional traits, and phylogeny are essential to understand the mechanisms behind diversity maintenance and informing conservation strategies. The plant family Velloziaceae, with about 260 species concentrated mainly in the CR, provides an excellent model for investigating these processes due to its remarkable microendemism and functional diversity. Here, we compiled spatial, morpho-functional, and phylogenetic data, evaluated species sampling trends, and estimated the effects of simulated species extinctions on patterns of taxonomic, functional, and phylogenetic diversity in the two largest genera of the family: B*arbacenia* Vand. and *Vellozia* Vand. Our analysis of potential sampling biases revealed a correlation between species occurrences and proximity to roads. Rarefaction curves indicate a continuing potential for species discovery, especially within the Cerrado and Caatinga domains. Simulated extinctions suggest significant reductions in functional and phylogenetic diversity across eastern Brazilian mountain communities. These findings highlight the vulnerability of CR ecosystems to biodiversity loss and emphasize the importance of integrative, multidimensional approaches that incorporate distributions, traits, and evolutionary history to understand and conserve biodiversity in threatened montane systems.

543. The biogeography and evolution of derived woodiness in tropical and sub-tropical angiosperms

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The repeated evolution of woodiness in herbaceous lineages has long been perceived as defining feature of island floras, in particular in the Tropics and sub-Tropics (“insular woodiness”). However, scattered evidence indicated comparable transitions of herbaceous lineages towards woody growth on continents, for instance on tropical mountains (“derived woodiness”). Here, we contrast recent results on the evolution of insular woodiness with a novel dataset on derived woodiness on continents. We identified numerous independent transitions towards woodiness in 57 eudicot angiosperm families, resulting in more than 6,500 recent derived woody species. We found more transitions and derived woody species on continents than on islands but derived woodiness on islands was more common when accounting for total angiosperm richness (on average 0.77% of the total flora on continents vs

1.85% on islands). Furthermore, we identified four global continental centers of derived woodiness, mostly in the Tropics and sub-Tropics: The Andes, Southern Africa, parts of Australia, and the Old-World dry belt. Our results reveal the re-evolution of woodiness in herbaceous lineages as widespread phenomenon on island and on continents driven globally by environmental conditions, albeit with important regional and systematic idiosyncrasies.

544. UV-B absorbing pollen compounds can reveal elevational histories of mountains

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Reconstructing past mountain elevations is a long-standing challenge with important implications for geology, climate science, and biogeography. A promising but still emerging approach involves analyzing elevational signatures preserved in pollen and spores, which record ultraviolet-B (UV-B, 280–315 nm) radiation levels in the chemistry of their outer walls. In this study, we applied Fourier transform infrared spectroscopy (FTIR) to: 1) quantify the relationship between elevation and UV-B absorbing compounds (UACs) in the pollen walls of 81 extant plant species distributed across elevational gradients in the Himalaya and Hengduan mountains; 2) to assess whether fossil pollen, spanning the Miocene to Pleistocene, preserves comparable signals of past. A total of 21 fossil samples were analyzed. Our results reveal a clear pattern: species growing at higher elevations consistently exhibit greater concentrations of UACs than those from lower elevations. Moreover, herbaceous species show higher UACs concentrations compared to woody life forms. These findings establish a strong relationship between elevated UV-B irradiation and UAC abundance at high altitudes. Preliminary results from fossil pollen further indicate that UAC intensity can serve as a proxy for inferring past elevations. We propose that this method offers a valuable new tool for reconstructing paleoelevation profiles and, when integrated with existing techniques, has the potential to refine current reconstructions.

545. Dispersal, diversification, and distribution in tropical Asia: biogeography of Dissochaeteae (Melastomataceae)

Linde Wieringa, Systematik, Biodiversität & Evolution der Pflanzen, University of Munich; Elizabeth M. Joyce, Systematik, Biodiversität & Evolution der Pflanzen, University of Munich; Darin Penneys, University of North Carolina Wilmington; Marie Claire Veranso-Libalah, Senckenberg Forschungsinstitut und Naturmuseum Frankfurt; Gudrun Kadereit, Systematik, Biodiversität & Evolution der Pflanzen, University of Munich

Southeast Asia is home to one of the most diverse floras worldwide, but the processes that generated and shaped this richness remains poorly understood. Despite being one of the largest and most diverse angiosperm families in the tropics, Melastomataceae remains understudied in the biogeographically unique region. Melastomataceae includes several Southeast Asian lineages varying in origin, age, habitat, and dispersal ecology. These contrasts provide a powerful framework for exploring the region's complex geological and biogeographical histroy. The tribe Dissochaeteae comprises c. 70 species of lianas and shrubs distributed in primary and secondary forests from Thailand to New Guinea, with peak species diversity in Borneo. We present a comprehensively sampled phylogenomic framework of the tribe utilizing high-throughput sequencing data, shedding light on patterns of diversification and dispersal across Southeast Asia. This phylogeny shows that Dissochaeteae followed the predominant eastward dispersal patterns in the region, including several expansions from Sunda into Sahul, with multiple bursts of diversification since the Miocene. However, it also provides new insights into the drivers of diversity patterns, with our climatic niche analyses suggesting that suitable climate is not the major factor structuring diversity, contrary to evidence from other Southeast Asian clades. Ongoing work will compare phylogenetic patterns across multiple Melastome lineages within the region, thereby contributing to the broader discussions on the evolution of the region’s megadiverse flora.

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

Christian Hof, *Global Change Ecology, University of Würzburg; Imran Khaliq, Ghazi University*

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.

Aquatic Biogeography

551. Scale and Process of Coral Reef Fish Assemblages across Longitude, Latitude, and Depth

Chancey MacDonald, *Newcastle University; Hudson Pinheiro, University of São Paulo; Luiz Rocha, California Academy of Sciences; Juan Pablo Quimbayo, University of Miami*

The relative contribution and scales of biological and environmental filters acting on species and their traits determines local assemblage structures and connective potential between assemblages along environmental gradients. This will influence interregional migration, shape biodiversity redistribution and limit migration-related rescue effects in response to disturbances and changing environmental conditions. Mesophotic reefs have been touted and negated as potential refugia for coral reefs suffering shallow water heat stress and associated degradation. Yet, we still understand very little detail about the ecological processes driving distinct assemblages in shallow and deep reefs, and how those processes scale along other major geographic gradients. In this talk I will share my investigations of the geographic scale and depths at which random and deterministic ecosystem processes shape evolutionary and ecological distinctness of coral reef fish assemblages along all three principle spatial gradients (Latitude, Longitude, and Depth [0-130m]). Using diversity metrics informed by species' similarities in functional traits, I will identify the spatial scales at which local reef fish assemblages are formed by similar processes and where along these gradients abrupt changes in assemblage composition are forced by deterministic processes such as environmental filtering or inter-species competition. This will reveal important controls on community structure and assembly filters that determine levels of similarity between adjacent assemblages and the future inter-compatibility of assemblage components.

552. Drivers of diversification in the northeastern Pacific rocky intertidal: a multi-species perspective

Michael N Dawson, University of California, Merced; Carmen del R Pedraza-Marrón, University of California, Merced

Understanding how scales of environmental heterogeneity shape the distribution of biodiversity is a central question in biogeography. Here we ask how large-scale latitudinal gradients (~1000 km), regional variation (~10 km) and small-scale intertidal gradients ~0.01 km) intersect to shape the distribution of genetic diversity in intertidal invertebrates. We generated chromosome-level reference genomes and 10X whole-genome resequencing data for ~150 individuals from across ~25 localities in each of 6 species. Analyses reveal familiar patterns including a relationship between life history and genetic differentiation likely mediated by dispersal ability, and that biogeographic ecotones coincide with environmental clines and population genetic differentiation in lower-dispersal species. However, we also find, in species that are well-mixed across regional and latitudinal scales, a remarkable degree of genetic differentiation between conspecifics that are separated by just a few meters in higher versus lower intertidal habitats within a single location. We ask whether allele-specific patterns of differentiation across intertidal environmental gradients are paralleled across regional and latitudinal environmental gradients to understand whether, despite the contrasting patterns, there may be common mechanisms.

553. Marine heatwaves amplify long-term impacts on warm-edge fish biomass decline

Shahar Chaikin, Museo Nacional de Ciencias Naturales (CSIC); Juan David González Trujillo, Universidade de Evora; Miguel Bastos Araújo, CSIC

Long-term ocean warming, interannual temperature variability, and marine heatwaves (MHWs) pose serious but poorly quantified threats to marine species. To isolate their individual effects, we analysed 707,692 estimates of biomass change across 33,836 fish populations (1,562 species) between 1993 and 2021, covering major Northern Hemisphere basins. Long-term warming was associated with an average annual biomass decline of 0.41%. However, warmer years and MHWs were linked to sharp biomass losses of up to 43% in populations at the warm-edge of the species range and biomass increases of up to 179.89% at the cold-edge. We reveal that short-term thermal variability drives major marine biomass redistributions, necessitating population-specific conservation, adaptive fisheries, and aggressive carbon emissions reduction to buffer marine biodiversity against intensifying warming.

554. Fuzzy biogeographic modelling reveals key factors driving the establishment, expansion, and saturation phases of a Pacific macroalgae invasion in the Mediterranean Sea

Raimundo Real, *University of Malaga; Ana L. Márquez, Universidad de Malaga; Nathalie Korbee, Universidad de Málaga; Félix L. Figueroa, Universidad de Málaga; Lucrecia Souviron-Priego, Universidad de Málaga*

Rugulopteryx okamurae is a brown alga native to the north-western Pacific and invasive elsewhere. It was first sighted in the northern Strait of Gibraltar in 2016 and covered most of the northern Alboran Sea by 2021. We modelled the yearly distribution of *R. okamurae* in the northern Alboran Sea during this period using the fuzzy notion of favourability, which produces commensurable biogeographic models despite variations in species prevalence across years. We produced environmental models based separately on five explanatory factors, namely accessibility through dispersion, oceanographic characteristics, biotope, biocoenosis and coastal influence. Significant environmental models were assembled using two fuzzy logic operators, namely intersection and union. This resulted in two ensemble biogeographic models for each year, which were used to predict the distribution of the species in following years. The ensemble biogeographic models exhibited a high predictive capacity, as most years the identified driving factors accurately predicted colonisation in the following year or even multiple years ahead. Accessibility through dispersion and oceanographic characteristics were critical during the initial years of establishment, while complete establishment depended on all five factors together. Expansion to the whole northern Alboran coast was explained by favourable conditions for any of the explanatory factors, while all factors except coastal influence explained the saturation of the invasion. Given that understanding the factors that explain the different phases of colonisation is crucial for developing mitigation and control measures, biogeographic models may help prevent further colonisations and mitigate the ecosystem and commercial consequences of *R. okamurae's* invasion.

555. The future of biodiversity in the Mediterranean Sea

Paolo G Albano, *Stazione Zoologica Anton Dohrn, Naples, Italy*

The Mediterranean Sea is a temperate basin with a high biodiversity and many endemic species. It has been the cradle of major civilizations and thus exposed for millennia to increasing anthropogenic pressures. However, modern global change may cause a shift into a completely novel state. The current rate of warming is among the highest globally and it is pushing its environmental conditions to a state more proper of a tropical sea. Indeed, hundreds of Indo-Pacific species introduced into the basin through the Suez Canal are already thriving. What does the future of the basin look like? In this contribution, I will i) summarize the biotic and abiotic properties of the Mediterranean Sea in the context of global

warming, ii) point at the ongoing collapse of native biodiversity, iii) show how the fossil record of the previous interglacial (135 to 116 ka, Pleistocene) can offer insights into new invasion pathways. In the novel ecosystem that is building up in the Mediterranean, most native species will have smaller ranges or go extinct, tropical species of both Indo-Pacific and Atlantic origin will be widespread, and ecosystem functioning will be different and mostly supported by such non-indigenous and range-expanding species. These transformations are irreversible, unprecedented in human history, and thus require a profound rethinking of the aims and methods of mitigation, adaptation, and restoration.

POSTERS

Regional and clade-focused biogeography

1000. Environmental and anthropogenic factors influence the distribution of ecosystem types at different successional stages

Jorge González Le Barbier, University of Oviedo; Tristan Ubaldi, Ecologie et Dynamique des Systèmes Anthropisés (EDYSAN); Jonathan Lenoir, CNRS; Victor González-García, University of Oviedo; Jose V. Roces-Díaz, University of Oviedo; Borja Jiménez-Alfaro, Universidad de Oviedo

Understanding how habitat (or ecosystem) types are distributed across biogeographic regions is fundamental for achieving biodiversity conservation targets. Modelling the potential Area of Occupancy (pAOO) — areas with suitable abiotic conditions for a specific habitat type — can provide high-resolution spatial information to support ecosystem assessment, red listing, and management. Yet, the performance of ecosystem distribution models (EDMs) computed for different habitat types, especially along successional stages, remains poorly evaluated. We used a comprehensive vegetation database harmonised to the European EUNIS classification to model the pAOO of 57 habitat types across the Ibero-Atlantic bioregion (SW Europe). Our main aims were to evaluate (i) whether habitat types occupy regional environmental space across the ecological-successional gradient, (ii) how EDM performance and predictors' contribution vary among habitats and successional stages, and (iii) how anthropogenic variables correlate with successional stages. Our results showed that late-successional habitats consistently achieved higher predictive performance and occupied a narrower environmental space than early-successional habitats. Climatic predictors dominated distribution models for late-successional habitats, whereas anthropogenic variables contributed better to early-successional models. Our findings demonstrate that incorporating successional context is critical when modelling habitat distributions at regional scales: model performance, predictors, and disturbance responses all vary systematically with successional stage. These results further support the use of EDMs for ecosystem assessment and related initiatives following biogeographical principles.

1001. Naturalized and invasive species integrate differently in the trait space of local plant communities

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How alien plant species integrate into local native communities remains a widely debated but largely unresolved question. We used eight functional traits and quantified the distribution and overlap of native, non-invasive naturalized and invasive species in the functional trait space of 12,460 local communities of six major habitats of the Czech Republic. We found that naturalized non-invasive species integrate near the center of the multidimensional functional trait space of each community, whereas invasive species tend to occupy the edges. This pattern was driven mainly by specific leaf area, plant height and seed mass followed by genome size. These results suggest that functional similarity to resident native species supports successful naturalization of alien species through preadaptation to environmental conditions. In contrast, the functional dissimilarity of invasive species enables them to exploit new niches, potentially avoiding direct competition with co-occurring native species while still passing through environmental filters. The magnitude of differences between native, naturalized and invasive species was habitat-specific, reflecting both the local ecological conditions and the traits of the most widespread species in a given habitat.

1002. Revisiting regionalization of the Eastern Brazilian Highlands: Herbarium records suggest novel patterns

Luísa Lucresia, *Universidade de São Paulo; Paulo Takeo Sano, Universidade de São Paulo; Thomas Meagher, University of St. Andrews*

The Eastern Brazilian Highlands (EBH) are ancient uplifts that constitute an important Neotropical diversity center. While traditionally subdivided by geomorphology, evidence suggests that lithology and macroclimate are more determinants of species distribution – although the impact of these factors may vary across the EBH's vegetation types. Bioregionalizations synthesize biodiversity patterns, identifying unique areas that inform investigation of evolutionary history, enable mapping of future changes, and support conservation policy. This study reassesses biogeographical patterns of the EBH using herbarium data and compares the resulting pattens with prior schemes. Angiosperms recorded in the area with valid coordinates were collected from GBIF, Jabot, and Splink platforms. Synonyms were transferred to valid names, and the dataset was segmented by occurrence in the EBH and in its vegetation types (rock outcrops and forests). A network analysis using InfoMap Biorregions with a 0.125° grid was conducted, and similarity patterns among bioregions were explored with UPGMA. Results revealed distinct groups for outcrops

and forests. For forests, four main groups were delineated coinciding with surrounding lowland patterns and suggesting greater macroclimatic influence. Outcrops showed a novel pattern with five major groups of mountain systems that do not strictly reflect macroclimate, lithology or geomorphology alone. Multiple structures traditionally treated as cohesive units (e.g. Serra da Mantiqueira, Espinhaço Range and Serra do Mar) have been segmented in this new scheme. These results differ from previously published bioregionalization schemes, providing a new framework to assess the biogeographical history of the area and highlighting areas of particular significance for future conservation effort.

1003. From Forest to Savanna: phytolith evidence of vegetation dynamics in northeastern Brazil

Gustavo Luis Schacht, *Universidade Federal do Recôncavo da Bahia; Marcia Regina Calegari, Universidade Estadual do Oeste do Paraná; Marco Madella, Universidad Pompeu Fabra; Grace Bungenstab Alves, UFBA*

Vegetation dynamics respond directly to environmental factors, particularly climate and soil conditions, and cover has undergone various changes throughout the planet's history. Changes in vegetation can be observed in the interior of the state of Bahia, Brazil, using phytoliths, which are an essential proxy for semiarid areas such as this region. We aimed at identifying changes in the vegetation cover the last few thousands of years. Our goal was to study the vegetation dynamics in a Cerrado enclave, a type of savanna typical of Brazil, in the Morro do Chapéu, Bahia. Phytolith analysis was combined with carbon isotope analysis and dating techniques. Phytoliths samples were collected every 10 cm from soil profiles 2 m deep, extracted and identified. The results show a varied concentration of well-preserved phytolith morphotypes originating from semiarid context. However, the phytolith assemblages indicate a change in vegetation compared to what is currently found there, showing that approximately 3,200 years Cal BP, a denser forest, was dominant while drier conditions set in at approximately 4,500 years Cal BP. The current vegetation, which is more open and has significant grass cover, occupied the study area from approximately 1,750 years Cal BP. These results may contribute to a better understanding the pulse of rainforests in northeastern Brazil.

1004. Limiting factors of Northern Hemisphere tree species: revisiting Darwin's hypothesis through the Law of the Minimum

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University of Birmingham, Birmingham, UK; Adriane Esquivel-Muelber, University of Birmingham, Birmingham; Julien Barrere Barrere, Université Grenoble Alpes (INRAE), UR LESSEM, Saint-Martin-d` Hères, France; Georges Kunstler Kunstler, Université Grenoble Alpes (INRAE), UR LESSEM, Saint-Martin-d` Hères, France; Emil Cienciala, IFER - Institute of Forest Ecosystem Research, Jilove u Prahy, Czech Republic; Jonas Fridman, Swedish University of Agricultural Sciences, Umeå, Sweden; Leen Govaere, Nature and Forest Agency (ANB), Brussel, Belgium; Anja Leyman, Nature and Forest Agency (ANB), Brussel; John J. Redmond, Department of Agriculture, Food and the Marine, Johnstown Castle Estate,; Wexford, Y35 PN52, Ireland; Mart-Jan Schelhaas, Wageningen Environmental Research (WENR), Wageningen, Netherlands; Susanne Suvanto, Natural Resources Institute Finland (Luke), Helsinki, Finland; Andrzej Talarczyk, Forest and Natural Resources Research Centre, ul. Płomyka 56A, 02-491 Warszawa, Poland; André Thibaut, Service Public de Wallonie, Jambes, Belgium; Miguel A. Zavala, Universidad de Alcalá, Departamento de Ciencias de la Vida, Forest Ecology and Restoration Group (FORECO), Madrid, Spain; Sara Villén-Pérez, Universidad de Alcalá, GloCEE – Global Change Ecology and Evolution Research Group, Departamento de Ciencias de la Vida, Madrid, Spain.

Understanding which environmental factors limit the distribution and performance of species is a key question in biogeography. Darwin's classic hypothesis suggests that abiotic variables become more restrictive both towards higher latitudes and higher elevations, while biotic constraints predominate at lower latitudes and elevations. Although different approaches have been proposed to assess this hypothesis, it appears that the perspective of Liebig's Law of the Minimum has not been explicitly considered, which posits that a single variable limits species' performance at any given time and location. In this study, we use this law to test Darwin's hypothesis by analysing more than 260 tree species in c. 247,500 national forest inventory plots across Europe and North America. Specifically, we modeled tree species potential performance, represented by basal area, along latitudinal (15º-70º latitude) and elevation (0m-3500m) gradients of these forests using 0.95 quantile regressions. We estimated the limiting effects of biotic (density and mean tree size) and abiotic (winter temperature, aridity-index, soil pH and soil nitrogen) factors on tree species potential performance. The variable predicting the lowest potential performance in each plot was identified as the limiting factor. The results indicate that all biotic and abiotic variables considered act as limiting factors somewhere. We find that Darwin's hypothesis does not generally hold, with approximately 8,6% of species being consistent with the hypothesis in terms of latitude and 7,6% in terms of elevation. The results suggest revising classical biogeographical assumptions and highlighting new frameworks in ecology to assess species limitation and macroecological patterns.

1005. Borealization in Northern Finland: Impacts on Biodiversity and Carbon Balance

Gangotri Chattopadhyay, *University of Helsinki; Lea Opitz, University of Helsinki*

Climate-driven borealization is reshaping high-latitude landscapes by facilitating shrub and tree colonization of historically treeless tundra. Although many studies treat biodiversity shifts and carbon dynamics separately, their coupled responses across spatial scales remain poorly resolved. In the Kilpisjärvi and Pallas regions of northern Finland, we sample the full forest-treeline-tundra continuum with field measurements and multivariate analyses to characterize plant taxonomic and functional diversity alongside linked measurements of CO_2 fluxes and soil carbon stocks from plot to landscape scales. By dissecting shifts in community composition and key plant functional traits and incorporating plot-level microclimate data, we predict species distributions and carbon dynamics across habitat types and borealization gradients to identify how drivers of community composition change in the forest-tundra ecotone. Field-measured diversity and flux data are integrated with fine-scale satellite imagery and climate-driven borealization models to produce high-resolution maps that reveal principal drivers and project trajectories of woody expansion. Vegetation surveys, such as species abundances, are paired with plant trait data. Plot-level chamber CO_2 fluxes, soil organic carbon cores, and trait–environment models are then used to relate biodiversity and vegetation structure to ecosystem carbon balance. Linking taxonomic and functional diversity with carbon metrics across environmental gradients yields spatially explicit insights into where borealization may enhance sequestration or promote net emissions, with direct relevance to biogeographic theory and conservation planning.

1006. Uncovering the spatio-temporal patterns of 30 years of greening in South UK landscapes

Guilherme Castro, *Royal Holloway University of London, UK*

Anthropogenic global changes are increasingly threatening ecosystems through the disruption of ecosystem functions and patterns. Yet our understanding of how global and local drivers interact and impact ecosystems at the landscape scale remains limited. In particular, there is a lack of long-term empirical evidence exploring landscape pattern-process relationships to inform land management and restoration efforts. This study addresses this gap by evaluating spatio-temporal changes in Net Primary Productivity (NPP) over a 30-year period (1995–2024) across a temperate landscape in Sussex (UK). We assessed how climate trends and land cover changes influence spatial and temporal patterns of NPP using a satellite-derived vegetation index (Normalized Difference Vegetation Index – NDVI). Our results revealed a rise an overall increase in NPP, with spatially heterogenous NDVI change linked to climate and land cover changes. These findings highlight the importance of long-term evidence at the landscape level to advance our understanding of ecosystem functioning trends.

1007. Defining the Ward Line as the Biogeographical Boundary of the Himalaya

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The Ward Line, located at the eastern edge of the Tibetan Plateau, was first identified by F.K. Ward in 1921 as a major dispersal barrier for fauna. However, its exact position remains difficult to pinpoint due to the region's unique geological structure, characterized by three parallel rivers and two divides—the Salween–Mekong divide and the Mekong–Yangtze divide. The Southeast Asia monsoon system adds further complexity of understanding species distributions, raising the key question of whether climate or topographic divides play a stronger role in impeding dispersal. In this study, we collected 30 environmental DNA (eDNA) samples from the tributaries of the Salween, Mekong, and Yangtze rivers and employed ITS2 primers to analyse the species phylogenetic beta diversity of plant and fungal communities. We then applied a null model approach to disentangle the dispersal limitation process from the climate filtering process. Habitat preference analyses indicate that our eDNA samples predominantly capture mid-to-low elevation species. The spatial pattern of the PCoA plot from phylogenetic beta diversity revealed congruent distribution patterns between plant and fungal groups, with assemblage segregation across different river valleys and along latitudes. Our results highlight the efficiency of using river eDNA to detect the terrestrial plant and fungi communities and clearly identify the Ward Line as corresponding to the Salween–Mekong divide after taking account of climatic and distance effects.

1008. The historical and environmental factors driving the geographical patterns of phylogenetic diversity and endemism of Japanese seed plants

Masahiro Noguchi, *Toyota motor corporation; Buntarou Kusumoto, Think Nature Inc.; Hidenori Tanaka, Toyota motor corporation; Masakazu Ito, Toyota motor corporation; Yasuhiro Kubota, Lab. Biodiversity & Conservation Biogeography, University of the Ryukyus*

The contemporary biodiversity is constituted by the result of eco-evolutionary responses to the historical environmental changes. The island system of Japanese archipelago offers a suitable opportunity to evaluate the relative importance of respective environmental and geohistorical drivers of the origin and maintenance of biodiversity. In this study, we analyzed the geographical patterns of phylogenetic diversity and endemism for Japanese seed plants (4,656 species) using their phylogenetic tree and distribution maps at 1-km grid-cell level. We also examined their historical and environmental drivers. The Pacific coastal areas of the central archipelago exhibited higher phylogenetic diversity for trees and herbs. This area is

characterized relatively stable climate during the glacial period, which may have contributed to survival of old clades and radiation of new species. Meanwhile, the center to southwest parts of the archipelago showed higher phylogenetic endemism. We classified dominant endemism types (neo- and paleo-endemics) in each grid-cell. Neo-endemism was predominant in the central mountainous areas and the northern part of the archipelago, suggesting that recent speciation has proceeded at region with isolated harsh climatic conditions. On the other hand, neo-endemics and paleo-endemics tended to be mixed in the southwestern lowland areas, where regional extinction and recolonization was likely to be active because of the fluctuations of available habitats by sea-level changes during the glacier-interglacial cycles. Based on the results, we will discuss hierarchical mechanisms of hotspot formation for phylogenetic diversity and endemism by historical and environmental factors.

1009. Environmental drivers of multidimensional biodiversity in Euro-Mediterranean woodlands

Manuel Cartereau, *CNRS - UMR 7263 IMBE; INTEGRADIV Consortium; Agathe Leriche, IMBE, Université d'Aix-Marseille*

Biodiversity is a multidimensional feature where one can focus on different facets (taxonomic, phylogenetic, functional), taxa or conservation targets (diversity, rarity, vulnerability). Although most studies in ecology focus on only one or few dimensions of biodiversity (e.g., species richness), biodiversity multidimensionality is pivotal for ecosystem functioning, stability and provision of services, especially in the context of ongoing global changes. However, biodiversity dimensions do not necessarily follow the same spatial patterns, thus creating trade-offs between multiple dimensions within a focal pool of species. While how environmental drivers shape biodiversity dimensions one at-the-time has been extensively investigated, their effects on trade-offs between multiple biodiversity dimensions remains poorly understood. Gathering occurrences, phylogenies, trait and conservation status data for five different taxa (i.e., trees, mammals, birds, reptiles and butterflies) and using a new multidiversity approach, we assessed how past and current climate, human footprint and topography influence multidimensional biodiversity patterns in Euro-Mediterranean woodlands.

1010. Evolutionary imbalance in the naturalization success of alien plants across Mediterranean regions

Alexander Yamir Ortiz Rivera *and Trevor Fristoe, both at University of Puerto Rico - Río Piedras*

Invasive alien plants drive negative ecological and economic impacts within introduced regions, reshaping biodiversity globally. While anthropogenic factors drive species Invasive alien plants drive negative ecological and economic impacts within introduced regions, reshaping biodiversity globally. While anthropogenic factors drive species introductions, the characteristics of invaders, shaped by their evolutionary histories, will interact with ecological conditions to mediate invasion success. The Evolutionary Imbalance Hypothesis (EIH) states that potential invaders will present success if they originate from regions that are 1) large, with abundant populations driving effective selection, and 2) biodiverse, where intense biotic interactions must be overcome for survival. Global analyses provide broad support for the EIH, with successful aliens often originating from native ranges spanning multiple continents that overlap biodiverse regions. However, each continent is composed of diverse biomes, with each biome recurring globally as fragments distributed across continents. Focusing on the exchange of alien species between biome fragments thus presents a more precise analytical framework for testing the EIH. Here, we focus on the exchange of naturalized aliens among Mediterranean biomes, which are characterized by distinct climate and boasting uniquely adapted species, occurring as fragments varying in size and biodiversity across five continents. We identified native species unique to each Mediterranean region using Plants of the World Online and characterized their occurrences as naturalized aliens using the Global Naturalized Alien Flora dataset. Preliminary results indicate support for the second prediction of the EIH, with the small but ultra-diverse Fynbos of Southern Africa overrepresented in the naturalized alien floras in other Mediterranean regions. Our results support the idea that conditions in native distributions can preadapt species for success as invaders.

1011. Mapping azonal vegetation: From phreatophyte ecohydrological niches to groundwater-dependent vegetation in the Mediterranean biome

Léonard El-Hokayem, *University Halle-Wittenberg; German Centre for Integrative Biodiversity Science; Gabriella Damasceno, University Halle-Wittenberg; Francesco Maria Sabatini, University of Bologna; Pantaleone De Vita, University of Naples Federico II; Helge Bruelheide, University Halle-Wittenberg; Christopher Conrad, University Halle-Wittenberg*

Groundwater-dependent vegetation (GDV) plays a vital role in sustaining biodiversity and ecosystem services in water-limited regions, yet its extent across the Mediterranean biome remains poorly mapped. This work outlines a stepwise approach to identify GDV by integrating ecological theory, ground-truth vegetation data, remote sensing, and machine

learning. The first step developed a local framework that linked high-resolution imagery with field surveys and ecohydrological indicators. GDV was identified by vegetation vitality during the dry season and the presence of phreatophytes. This clarified the ecological niche of phreatophytes and identified key spatial predictors needed for broader mapping. The second step introduced a biome-wide GDV potential index based on eleven global geospatial layers. This index approximated the fundamental niche of phreatophytes and indicated areas with low to high suitability for GDV. The third step integrated global species-community data from sPlot and GBIF with high-resolution remote sensing variables in a Random Forest model. This produced the first 30 m resolution baseline map of GDV, highlighting its realised niche across the biome. Results show GDV covers about 482,000 km^2 of natural vegetation, with highest coverage in California and Chile, while only 25% falls within protected areas. GDV functions as ecological refugia for species, offering "green, wet, and cool islands" in otherwise dry landscapes. By supporting biodiversity, microclimate buffering, and groundwater resilience, mapping GDV is crucial to conservation and water management planning. The framework developed here not only identifies GDV across the Mediterranean biome but also provides a transferable method for safeguarding these ecosystems globally.

1012. Crop niche dynamics in dryland biomes during Holocene climate change: insights from Africa and the Mediterranean

Mudit Joshi, *Aarhus University; Alejandro Ordonez, Aarhus University*

Across Africa and the Mediterranean, Holocene climate change and expanding human land use reshaped where early farming could take hold. In this study, I reconstruct the paleobiogeography of four key cereals—sorghum, wheat, barley, and millets—across the last 10,000 years. I use high-resolution CHELSA-TraCE21k paleoclimate fields together with mechanistic niche models (Recocrop) and habitat suitability models (HSMs) to estimate potential climatic ranges. These are compared with archaeobotanical evidence and anthrome reconstructions to narrow down the realized niches that were actually used by past farmers. The analysis spans major Holocene events, including the African Humid Period, the 8.2 ka cooling, and the 4.2 ka aridification. Early results already point to some clear continental-scale dynamics: during the mid-Holocene aridification (6000–4000 BP), suitable niches shifted southward, with Central and North Africa losing potential while southern zones gained new high-suitability areas. Sorghum and millets consistently maintained wider ranges in Africa's dryland biomes, whereas wheat and barley were more stable in Mediterranean climates. These functional differences mattered—drought- and heat-tolerant cereals helped sustain agriculture through harsher phases, while temperate taxa thrived in cooler, wetter pockets. By linking crop niches with the broader climatic vulnerabilities of dryland biomes, this work offers a way to read deep-time signals of resilience. Many of today's food-insecure regions were already constrained by climate in the past. Tracing how niches contracted,

shifted, or persisted helps us understand not only the history of agrarian landscapes but also the stresses—drought, heat, and land-use pressure—that will shape their future.

1013. Forecasting Mediterranean Vegetation Dynamics under Climate Change using LSTM Neural Networks

Ioannis P. Kokkoris, *Department of Sustainable Agriculture, University of Patras; Alexandros D. Kouris, Department of Sustainable Agriculture, University of Patras*

Mediterranean ecosystems are highly sensitive to climate variability, making predictions of their future trajectories critical for biodiversity conservation. Traditional models often fail to capture the complex, nonlinear interactions between climate and vegetation. We applied Long Short-Term Memory (LSTM) neural networks with attention mechanisms to forecast vegetation dynamics across Natura 2000 sites in Greece. By integrating long-term satellite-derived vegetation indices (NDVI, EVI) with historical climate data in order to capture temporal dependencies and nonlinear vegetation-climate relationships. Future projections were derived from CMIP6 climate scenarios under multiple Shared Socioeconomic Pathways (SSPs). The attention mechanism improves interpretability, highlighting critical periods that drive vegetation trends. Preliminary analysis suggests diverse trajectories across sites: some areas maintain or increase productivity, while others may exhibit declines in greenness and shifts in seasonality. These patterns suggest that climate change will impact habitats differently, affecting quality, and resilience, with implications for species persistence. Our work aims to demonstrate the utility of LSTM neural networks with attention mechanisms for ecological forecasting. By capturing complex temporal patterns and nonlinear responses, these models offer actionable insights for conservation planning and management in Mediterranean landscapes. This approach contributes to the development of predictive tools that anticipate biodiversity responses under global change, supporting evidence-based strategies to maintain resilient ecosystems.

1014. Forest-steppe: the center of vascular plant diversity in northern Eurasia

Milan Chytrý, *Masaryk University; Irena Axmanová, Department of Botany and Zoology, Masaryk University; Jan Divíšek, Department of Botany and Zoology, Masaryk University; Klára Klinkovská, Masaryk University; Ilona Knollová, Masaryk University; Marcela Řezníčková, Masaryk University*

Research over the past 15 years has shown that the most species-rich plant communities in Europe occur in the peri-Carpathian forest-steppe. Their diversity may result from the landscape mosaic of forest and steppe, but also from the overlap of lowland and mountain floras. If vegetation mosaic were the main driver, forest-steppes would also be highly diverse

in the lowlands of Eastern Europe and Siberia, where they form the boundary between northern forests and southern steppes.

We studied plant diversity along a 2,900 km north–south transect across the lowlands of Western Siberia and Kazakhstan, from the Arctic Ocean to the Tien-Shan Mountains. This transect covered 11 vegetation zones: tundra, forest-tundra, northern, middle and southern taiga, subtaiga, forest-steppe, steppe, desert-steppe, semi-desert, and desert. Every 50 km, we recorded 5–8 vegetation plots (100 m^2) across both forested and open habitats. The highest vascular plant richness was found in the forest-steppe, followed by the neighboring subtaiga. The lowest diversity occurred in the dry steppe, semi-desert, and desert, where aridity and lack of forest reduce habitat diversity. Low values were also found in the northern and middle taiga due to the cold climate and the absence of grasslands. Our results confirm that the forest-steppe is the center of vascular plant diversity in northern Eurasia. Its richness likely stems from its heterogeneous mix of forest and steppe, moderate climate (neither too dry nor too cold), and the central location, which allowed forest-steppe species to survive both cold and warm climatic periods in the past.

1015. Implementing FAIR principles in European Vegetation Archive data

Milan Chytrý, *Masaryk University; Irena Axmanová, Department of Botany and Zoology, Masaryk University; Jan Divíšek, Department of Botany and Zoology, Masaryk University; Klára Klinkovská, Masaryk University; Ilona Knollová, Masaryk University; Marcela Řezníčková, Masaryk University*

The EVA-FAIR project advances the implementation of FAIR (Findability, Accessibility, Interoperability, Reuse) principles in European vegetation-plot databases, which have recently become an extremely important source of data for biogeographical research. These databases hold over a century of plant occurrence and abundance records. Building on the European Vegetation Archive (EVA), which currently integrates more than 2 million plots from 108 providers, the project seeks to overcome long-standing restrictions on data openness by developing FAIR workflows and publishing data in trusted repositories. The first project stage was a national pilot focused on the Czech National Phytosociological Database, one of Europe's largest vegetation-plot databases. We created its publicly accessible version and a taxonomically harmonized and geographically and environmentally stratified subset optimized for research. Species-occurrence records from CNPD were uploaded to GBIF, thereby improving global biodiversity coverage. To ensure reproducibility and future updates, we developed R scripts for taxonomic harmonization, stratified resampling, and Darwin Core Archive export, all openly released on GitHub and Zenodo with version control. This national pilot provides a replicable model of "FAIRification" for vegetation-plot databases. In the second stage, these tools and workflows will be scaled to the European level. Through workshops, training, and community building, EVA data providers will be encouraged to open their datasets. We will also prepare an open, stratified version of the European Vegetation

Archive. Ultimately, EVA-FAIR will unlock unprecedented access to vegetation-plot data, supporting biodiversity science, conservation, restoration, and citizen science across Europe.

1016. Hemiparasite-legume co-occurrence patterns in European grasslands

Nina Fahs, *Masaryk University, Brno, CZ; Kryštof Chytrý, University of Vienna; Jakub Těšitel, Masaryk University*

Legumes, as well as parasitic plants, display specialised strategies of resource acquisition that deviate from the usual plant physiology. These strategies allow the plants to escape ecological constraints associated with a deficiency of resources. Further do both legumes and parasitic plants exert multiple effects on the communities and the ecosystems they inhabit. Some preliminary observations and pieces of indirect evidence scattered in the literature suggest, aside from the known hemiparasite-host relationship, the existence of mutualistic aspects in the interaction between these two functional groups. Legumes may benefit from the effects the parasites exert on the communities, such as the suppression of competitors, while the parasites may benefit from the additional nitrogen, legumes provide to the community. This may facilitate the coexistence of these functional groups in plant communities. Our study investigates the co-occurrence patterns of legumes and hemiparasitic plants in grassland ecosystems in European grassland ecosystems. We use several vegetation-plot datasets to test the co-occurrence pattern of these two functional groups across different spatial scales. Information on the management was added for a subset of the dataset to be able to relate the patterns to different management methods, e.g. grazing and mowing. We found notable co-occurrences between *Rhinanthus* hemiparasites and the legumes *Trifolium repens, T. pratense, L. corniculatus,* and *V. cracca*, which were also the most common species of both functional groups in European grasslands.

1017. Species assembly in temperate seminatural grasslands: geohistorical drivers of endemicity and species turnover

Shogo Ikari, *University of the Ryukyus; Yasuhiro Kubota, Lab. Biodiversity & Conservation Biogeography, Univ. of the Ryukyus; Tanaka Kenta, Sugadaira Research Station, Mountain Science Center – Japan*

Semi-natural grasslands represent a form of grassland that can arise independently of climatic suitability. In recent years, it has become increasingly recognized that grasslands maintained in close association with human livelihoods over long periods (often centuries or more) develop plant communities that differ entirely from the surrounding vegetation. In Japan, where such grasslands are scattered across the archipelago, these habitats are likely to have functioned as modern refugia for grassland species that dispersed from the continent

during the Pleistocene. Indeed, many widespread continental species now are known to occur in isolated and declining populations. At the same time, numerous endemic species that have speciated more recently are also well documented in these grasslands. This study addresses the previously missing mesoscale (thousands-of-kilometers) perspective on biodiversity gradients in semi-natural grasslands, by comparing them with natural grasslands. Specifically, we examined diversification processes in grasslands and the beta-diversity gradient through historical range-contraction dynamics, showing high endemism in rain-rich grasslands and refugia-driven diversity patterns. This study makes a conceptual contribution by linking community assembly processes in semi-natural environments to macro-scale climatic variation, while also highlighting the conservation value of ecosystems that are becoming regionally rare due to change in human resource utilization and land uses.

1018. Shifting the Baseline: A Biotic Integrity Index for Restoration in Temperate Europe

Skjold Alsted Søndergaard, Aarhus University; Rasmus Ejrnæs, Aarhus University

The natural target of ecological restoration with a conservation aim is integrity in terms of both biota and processes. What constitutes an intact species community depends on the chosen baseline, so ecological restoration is vulnerable to the shifting baseline syndrome. Careful consideration of historic and prehistoric human impact on ecosystems is necessary for meaningful estimates for ecological integrity. Paleontological evidence has shown that open-habitat specialists persisted in parts of temperate-humid Europe previously thought to be densely forested during interglacials, challenging the typical use of closed forest as the vegetation baseline for temperate Europe. Acknowledging that natural processes – particularly those associated with large and mega-herbivores – have completely vanished from Europe, we focus our investigation on biotic integrity of plants, invertebrates and microorganisms. Paleontological evidence suggests that a grassland-woodland mosaic is a good candidate for an ecosystem baseline and we argue that hotspots of species diversity might also be hinting to high biotic integrity. Guided by species pool theory and patterns of plant species richness records and woodland indicator species, we have investigated ecosystems hypothesized to represent the highest remaining biotic integrity in temperate Europe. We have collected species composition data from vegetation and soil eDNA and compared these with reference data from other parts of temperate Europe to develop a new index for biotic integrity. The index reflects both species richness and composition. We further propose to combine biotic integrity with an assessment of process integrity as a combined indicator of restoration success.

1019. How have the biogeographic shifts of Aglaia (Meliaceae) influenced fruit evolution?

Lara Iaboli, *Caroline Pannell, Julius Jeiter, Omer Nevo, Gudrun Kadereit, Elizabeth Joyce, all at Ludwig Maximilians University Munich, Germany*

Aglaia is the most speciose genus in the mahogany family (Meliaceae), with c. 128 species endemic to the lowland tropics of India, South-East Asia, Australia, and the Pacific Islands. Fruit morphology is highly variable, with primate, bird and Cassowary dispersal syndromes common in the genus. It remains to be understood how this fruit diversity evolved in *Aglaia*, and whether the different fruit types have switched in conjunction with the biogeographic shifts across the region. We have reconstructed the phylogeny of all *Aglaia* species using a target-capture approach combining custom and Angiosperm353 loci. By characterising the fruit morphology of *Aglaia* through detailed fruit developmental and anatomical studies and fruit chemistry through analysis of volatile organic compounds (VOCs) and macronutrients, we will define dispersal syndromes in the genus to understand their evolution in a phylogenetic context. We will then test for correlations of biogeographic shifts with shifts in the evolution of fruit characters through Ancestral State/Area Analysis and simulation modelling. This study aims at gaining new insights in the effects of the Sunda-Sahul Biotic Exchange on plant diversification, and more in detail whether diversification in *Aglaia* has been driven by switching disperser communities after jumping Wallace's Line.

1020. Paleobiogeography of Ebenaceae: Tracing tropical plant migrations from Africa to Asia

Mahi Bansal, *National Centre for Biological Sciences; Vandana Prasad, Birbal Sahni Institute of Palaeosciences*

Establishing convergence between fossil evidence and molecular timelines helps in bridging the gap between rocks and clocks, and is a fundamental challenge in paleobiogeographic studies. The present study employs high-taxonomic-resolution fossil pollen of the plant family Ebenceae to calibrate a phylogenetic tree constructed from integrated molecular and morphological data, with the aiming of identifying the global tectono-climatic processes that shaped its origin, diversification, and distribution. Our results suggest that Ebenaceae originated in western Gondwana ~108 Ma. The concurrent separation of Africa and South America caused vicariant divergence, leading to the emergence of subfamily Lissocarpoideae in South America (~53.6 Ma) and Ebenoideae in the lowland tropical rainforests of Africa (~102 Ma). We propose the further dispersal of Ebenoideae from Africa to: i) Eurasia via a South Turkey-Balkan-Italy lineament during the Campanian, followed by passage through boreotropical latitudes, and adaptation to fluctuating early-Paleogene climate of East Asia before reaching India and Southeast Asia; ii) to India via Kohistan-Ladakh Island Arc during the Maastrichtian-Paleocene, with further adaptation to temperature-driven seasonality of the Indian Paleocene; iii) to Sahul via Southern Gondwanan remnants in the early-Paleogene,

with Sunda-Australia collision (Oligocene) and emergence of New Guinea (Miocene) facilitating movement across Wallace's line, iv) to Southeast Asia again along the northern Tethyan belt post Afro/Arabia-Asia collision during the Miocene. The adaptation of Ebenaceae members to diverse ecological conditions reflects its complex past dispersal patterns, and potential deep-time corridors that enabled the movement of tropical plant lineages, from Africa to tropical Asia, across climatic barriers.

1021. Palm Phylogenomics and the origins of rainforest diversity

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Botanic Gardens, Kew; Serafin J. R. Streiff, DIADE, Univ Montpellier; Maria Fernanda Torres Jimenez, Vilnius University, Lithuania; Oscar Wrisberg, Aarhus University; Alexander Zizka, University Marburg; Alexandre Antonelli, Royal Botanic Gardens, Kew; Christine D. Bacon, Department of Biological and Environmental Sciences, University of Gothenburg; Sidonie Bellot, Royal Botanic Gardens, Kew; Ángela Cano, Cambridge University Botanic Garden; Benedikt Georg Kuhnhäuser, Royal Botanic Gardens, Kew; Bill J. Baker, Royal Botanic Gardens, Kew; Wolf L. Eiserhardt, Aarhus University

With 87% of their species diversity in tropical rainforests (rainforest), palms are a model group for studying the origin and evolution of this biome. However, Previous phylogenetic studies lacked broad sampling of palms, limiting our understanding. Here, we built a comprehensive phylogenomic tree for palms, which includes genomic data for 1,929 species (77% of the family) covering all subfamilies, tribes, and subtribes. Using a global survey of the palm fossil record, we time-calibrated the tree and found that the diversification of extant palm lineages commenced approximately 110 Ma in the Northern Hemisphere. Diversification rates across the tree are highly heterogeneous, yet all subfamilies show a similar pattern, with rates increasing during the Cenozoic. We reconstructed biome history and contrary to previous studies, our results strongly suggest that the ancestral palms did not inhabit rainforests. However, phylogenetic evidence for rainforest occupancy in the lower-mid Cretaceous remains strong, particularly among the ancestors of Calamoideae, Ceroxyloideae, and Arecoideae in the Northern Hemisphere. Notably, long-term association with rainforest alone is insufficient to explain the high diversity of palms in this biome. Moreover, palms appear to have diversified at higher rates in rainforest compared to other biomes throughout most of their history, contradicting recent findings of slow plant and animal diversification in the tropics. This discrepancy is probably due to different mechanisms driving species richness at different spatial scales: while global variation may be caused primarily by time for speciation, the variation within the tropics may be driven by diversification rates.

1022. Mapping the distributions of 2,238 palm species to test the drivers of range size in a keystone tropical plant family

Hanchen Shuai, *Aarhus University; Bill J. Baker, Royal Botanic Gardens, Kew; Paola De Lima Ferreira, Aarhus University; Jens-Christian Svenning, Center for Ecological Dynamics in a Novel Biosphere (ECONOVO), Aarhus University; Wolf L. Eiserhardt, Aarhus University*

With 87% of their species diversity in tropical rainforests (rainforest), palms are a model group for studying the origin and evolution of this biome. However, Previous phylogenetic studies lacked broad sampling of palms, limiting our understanding. Here, we built a comprehensive phylogenomic tree for palms, which includes genomic data for 1,929 species (77% of the family) covering all subfamilies, tribes, and subtribes. Using a global survey of the palm fossil record, we time-calibrated the tree and found that the diversification of extant

palm lineages commenced approximately 110 Ma in the Northern Hemisphere. Diversification rates across the tree are highly heterogeneous, yet all subfamilies show a similar pattern, with rates increasing during the Cenozoic. We reconstructed biome history and contrary to previous studies, our results strongly suggest that the ancestral palms did not inhabit rainforests. However, phylogenetic evidence for rainforest occupancy in the lower-mid Cretaceous remains strong, particularly among the ancestors of Calamoideae, Ceroxyloideae, and Arecoideae in the Northern Hemisphere. Notably, long-term association with rainforest alone is insufficient to explain the high diversity of palms in this biome. Moreover, palms appear to have diversified at higher rates in rainforest compared to other biomes throughout most of their history, contradicting recent findings of slow plant and animal diversification in the tropics. This discrepancy is probably due to different mechanisms driving species richness at different spatial scales: while global variation may be caused primarily by time for speciation, the variation within the tropics may be driven by diversification rates.

1023. Explaining differences in species richness by comparing distribution patterns across subfamilies in Leguminosae

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The enormous differences in species richness among lineages have long intrigued evolutionary biologists. Biogeographical processes, such as long-distance dispersal and niche adaptation, undoubtedly play an important role in generating differences in richness. However, testing the effect of these processes by direct comparisons of lineages is confounded by differences in age and evolutionary relatedness between study groups. The six subfamilies of the legume family provide an ideal natural experiment to address this question. Since the origin of Leguminosae is a phylogenomic tangle which gave rise to all subfamilies within a very short time frame, the subfamilies are practically identical in terms of age and relatedness. Notwithstanding this identical origin, this natural experiment yielded

vastly different results, ranging from subfamily Duparquetioideae, consisting of a single African species, to subfamilies Caesalpinioideae and Papilionoideae, which have respectively circa 4,700 and over 14,000 species across the globe. Using detailed occurrence data of all c. 20,000 legume species, assembled in collaboration with legume experts from across the globe, we quantify differences between subfamilies and lower-level clades in areas of species richness, ecological versatility, and geographic extents. Furthermore, by combining this new geographic dataset with existing legume-wide and subfamily-specific phylogenies, we compare rates of long-distance dispersal and niche shifting through time to examine the roles of evolvability and phylogenetic conservatism in generating species richness. We recover important roles for niche breadth and the number and timing of niche shifts in explaining differences in richness, shedding new light on why some lineages are more successful than others.

1024. The global drivers of mangrove faunal specialist diversity

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Mangrove forests are highly dynamic coastal woodland ecosystems that serve as important foraging sites for a variety of marine and terrestrial organisms. Despite this, the number of mangrove specialist taxa is surprisingly small, with the majority occurring in Australasia and Southeast Asia. To understand the macroecological drivers of mangrove specialisation in terrestrial vertebrates, we reconstructed the global distribution of mangrove forests throughout the late Pleistocene and modelled the relationship between historical mangrove distribution patterns and the number of extant terrestrial vertebrate specialist species. Our results showed that across all vertebrate taxa, larger mangrove patches in more biodiverse areas tended to have more mangrove specialists, suggesting that the physiological challenges of mangrove specialisation may be buffered by greater habitat heterogeneity and source population diversity. Counterintuitively, our models also showed that older mangroves had fewer specialists, which indicate that mangrove specialists may experience high extinction rates due to the impact of natural disasters, or tend to expand their niche breadths over time. Additionally, our models showed that isolation from forests and the temporal contiguity of mangroves were not significant predictors of mangrove specialist diversity. We therefore show that at macroecological scales, the overall paucity of mangrove specialist taxa is likely driven by the challenges associated with specialising and surviving in mangroves, and not because of mangrove range shifts throughout the late Pleistocene. Our findings also highlight the need to better understand the physiological adaptations required for mangrove specialisation, and to distinguish between different drivers of mangrove specialist declines over time.

1025. Gliding towards and uncertain future: Phylogeography and conservation genomics of the elusive Siberian flying squirrel (*Pteromys volans*)

Stefan Prost, *University of Oulu; Angelika Kiebler, University of Oulu, Finland; Gerrit Wehrenberg, University of Oulu, Finland; Jaana Kekkonen, University of Helsinki, Finland; Fernanda Ito dos Santos, Finnish Museum of Natural History*

Environmental and human-mediated changes are threatening key and umbrella species. One such species is the Siberian flying squirrel (*Pteromys volans*). In order to enable informed conservation decisions, we investigated their genetics and populations structure within their global distribution using genome-wide SNP data. These analyses revealed a gradual decline in genetic diversity from Eastern Russia westwards, with individuals from Finland and Estonia showing highly depleated genetic diversity. Their rapid expansion after the last glacial period from refugia in Eastern Russia make them a prime example to study evolutionary forces such as allele surfing. Indeed, we found the same mitochondrial genome haplotypes within Finland over a distance of 500km. To take a look at the genomic effects of allele surfing on genetic diversity, inbreeding and mutational load (amount of potentially harmful mutations) we generated a chromosome-level reference genome for this species and re-sequenced over 60 genomes using modern and historic samples. This analysis has important implications for conservation management, especially in light of considered reintroductions from ex situ populations. Furthermore, we are developing reduced genetic marker sets for large-scale landscape genomic analyses using non-invasively sampled droppings to study the impact of landscape features, such as roads or clearcuts for forestry, on the connectivity of populations. Recently, the gap between science, society and policy has been highlighted as a major problem for the effectiveness of conservation. To bridge this gap our project is run together with several national and international stakeholders and local communities.

1026. Population genetics of the Siberian flying squirrel (*Pteromys volans*) in Finland - Shaped by glacial retreat and land uplift during the Holocene

Angelika Kiebler, *University of Oulu, Finland; Stefan Prost, University of Oulu; Gerrit Wehrenberg, University of Oulu, Finland*

The Siberian flying squirrel (*Pteromys volans*) is the only flying squirrel species in Europe, with Finland hosting the largest EU population across its southern half. Despite this range, it is classified as “vulnerable” in the Finnish Red List following a >30% decline in one decade. Knowledge of the species’ genetic structure remains limited. Due to low genetic diversity in the West-Eurasian phylogroup, standard markers such as cyt b are uninformative. Therefore, we analyzed whole mitochondrial genomes (mitogenomes) for higher resolution. We sequenced 54 individuals (16,511 bp), 52 from Finland and two from Estonia, yielding 41 haplotypes. Median-joining network analysis, including Korean sequences (Far Eastern phylogroup), revealed three Finnish clusters. Two clusters, dominant in southwest and

northeast Finland, show star-shaped networks and neutrality test signals of recent expansion. The third cluster occurs mainly in central Finland but also as scattered individuals across the country. Estonian and Korean haplotypes connect most closely to this cluster, suggesting it represents the ancestral population that first colonized Finland after the Last Glacial Maximum. We hypothesize initial colonization of *P. volans* after glacial retreat and forest succession in Finland (approx. 11,700–10,300 years ago). The Weight of the ice sheet depressed the Earth's crust, and large parts of Finland remained underwater after the ice sheet retreated. As the crust rebounded (land uplift), relative sea levels dropped, exposing new habitats (approx. 10,300–9,000 years ago). Thus, we propose that rapid expansion events occurred as land emerged and suitable habitats connected, shaping the present-day genetic structure of *P. volans* in Finland.

1027. A global comparison of thermoregulatory phenotypes in Sciuridae

Eric Brown, *University of Maine; Danielle Levesque, University of Maine*

The role of climate in the distributions of organisms is fundamental to biogeographical analysis. Appreciation for the physiological patterns and mechanisms of thermoregulation that underlie such distributions is accordingly increasing, such as in the latitudinal and geographic patterns of body size and metabolic rate in mammals. Among mammals, sciurids (ground, tree, and flying squirrels) have long been a model clade for studying endothermic phenotypes due to their near-global distribution and ecological and thermos-physiological diversity. Much work has been done in recent years to resolve questions about their diversification and dispersal since the Oligocene, yet how thermoregulatory traits are distributed phylogenetically and geographically within Sciuridae remains unexplored. Here we compile environmental and trait information relevant to the thermal ecology of squirrels and test how thermoregulatory phenotypes compare among life histories, zoogeographic regions, and lineages using phylogenetic regression. We expect that the thermoregulatory phenotypes (i.e. heterothermy and homeothermy) of squirrels will be best explained by the environmental variability of a species' range (e.g. seasonality), in addition to lineage and life history. Not least of all because of the trophic importance of squirrels in ecological communities, linking thermos-physiology to the present distribution of Sciuridae will better prepare us to predict how they might respond to ongoing climate change.

1028. Urbanization facilitates biological invasions into otherwise unsuitable regions

Jan Lenc, *University of Florida; Brett Scheffers, University of Florida*

Urbanization alters local climates, potentially promoting biological invasions by reshaping species' thermal environments. For tropical ectotherms introduced into subtropical or temperate regions, cold winters constrain survival by limiting thermoregulatory opportunities.

However, urban heat islands (UHIs) with warmer and more variable microclimates may offset these constraints and enable persistence beyond climatic limits. We tested this mechanism in the brown anole (*Anolis sagrei*), an invasive tropical lizard widespread in Florida, USA. During winter, we surveyed anole occupancy, abundance, and activity in urban and forest habitats at the northern and southern non-native range edges, including one-season survey in subtropical South Florida and temperate North Florida, plus a five-year survey in North Florida. At the northern edge, we also quantified fine-scale thermal heterogeneity to test whether urban microclimates enhanced thermoregulatory opportunities. We found that at the cold range edge in North Florida, anoles had higher occupancy, abundance, and activity in urban than forest habitats, indicating a thermal advantage under winter conditions. By contrast, at the warm edge in South Florida, urban–forest differences were absent, reflecting the reduced importance of UHIs where cold constraints are minimal. Thermal measurements in North Florida further revealed greater microclimatic heterogeneity and decoupling between ambient and lizard temperatures in urban than forest habitats, indicating enhanced thermoregulatory opportunities tied to persistence. Together, our results show that UHIs act as thermal refuges at cold non-native range edges, providing a general mechanism by which urbanization can facilitate the persistence and expansion of invasive ectotherms into otherwise unsuitable regions.

1029. Biodiversity estimates in South America from range maps do not always reflect current climate or habitats

Ethan Andrew Shirley, *University of Michigan; Emma Risch, University of Michigan*

Certain areas of Earth have higher biodiversity than others. Different levels of biodiversity are driven largely by geography, climate, and, in turn, habitat. However, this is not always the case. Natural ways in which differences in biodiversity do not reflect climate and habitat include: (1) historic, not current climate, has limited ranges in ways that require a long time to bounce back, and (2), complex behavior of animals and plants that interact in communities permitting greater or fewer species in a region independent of habitats. In mammals, first-order patterns in biodiversity in tropical South America are related to presence or absence of forest. Three-toed sloths (Bradypus variegatus) may represent a species limited by past extent of climate and habitats and slow dispersal that has not yet permitted expansion into adequate habitats today. In birds, mixed multispecies flocks may develop constructed niches and permit greater diversity than habitat alone would predict. Focusing on biogeography of functional and phylogenetic groups helps elucidate the nuances of these patterns, as bird species in certain dietary categories and living in certain parts of the canopy may be more likely to form mixed flocks, and numbers of arboreal mammal species may be more limited by habitat than those living principally on the ground. Efforts to understand the nuances of species distributions and their suitable climate zones and habitats are hampered by

imperfect range maps, habitat maps, and ecozone boundaries; all of these problems are manifest in global datasets, and may mislead assessments of biodiversity for conservation.

1030. Hot or not? Trait-dependent thermoregulation of Orthoptera along an elevational gradient

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Ectotherms are particularly threatened by climate change as fluctuations in environmental temperatures directly affect their body temperature and thus crucial physiological processes. Thermoregulation can be an effective strategy to maintain the body temperature within an optimal range, which makes individuals less vulnerable to changing environmental conditions. However, there is still a lack of research on the ability to thermoregulate in Orthoptera, on their traits influencing thermoregulation, and on how this varies spatially along environmental gradients.

Aim of this master thesis is to investigate the ability of Orthoptera species to buffer their body temperature against variable ambient temperatures along an elevational gradient. Additionally, the effect of certain traits such as body size, dispersal ability and colour intensity on thermoregulation at the community- and species-level will be analysed. We measured body temperature and morphological traits of 530 individuals and 20 species of Orthoptera along an elevational gradient of 1200 m in the German Alps. Measures of air temperature and information on microclimatic variation and habitat structure were collected as well. We tested whether thermoregulation changes at the community- or species-level in Orthopterans to determine whether communities or species adapt to local climatic conditions, or whether thermoregulation is a fixed trait. We also highlight the traits that influence this relationship. Our study emphasizes the value of integrative approaches for unravelling the links between physiology, ecology, and geography, offering a basis for predicting how insects will respond to rapid environmental shifts in mountain ecosystems.

1031. Dark matters: elevational trends in grasshopper coloration

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Insect coloration fulfills multiple ecological functions, including thermoregulation, camouflage, and signaling. Coloration may vary predictably along elevational gradients, with their variation of abiotic and biotic condition such as temperature, radiation, and vegetation structure. The thermal melanism hypothesis predicts that darker individuals should

predominate in cooler environments; however, inter- and intra-specific empirical evidence from living individuals across elevational ranges remains limited. We investigated variation in color lightness of grasshoppers (Orthoptera) along an elevational gradient spanning more than 1200 m in Berchtesgaden National Park, Germany. Using standardized digital imaging of 535 living individuals of 20 species overall, we quantified coloration and tested its associations with other traits related to dispersal and thermoregulation, as well as with spatial variation in climate and habitat structure. Our results advance the understanding of biogeographic patterns in insect coloration by linking color variation to both environmental gradients and species-specific traits. Our work highlights the importance of integrative approaches in disentangling the interactions among physiology, ecology, and geography, and they provide a framework for predicting insect responses to rapid environmental change in mountain ecosystems.

1032. DNA barcode reference library for European ants: a roadmap for phylogeography and species discovery

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We present a comprehensive DNA barcode library for European ants with the aim of tackling the Linnean, Wallacean, and Darwinian shortfalls by providing an updated checklist, updated distributional ranges, genetic diversity maps, and mitochondrial gene trees. The European ant fauna is here estimated to include 650 species, including one species reported for the first time from the continent and 24 species for the first time from 11 countries. Our genetic dataset covers 78% of this fauna (507 species), with 6,529 georeferenced COI sequences of which 62.2% are newly generated. We calculated intra- and inter-specific genetic distances and generated a total of 52 genus-level trees, genetic diversity, and specimen maps for 490 species, and haplotype networks for 288 species, all available in the Supplementary file as the atlas “The Genetic Diversity Maps of European Ants”. DNA barcoding performance largely varies among genera and species groups, likely reflecting biological (e.g., hybridisation, incomplete lineage sorting) and operational factors (e.g., taxonomy), and highlights the existence of potential cryptic taxa and the need for taxonomic revisions. The intraspecific genetic maps we have generated provide insights into the mtDNA phylogeographic structure of European ants. The degree and patterns of population differentiation observed may be linked to species traits, human introductions, and genetic differentiation in glacial refugia and islands. The data produced in this study offer a significant contribution to the evolving understanding of the biogeography of European ants, aiming to facilitate future research and species discovery.

1033. Environmental drivers of mycoheterotrophic plant distribution in Europe

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Plant mycoheterotrophy is a specialized nutritional strategy that enables plants to acquire organic carbon, in addition to mineral nutrients and water, through mycorrhizal symbiosis with fungi. The acquisition of organic carbon at various life stages reduces reliance on seed nutrient reserves and photosynthesis. Obligatory dependence on different mycorrhizal fungi may shape the environmental requirements of mycoheterotrophic plants. We aimed to disentangle the environmental drivers influencing the distribution patterns of European

mycoheterotrophic plants, incl. those using mycoheterotrophic nutrition only for part of their life cycle. We classified these plants into functional groups based on their mycorrhizal associates. We modelled their ecological responses to climatic, topographic, and habitat variables using vegetation plot data and ecological indicator values. The three groups of mycoheterotrophs respond differently to the studied predictors. Ectomycorrhizal fungi-associated mycoheterotrophs (some orchids, Monotropaceae, and Pyrolaceae) strongly avoid open habitats, and their distribution is further influenced by temperature-related factors. Saprotrophic fungi-associated mycoheterotrophs (most orchids) are positively affected by higher precipitation, with temperature playing a lesser role. Both groups preferentially occur in Mediterranean, Baltic, and mountainous regions, while the latter also thrives in warm oceanic areas. Arbuscular mycorrhizal fungi-associated species (Lycopodiaceae, Ophioglossaceae) are influenced by both precipitation and temperature, favoring mountain and eastern Baltic regions with cool, wet summers. Most species prefer low-nutrient habitats. In light of ongoing climate change, land-use shifts—including the encroachment of open habitats—and increasing habitat eutrophication, which leads to the loss of suitable environments, mycoheterotrophic plants face a growing risk of endangerment.

1034. Exploring Nutrient Foraging Patterns of Ants Along Urban Greenways in Relation to Socio-Environmental Gradients Across Three U.S. Cities Shannon

Shannon McCarragher, *Southern Illinois University Edwardsville; DeAnna E. Beasley, University of Tennessee at Chattanooga*

Urban greenways offer critical habitat corridors that can influence biodiversity patterns across cities. This exploratory study examined nutrient resource use in ant communities along greenways in three U.S. cities (Chattanooga, TN, Cleveland, TN, and Edwardsville, IL) representing a gradient of urban size, population density, and housing density. More specifically, ant abundance and genus richness were recorded during standardized morning and afternoon surveys (120 minutes each) at a total of 135 bait stations placed across sites varying in structural habitat complexity. Baits included liquid sugar, extra virgin olive oil, amino acids, salt, and water, representing key nutrient categories relevant to ant physiology. Socio-environmental variables (e.g., ground temperature, herbaceous vegetation height, distance to road) were measured at each station and incorporated into an AIC-based model selection framework to evaluate competing hypotheses about urban habitat structure and ant nutrient preferences. We hypothesized that ants in low-complexity habitats would favor fat-based baits, while those in higher-complexity habitats would prefer sugar baits. Model rankings based on AIC scores enabled robust ecological inference across gradients and regions. The preliminary results presented in this study contribute to a growing understanding of how urbanization gradients influence ecological function and community abundance in fragmented landscapes.

1035. Walking on treacherous silk grounds: Integrative systematics and biogeography of the spider genera Inermocoelotes and Urocoras (Arabeae, Aglenidae)

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Although well-known to both science and the public, the spider family Agelenidae, popularly known as funnel web spiders, remains one of the most challenging groups in terms of taxonomy and phylogeny. It belongs to the informal "marronoid" clade, classified as a "tailor's drawer" because of its complexity and lack of support. Apart from its uncertain position in the clade, the relationships within the family itself are also insufficiently resolved. This is especially true for the subfamily Coelotinae, which comprises numerous poorly defined genera with insufficient diagnoses, leading to the incorrect generic placement of many species, particularly in Asia, where the subfamily is extremely diverse. In this study, we focus on the phylogeny and biogeography of the coelotinae genera *Inermocoelotes* and *Urocoras*. We present the results of a time-calibrated target-gene phylogenetic analysis, based on six genes sampled from all 15 valid I*nermocoelotes* species, plus two new, undescribed ones, and three out of four species of *Urocoras*. Most of the European Coelotinae were also included in the analysis. Because of the lack of fossils in the subfamily, we estimated divergence times based on universal substitution rates and compared the results to a recently published study, calibrated using fossils from the subfamily Ageleninae. Furthermore, we conducted ancestral climatic niche reconstruction and estimated the area of origin of the target group. Our results confirm the monophyly of the two genera and reveal the Southeastern European Mountain System as a center of origin for a unique component of European terrestrial biodiversity.

1036. Using Leaf-Level Reflectance Spectroscopy to Assess Ecotypic Variation in Fern Species

Jessica Lira Viana, *Aarhus University; Flávia Durgante, Karlsruhe Institute of Technology (KIT); Institute of Geography and Geoecology; Floodplain Institute Department; Hanna Tuomisto, Aarhus University and University of Turku*

Understanding how plant populations adapt to local environments requires methods that can capture both genetic differentiation and phenotypic plasticity. Leaf traits such as pigment concentrations, structural characteristics, and chemical composition influence how light is absorbed or reflected across different wavelengths of the spectrum, which are important features for species discrimination. Leaf-level reflectance spectroscopy provides a non-destructive tool to explore hidden dimensions of biodiversity and has the potential to reveal ecotypic variation within species. In this study, we aim to test the extent to which leaf-level reflectance spectroscopy can differentiate populations of widespread fern species growing

under contrasting environmental conditions. We collected spectral data in the 900–2500 nm range from herbarium specimens deposited at AAU and TUR. Specimens were collected across a wide geographical extent of neotropical rainforests covering distinct ecoregions. We will assess the relative importance of intraspecific versus geographical variation in the spectral data using multivariate statistical and machine learning approaches to evaluate their capacity to detect population-level differences. This study will provide insights into the potential of spectroscopy for investigating intraspecific variation and the detection of a valuable dimension of biodiversity detection and monitoring.

1037. The build-up of fern diversity in the American tropics

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The American tropics are home to some of the richest biodiversity on Earth, but we still don't fully understand how this diversity developed. We explored how speciation and dispersal have shaped the distribution of ferns (Polypodiopsida) across this area with a complex geological history. We combined timed phylogenetic trees with geographic occurrence data and applied biogeographic models to reconstruct species movements and diversification through time, comparing results from a broad dataset of 56 fern clades encompassing 67 genera obtained from GBIF with those of a single genus with taxonomically curated observations. Our results show that the American tropics act as a network of connected corridors, unlike the more isolated tropical regions of Southeast Asia. The wind-borne spores of ferns are expected to spread more easily across landscapes than the seeds of flowering plants, and ferns were found to disperse about twice as often as angiosperms in the same area. Fern diversity patterns also differ from those of flowering plants. The diversity of flowering plants peaks in Amazonia, whereas fern diversity was centred in the Andes, which both promoted speciation and acted as a hub for dispersal. Ferns likely thrive in the moist environments of the Andes because of their poorer ability to control water loss. In the taxonomically curated genus, however, diversity peaked in Amazonia, possibly due to better resolved species boundaries in this poorly known area. Our findings also show how both speciation and dispersal have varied through time in response to geological change, shaping today's biodiversity patterns.

1038. Different roads to diversity: Adaptive radiation and geographic isolation in tropical American ferns

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Understanding the processes that generate and maintain tropical plant diversity remains a central question in biogeography. Ferns, with their ecological breadth and diverse life-history strategies, offer a valuable system for studying how geography and environment shape evolutionary trajectories. Here, we present the first nuclear phylogenetic trees of the tropical American clades within two widespread fern genera, *Tectaria* and *Trichomanes*, constructed using the GoFLAG probe set. These phylogenetic trees reveal some evolutionary patterns that are incongruent with previous plastid-based reconstructions and highlight contrasting modes of diversification. In *Tectaria*, species are restricted to nutrient-rich soils, and the phylogenetic tree uncovers well-defined, geographically clustered clades. This suggests that geographic isolation, potentially driven by vicariance, could have been the dominant force shaping diversification in the genus. In contrast, *Trichomanes* displays a pattern where individual species are specialised to different kinds of soil conditions, but their geographical distributions can be very broad. This points toward adaptive radiation, mediated by ecological differentiation, as a key driver of diversification. The comparison between *Tectaria* and *Trichomanes* suggests that some tropical plant groups diversify primarily through niche specialisation and adaptive radiation, while others diversify through geographic isolation. This comparative framework underscores how ecological context, life-history traits, and geographic history may predispose lineages toward distinct evolutionary pathways, shedding light also on broader principles governing the origins of tropical biodiversity.

1039. Effects of intraspecific trait variability on leaf trait space across habitat types

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Trait-based ecology has identified key, independent axes of trait variation that define functional trait spaces and summarize plant adaptive strategies. However, it remains unclear how these axes are altered by intraspecific trait variability (ITV), a facet of trait variation that is relevant to define the potential for acclimatization and adaptability of species. We tested how ITV modifies a functional trait space defined by two independent dimensions of leaf form and function (leaf size and leaf mass per area) using a standardized empirical dataset spanning 3153 individual trait measurements for 167 species across five habitat types (coastal dunes, forests, grasslands, heathlands, wetlands) in Italy. We found that ITV: (i) rotates the axes of trait variation defining the target trait space; (ii) increases the variance explained by these axes and (iii) modifies both the internal structure and outer boundaries of the trait space.

Despite these effects, their magnitude was generally small and varied by trait dimension and habitat type. Our findings underscore the context-dependence of ITV and caution against broad extrapolations of ITV patterns across traits and spatial scales. At the same time, our study paves the way towards developing a new framework to routinely integrate ITV into functional trait space analyses. This will help elucidate the impact of ITV on plants' functional strategies and resolve the functional biogeography of ITV.

1040. Seasonal variation of leaf functional traits in sub-Arctic plants

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Leaf functional traits are informative of plant fitness and functions in ecosystems. These functional traits and their variation across geographic extents is much studied but less is known about their temporal variation, especially how phenology affects functional trait variation over a growing season. Here, we provide an analysis of the seasonal variation in six leaf functional traits of 11 sub-Arctic vascular plant species in northern Finland, highlighting significant temporal dynamics over a growing season. Our findings reveal that functional traits, including specific leaf area, leaf dry matter content, leaf area, leaf dry mass, brightness index, and greenness index, exhibit considerable variation across the 15-week growing season. These temporal variations are influenced by plant growth forms, with distinct patterns observed among forbs, deciduous shrubs, and evergreen shrubs. Our analyses show that the rank of species is rather well preserved through the growing season in the most commonly used traits, and for this reason, the timing of sampling has a rather minor impact on the relative trait differences across species. However, if different species are measured at different times of the year, the seasonal effect can be notable. The growth forms often followed roughly similar temporal dynamics, and therefore, the error can be especially strong when comparing species across different growth forms.

1041. Pathogens and pests constrain climate-driven poleward range shifts

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Understanding species' response to climate change is critical for forecasting future dynamic and distribution of biodiversity. Although ecologists have long recognized that species shift their geographic distribution towards cooler regions to track climate niche, more recent works suggest that these shifts can be overwhelmingly altered by biotic interactions including with parasites and pathogens. However, integrating these interactions into large-scale predictive models remains challenging due to the limited understanding of how interaction outcomes change with climate. Here, we evaluate impacts of climate change on pest and pathogen intensity in forested ecosystems using data from one million individual trees across

North America. We show greater pest and pathogen pressure at species current warmer range limits. As temperatures rise, pest and pathogen intensity will decrease at species' warm range edges and increase at their colder edge. This asymmetry reverses biogeographic gradients in pest intensity from being higher at species' warmer range limits to being higher at their cooler range limits. We estimate that climate-driven shifts in pest pressure will constrain 20% of species predicted poleward migration required to offset warming trends, and reduces climatically suitable habitat area by an average of 23%. We thus suggest that impacts of warming climates on species' range extents and estimates of species extinction risks from climate niche models may be substantial underestimates.

1042. Sky Island Mammals of North America: biogeography and conservation

Kimberly Cook, *University of Kentucky; Binaya Adhikari, University of Kentucky; Dakota Rowseg, Science Museum of Minnesota; Nathan Steadman Upham, Arizona State University; Robbie R Burger, University of Kentucky*

We present a synthesis of a forthcoming series of Feature Articles in the Journal of Mammalogy that address new biogeographic approaches and conservation challenges relevant to the Sky Island Mammals of North America (SIMONA). Covering topics from endangered species management to comparative analyses of montane archipelagos, the collection is designed to engage a broad audience including biogeographers, macroecologists, ecologists, and specimen-based researchers. The papers examine similarities and differences among major sky-island systems—including the Great Basin, southern Appalachians, Madrean Archipelago, and Sierra Madre ranges—in biodiversity, geodiversity, evolutionary history, habitat diversity, climate, and land-use history. These comparative perspectives reveal how sky-island systems provide powerful opportunities to test biogeographic theory while also informing conservation priorities. Collectively, the ten articles introduce new concepts and leverage existing tools (e.g., sky-island delineation, species distribution modeling), apply a novel Constraint-based model of Dynamic Island Biogeography (CDIB, linking traits and environmental history to species' distributions across time), and integrate population genetics with regional biogeographic studies. These articles also create a forum for transnational collaboration on topics of practical and theoretical concern to sky island systems in the United States, Mexico, and elsewhere. This synthesis advances understanding of the origins and dynamics of sky island biodiversity and provides a framework for predicting how ongoing environmental change may reshape these unique mammalian communities.

1043. A Century+ of Surveys: Small Mammal Change Over Time

Reina Warnert, *UC Merced; Jessica L. Blois, University of California, Merced*

As rates of global change accelerate, understanding the continuing effects of climate change on ecosystems is essential. Small mammals are key components of healthy ecosystems as seed and fungal dispersers, prey, and habitat engineers, and have been shown to be sensitive to changes in climate and habitat. In particular, montane species living along elevational gradients tend to be highly vulnerable to global change. Small mammal surveys conducted as part of the Grinnell survey and resurvey efforts over the last century provided high-quality occurrence data in the Sierra Nevada mountains, USA, establishing range shifts as an important global change response. In 2023 - 2024, we resurveyed 20 historic sites in Yosemite National Park, focusing on mid-elevation locations that were likely impacted by drought and fire, and to capture additional small mammal range shifts. In addition to community-level data for each site, we collected morphological data from individual specimens, including total length and mass. By analyzing data across three time periods – 1900s (historic), 2000s (modern), 2020s (current) – and integrating changes in temperature and precipitation, we explore drivers of small mammal community and population change. We found that small mammal ranges have shifted little between modern and current time periods, with some species returning to lower elevation sites that were unoccupied during modern surveys. However, *Peromyscus maniculatus* body size has changed significantly across the three time periods, coinciding with trends in precipitation and temperature. Overall, our results increase our understanding of the ways small mammals may be influenced by global change.

1044. Multilocus phylogeny of North African wall geckos (genus *Tarentola*) illuminates the history of western Sahara-Sahel ecoregions

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Paleoclimate and habitat heterogeneity have strongly shaped the ecology and evolution of North African biodiversity. However, these patterns remain poorly understood, even for some of the region's most conspicuous taxa. Here, we investigate the biogeographic and evolutionary histories of Sahara-Sahel wall geckos, genus *Tarentola* (Phyllodactylidae), which comprise seven putative taxa with unclear phylogenetic relationships and species status: T. *annularis, T. chazaliae, T. parvicarinata* and the *T. ephippiata* complex (including *T. ephippiata sensu strito, T. hoggarensis, T. panousei* and *T. senegambiae*). To this end, multi-locus

phylogenetic analyses were conducted on a representative dataset of 234 samples, targeting two mitochondrial (12S, COI) and three nuclear (MC1R, ACM4, Cmos) markers, totalling 2,233 base pairs. The resulting clades partially contradict existing taxonomic and distribution knowledge. Specifically, five candidate lineages were recovered, corresponding to *T. annularis, T. chazaliae, T. parvicarinata, T. ephippiata* and *T. senegambiae*. The latter two constitute the *T. ephippiata* complex, where the lack of genetic differentiation across the western half of the Sahara suggests that *T. panousei* and *T. hoggarensis* are embedded within *T. ephippiata*. In addition, T. annularis shows little genetic structure throughout its range, whereas *T. chazaliae* and *T. parvicarinata* exhibit remarkable intraspecific diversity, which is geographically structured only in the latter. These findings underscore persistent biodiversity shortfalls that hinder a comprehensive understanding of biogeographic and evolutionary processes in the Sahara-Sahel.

Global Biogeography

1045. Evaluating a protected area portfolio against global biodiversity and climate goals

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Protected areas are one of the most important tools to preserve species and biodiversity. Due to limited conservation funding, expectations and demands on protected area networks are manyfold, e.g. species protection, continued ecosystem functioning, or climate change mitigation. This necessitates rigorous prioritization of conservation effort and continuous evaluation of protected area portfolios against individual targets and goals. Here, we use the case study of a large government-funded development bank to develop an approach that evaluates areas against the global biodiversity and climate goals set by the United Nations Framework Convention on Climate Change and the Convention on Biological Diversity. We identify key indicators for assessing areas, and apply these to evaluation examples at three spatial levels, i.e. biogeographical realm, biome, and country. At each spatial level, our approach evaluates the contributions of i) a portfolio of protected areas such as financed by development banks or conservation agencies or ii) an individual selected protected area; contributions to conservation objectives are assessed by contrasting key indicator values for the selected portfolio or area with values for a random selection of protected areas in the same realm, biome, or country. The results of our case study highlight challenges for meeting diverse conservation objectives with limited numbers of protected areas. Our approach provides a basis for informed decision-making, and contributes to more effective quality control in area-based conservation.

1046. Red List criteria underestimate climate-related extinction risk of range-shifting species

Raya Keuth, *University of Potsdam; Susanne Fritz, German Centre for integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & University of Jena Damaris Zurell, University of Potsdam*

Climate change is a major threat to biodiversity, elevating extinction risks and causing global redistribution of species. Early identification of the most vulnerable species is urgently needed to apply conservation measures with sufficient warning time. The IUCN Red List provides guidelines for assessing species at risk from climate change, relying on species distribution models (SDMs) and spatially explicit population models (SEPMs). Yet, it has never been systematically tested how well these guidelines work for species not only undergoing range declines but also range shifts. In this study, we used a simulation approach to investigate the ability of the Red List criteria to detect climate change risks for species with different life history traits and climate vulnerability. For this, we used SEPMs to simulate virtual species (varying in four traits: niche position, niche breadth, growth rate and dispersal distance) under climate change and fitted different SDM algorithms to the data. Among all traits tested, the niche position proved most important for the accuracy of the Red List assessment. Specifically, SDM-based Red List assessments underestimated extinction risk of warm-adapted, range-shifting species because dispersal limitations prevented colonisation of newly available habitats. In contrast, for cold-adapted, range-contracting species, SDM predictions accurately approximated expected range loss and related extinction risk. Red Listing based on SEPM-based extinction probability, rather than SEPM-based abundance predictions, provided delayed warning for all species. Based on our findings, we provide tentative recommendations for updating the IUCN Red List guidelines for assessing extinction risk imposed by climate change.

1047. European flora habitat requirements in relation to species conservation status

Daria Panasiuk, *University of Tartu; Riin Tamme, University of Tartu; Meelis Pärtel, University of Tartu*

Effective nature conservation requires a clear understanding of the habitat conditions that species depend on. We address whether threatened species of the European flora occupy more likely ecological extremes conducting an analysis on a recently compiled dataset of Ellenberg indicator values for vascular plants. We examined species distributions across five ecological indicator value gradients—soil moisture, soil nutrients, soil reaction, light, and temperature—in relation to their IUCN Red List status. Using a randomization approach, we assessed whether the optimum positions and niche widths of threatened species are concentrated at ecological margins in two-dimensional ecological requirements spaces. Our results revealed zones of under- and overrepresentation of threatened species and identify which data-deficient taxa might merit special attention by conservationists. These findings

provide new insights into the ecological drivers of species vulnerability and support more targeted approaches to conservation policy and Red List assessments.

1048. The role of niche characteristics on plant extinction risk

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Understanding how and what drives plant extinction risk is crucial for anticipating biodiversity dynamics under current global changes. Species niches, defined by their geographic distributions and environmental space, influence their vulnerability to regional extinction. Therefore, extinction risk is unlikely to be evenly distributed across niche gradients. In this study, we investigate how proxies for niche characteristics, particularly range center and margins, influence plant extinction risk. We hypothesize that species' populations at niche margins experience increased extinction risk due to potential unsuitable environmental conditions. Using a recently unified dataset that harmonizes regional and sub-national Red Lists of plant species worldwide, we quantify extinction risk across geographic range and macroecological niche, including center and margins. We also assess whether risks at range margins align with underlying plant traits, including dispersal capacity and growth form, which mediate the ability of species to persist under marginal conditions. Specifically, we test whether growth form, for example, woody vs. herbaceous, interacts with niche position to shape extinction dynamics. We expect a consistent pattern of higher extinction risk at environmental and geographical margins, along with growth form modifying the intensity of marginal risks. By integrating geographic, environmental, and trait dimensions, we help understand how regional extinction risk is distributed within a species' range. These insights are key for prioritizing conservation efforts related to the niche space of plant species and their persistence in changing environments.

1049. Towards a Trait-Climate-Coupled Biome Framework

Haozhi Ma, *Swiss Federal Research Institute for Forest, Snow and Landscape Research; Philipp Brun, WSL; Niklaus E. Zimmermann, Swiss Federal Research Institute WSL*

Biomes are fundamental units of global vegetation, representing physiognomically distinct plant formations that reflect the collective adaptations of plants to environmental conditions. Continuous shifts in climate are reshaping the adaptative boundaries of vegetation types, leading to biome transitions. By definition, biomes are inherently shaped by both climate and functional traits, as traits directly reflect adaptation strategies. Previous biome classifications have relied on 1) simple climate schemes that assign biomes, 2)

physiognomic criteria that indirectly reflect climate yet lacks explicit links to functional traits, or 3) trait-based classifications without integration of climate drivers. Here, we propose a novel framework that explicitly links climate conditions with functional traits to define state-of-art biome classifications across the globe. Our framework incorporates dominant and co-occurring plant functional types and their corresponding functional traits, linking them to climatic boundaries related to temperature, humidity and seasonality. We identified approximately 20 biomes worldwide, spanning five thermal bands and four distinct humidity states. For the first time, we provide a biome definition that captures both distinct vegetation forms and their relationships with climates, offering a benchmark for future studies on biome shifts and ecosystem functioning under climate change.

1050. Global assessment of biome conservatism and drivers of biome shifts

Gengchen Yang, *Swiss Federal Research Institute WSL; Niklaus E. Zimmermann, Swiss Federal Research Institute WSL; Wen-Na Ding, Swiss Federal Research Institute WSL*

Phylogenetic niche conservatism, the tendency of species to retain their ancestral environmental distributions, extends to the broadest spatial and temporal scales as phylogenetic biome conservatism, given that biomes are global vegetation assemblages shaped by convergent evolution under similar environmental conditions. However, a comprehensive synthesis testing phylogenetic biome conservatism across lineages and biomes remains lacking. Here, we present the first global, multi-lineage assessment of biome conservatism and biome shift dynamics across diverse biomes using time-calibrated phylogenies of 160 vascular plant lineages representing ~20,000 species. We found strong evidence for phylogenetic biome conservatism, evidenced by a low overall biome shift frequency (17%). Biome shift is more likely to occur from biomes with higher inter- and intra-annual climatic variabilities and more eco-geographical opportunities in herbaceous lineages, explaining the higher biome shift frequencies in colder regions and grassland biomes. Biome shifts occurred more frequently between geographically closer and environmentally more similar biomes. Biome shifts are directional and asymmetric, with larger, younger, and less species rich biomes more likely to function as recipients than donors of biome shifts. Our findings reveal that the evolutionary dynamics of biome occupancy are shaped by the interplay of environmental change, geographic structure, and evolutionary history, providing an integrated evolutionary perspective to understanding the dynamics of global biomes.

1051. Trends and drivers of wildfire occurrence across global biomes

Manuel Richard Popp, *Swiss Federal Institute WSL; Philipp Brun, WSL; Niklaus E. Zimmermann, Swiss Federal Research Institute WSL*

Wildfires strongly affect terrestrial ecosystems, shaping vegetation dynamics and carbon and nutrient cycling. Scientific investigations of wildfires have focused on fire-prone regions with high human or economic exposure or on fire weather, whereas comparative analyses at the biome scale are sparse. We analysed MODIS burned area data over recent decades to investigate biome-specific wildfire dynamics, dominant drivers, and the roles of regional climate and extreme events. We observed a global decline in wildfire extent, primarily driven by reduced burned area in fire-prone biomes, which may be linked to intensification of agricultural activities and management in African grasslands. Atmospheric conditions were key predictors of wildfires in tundra and coniferous forest biomes, whereas productivity and ignition sources played an important role in Mediterranean, subtropical, and tropical biomes. Our study provides new insights into global wildfire patterns and their biome-specific trends and determinants, offering a baseline to assess how future climate change and land-use shifts may alter wildfire dynamics.

1052. Biome.jl: A Flexible Package for Mechanistic Biome Simulations

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Understanding how biomes respond to climate change requires models that explicitly capture physiological processes and the interactions among plant functional types (PFTs) that shape their distribution. Traditional biome classifications have offered useful descriptive frameworks but have largely relied on correlative methods tied to predefined climatic thresholds. Mechanistic models such as BIOME4 advanced the field by incorporating ecophysiological principles, yet their broader applicability was constrained by simplifying assumptions and the computational limitations of their time. Today, access to high-resolution climate data, refined species distribution records, and high-performance computing removes many of these barriers, enabling more detailed and flexible mechanistic modeling. Here we introduce Biome.jl, a modular platform for developing, calibrating, and running mechanistic biome models at various resolution and structural detail. Designed to merge data-driven approaches with mechanistic realism, Biome.jl supports both climate-envelope classifications and physiology-based equilibrium models. Building on the foundations of BIOME4, the framework allows users to define new PFTs, modify or expand biome classification systems, and calibrate physiological parameters with empirical data. It

integrates diverse climate and ecological inputs at both global and high-resolution scales, supporting applications ranging from treeline dynamics to paleoecological reconstructions based on fossil pollen. As an open-source and extensible package, Biome.jl is intended as a community resource that grows with evolving research needs. By coupling ecological processes with modern datasets and computational tools, it provides a configurable and testable framework for exploring biome distributions under past, present, and future climate scenarios.

1053. Gbif.range: An R package to generate ecologically-informed species range maps from occurrence data with seamless GBIF integration

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Accurate mapping of species distributions and monitoring their temporal changes are essential for ecological research, biodiversity assessment, and conservation planning, particularly amid accelerating global change. Current methods, such as expert-derived maps and species distribution models (SDMs), often face limitations like taxonomic and geographic incompleteness, sampling biases, and insufficient spatial coverage. In contrast, classical range-mapping approaches based on species occurrence geometry, while simpler and more accessible than SDM, often lack ecological grounding and precision. Here we present gbif.range, an R package designed to generate ecologically informed species range maps across diverse geographical scales. The package integrates occurrence records from the Global Biodiversity Information Facility (GBIF) with expert-based ecoregion layers, offering tailored functions for data retrieval, filtering, and customization. This streamlined workflow reduces technical complexity and enhances data integration, making the tool accessible to researchers of all expertise levels. We demonstrate gbif.range's functionality by inferring species richness distributions at both global and regional scales. Globally, we validate the package using data from 381 species, showing strong concordance with IUCN expert-derived distributions (Lin's ccc ~0.76) and species range areas (Lin's ccc ~0.73). Regionally, we highlight its capacity to assess range map accuracy using diverse validation data sources. By overcoming barriers like technical complexity and data availability, gbif.range empowers researchers—from novices to experts—to generate, refine, and evaluate species distributions. As ecological datasets continue to expand, gbif.range is poised to mitigate current limitations in range mapping, enhancing the ecological accuracy and practical relevance of species distribution maps.

1054. Mobilisation of data from natural history collections can increase the quality and coverage of biodiversity information

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The surge of biodiversity data availability in recent decades has facilitated research on previously unthinkable scales, but knowledge gaps persist. Here, we quantify potential gains to insect data on the Global Biodiversity Information Facility (GBIF) through further digitisation of natural history collections, assess to what degree this would fill biases in spatial and environmental record coverage, and deepen understanding of bias with regard to climate rarity. Using Afrotropical records for Catharsius Hope, 1837 (Coleoptera: Scarabaeidae), we compared inventory completeness of GBIF data to a dataset which combined these with records from a taxonomic revision. We analysed how this improved dataset reduced regional and environmental bias in the distribution of occurrence records by identifying well-surveyed spatial units of 100 × 100km and using emerging techniques to classify rarity of climates. The number of cells for which inventory completeness could be calculated, and coverage of climate types by 'well- sampled' cells, increased threefold when using the combined set compared to the GBIF set. Improvements to sampling in Central and Western Africa were striking, as were those of rare climates, as not a single well-sampled cell from the GBIF data occurred in the rarest climate types. Findings support literature highlighting continuing data gaps on GBIF, especially for insects and in the tropics, agreeing that it is not yet ready to serve as a standalone data source for all taxa. However, we show that natural history collections hold the necessary information to fill many of these gaps, and their further digitisation should be prioritised.

1055. A cross-disciplinary framework for temporal dynamics across community ecology, landscape ecology, and remote sensing

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Ecosystems are increasingly shaped by humans, yet approaches to study their temporal dynamics remain fragmented across disciplines. Community ecology, landscape ecology,

and remote sensing often pursue similar questions but rely on different concepts, scales, and methods, which make cross-disciplinary comparison difficult. We propose a unifying framework that bridges these fields by clarifying the role of spatial and temporal dimensions—grain, resolution and extent—and by aligning key concepts. For example, the notions of individual, species, and diversity in community ecology parallel to patch, habitat, and patch diversity in landscape ecology, and to pixel, spectral species, and spectral heterogeneity in remote sensing. To evaluate how research aligns with this framework, we reviewed empirical studies across disciplines. Despite some differences, translating terminology into shared categories revealed consistent patterns and persistent gaps. Community ecology frequently emphasizes diversity, particularly richness and beta diversity, relying on long time series (decades to centuries) and fine-grain yet globally distributed datasets. Landscape ecology tends to address heterogeneity and fragmentation, often using historical maps to extend temporal depth, and relies on coarse temporal resolution. Remote sensing commonly investigates spectral heterogeneity through vegetation indices, but it is constrained by short or irregular time series and sensor inconsistencies; high- temporal frequency monitoring is uncommon, and ecological concepts (e.g. beta diversity) are rarely captured directly. By translating discipline-specific concepts into a shared conceptual language, our framework enables direct comparison of studies and opens opportunities for integration. We argue that such unification is not only feasible but essential for monitoring, interpreting and predicting environmental change.

1056. Latitudinal genetic diversity gradients steepen toward the poles

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Comparing and contrasting different components of biodiversity is necessary to test competing hypotheses about processes maintaining latitudinal biodiversity gradients. There is considerable interest in understanding whether genetic diversity covaries with other biodiversity components, however evidence for a latitudinal gradient in genetic diversity is equivocal. This is partly due to a lack of consensus on the type of genetic diversity gradient described. Genome-wide diversity varies both within and across species: thus, genetic diversity gradients might arise due to the existence of parallel latitudinal gradients within species, or due to species turnover and differences in average genetic diversity across species and latitude. We used a compilation of nuclear genetic data from 100 mammal species across 1,426 locations to test for latitudinal genetic diversity gradients using Bayesian hierarchical regressions. We detected no latitudinal genetic diversity gradients within or across species, but the direction of within-species gradients was associated with species attributes. Notably, the slopes of intraspecific gradients became increasingly positive for species distributed at higher latitudes. Interactions between species-level traits

and population-level processes appear to broadly shape the biogeography of genetic diversity.

1057. Disentangling spatial trends in global plant species richness

Anastasia Luna Andrews, *Radboud University Nijmegen; Patrick Weigelt, Radboud University*

Leveraging ensembles of machine learning algorithms, we created species richness distribution models for almost all plant families, covering nearly the full diversity of vascular plants. From here, we assessed the universality of tracheophyte species richness patterns such as the latitudinal diversity gradient. The family level distributions further allowed us to identify spatial trends present across multiple taxa though partially concealed by other patterns in the distribution of plant species richness and evaluate support for different theories explaining the distribution of plant diversity. The composition and distribution of these sets of families and the environmental factors associated with them indicated climatic history and productivity to be of greater relevance only in the tropics. Most primarily temperate families were associated with mountain regions though not environmental heterogeneity in itself, which may gain importance above the family level. Identifying such spatial and taxonomic contexts of different trends and drivers of plant diversity thereby contributes to explaining global differences in species richness.

1058. Why are certain morphological configurations more common in nature than others?

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Evolution is the key mechanism underlying the remarkable diversity of morphological forms observed in nature. This diversity arises from a complex interplay between abiotic and biotic forces that continually shape species over time. Yet, some morphological arrangements are disproportionately common compared to others, and the mechanisms driving this imbalance remain poorly understood. Here, we examine patterns of morphological commonness in global birds using a novel framework that investigates macroecological patterns in morphological space. Avian morphological diversity was represented in a simplified two-dimensional space, discretized into cells. Each cell represents a set of morphologically similar species, independent of evolutionary history, and the number of species within a cell reflects its morphological commonness. To explore the potential factors influencing commonness, we projected the species composition of each morphological cell into geographical and environmental spaces, and quantified occupied area, climatic conditions, and degree of isolation in each space. We assessed the influence of these factors using

regression models. We found that morphological commonness is not randomly distributed but is influenced by geographical and environmental factors. By shifting focus from geographical to morphological space, our approach provides new insights into why certain trait combinations dominate global avifauna while addressing longstanding questions in macroecology. Furthermore, it demonstrates that morphological space itself offers a powerful and independent perspective for investigating fundamental questions in ecology and evolution.

1059. The Effect of Environmental Fluctuations on Biodiversity Patterns

Daniel Pokorny, *Center for Theoretical Studies; Irena Simova, Charles University in Prague; David Storch, Center for Theoretical Study, Charles University*

Processes governing species richness patterns are modulated by environmental productivity. Equilibrium Theory of Biodiversity Dynamics postulates that species richness depends both on environmental productivity and its fluctuation as they both directly influence minimum viable population size and, consequently, probability of extinction. However, neither the effect of productivity fluctuations on current species richness, nor the temporal scale which it would operate at has been directly tested. We calculated mean productivity, its fluctuation (standard deviation) and its minimum per time window utilizing Miami model across prolonging time windows spanning 2 kY to 5 MY BP. We then related these measures to current species richness at the ecoregion scale. Past fluctuations affect current species richness negatively when accounting for mean productivity. The effect is strongest at the time scale of around 20kY. However, when minimum of mean productivity is included in the model, past fluctuations explain almost no variability in current species richness and minimum of mean productivity becomes a slightly better predictor of current species richness than mean productivity. The results confirm that productivity fluctuation reduces current species richness, potentially through elevated extinction rate affected by increased minimum viable population size (in harsher periods). The fact that minimum of mean productivity both explains slightly more variability than mean productivity and renders productivity fluctuation redundant in the model also suggests that the reduced species richness may reflect historical bottlenecks in population size.

1060. VegVault: Database linking global paleo-, and neo-vegetation data, functional traits, and climate

Ondřej Mottl, *Charles University; Franka Gaiser, University of Bayreuth; Irena Simova, Charles University in Prague; Suzette Flantua, University of Bergen*

Understanding the dynamics and persistence of biodiversity patterns over short (contemporary) and long (thousands of years) time scales is crucial for predicting ecosystem

changes under global climate and land-use changes. A key challenge is integrating currently scattered ecological data to assess complex vegetation dynamics over time. Here, we present VegVault, an interdisciplinary SQLite database that uniquely integrates paleo- and neo-ecological plot-based vegetation data on a global and millennial scale, directly linking them with functional traits, soil, and climate information. VegVault currently comprises data from BIEN, sPlotOpen, TRY, Neotoma, CHELSA, and WoSIS, providing a comprehensive and ready-to-use resource for researchers across various fields to address questions about past and contemporary biodiversity patterns and their abiotic drivers. To further support the usability of the data, VegVault is complemented by the {vaultkeepr} R package, enabling streamlined data access, extraction, and manipulation. This study introduces the structure, content, and diverse applications of VegVault, emphasizing its role in advancing ecological research to improve predictions of biodiversity responses to global climate change.

1061. From native to alien: understanding the biogeography and drivers of donor regions of alien species

Manuela Gomez Suarez, *Justus Liebig University Giessen; Philipp Laeseke, Justus Liebig University Giessen, Germany; Hanno Seebens, Justus-Liebig University Giessen, Germany*

Alien species (AS) may pose significant challenges to ecological communities, ecosystems, and human well-being, prompting extensive research efforts over recent decades. While many studies have concentrated on spatial trends and drivers in regions where AS have been introduced, data availability has hindered the viability of studies examining their donor regions (i.e. here: native regions). Identifying donation hotspots and their underlying characteristics is critical for predicting biological invasions, and thus preventing future introduction events. To address this knowledge gap, we developed SInAS, a cross-taxonomic dataset on global alien and native AS distributions, encompassing countries and key sub-national units. It offers information of alien and native regions, enabling analyses of biogeographic patterns and species spread dynamics. We analyzed the drivers behind AS' donor regions and found that regions with high native species richness (NSR) and low gross domestic product (GDP) are significant AS' donors. This contrasts with recipient regions, which are often characterized by high GDP and lower NSR. However, when accounting for global biogeographical patterns, the amount of donated AS relative to NSR of a region is higher in countries with high GDP and high population density. Notably, over 80% of mammals native to Europe have been introduced elsewhere. In contrast, biodiverse regions like South America and Southern Asia exhibit a lower ratio of donated AS relative to their NSR. Our study provides a comprehensive overview of the biogeography of AS native regions, enabling further exploration of global trends in species introductions and flows, thereby improving future predictions.

1062. How regional and local factors influence taxonomic, phylogenetic and functional diversity in global plant communities?

Riin Tamme, *University of Tartu; Meelis Pärtel, University of Tartu; DarkDivNet Consortium, University of Tartu*

Local plant communities are the outcome of multiple ecological filters acting at different spatial scales. These filters determine how many and which species are ecologically suitable to the local conditions, and able to disperse and persist there. The species pool framework allows to distinguish species that are either observed in the community or have been filtered out (dark diversity), giving a unique opportunity to test how regional and local factors have shaped the taxonomic, phylogenetic and functional assembly of local communities. Using data from the global research collaboration network DarkDivNet, where vegetation has been sampled from >100 study areas, we explored how large-scale environmental factors and in situ measured soil conditions influence observed and dark diversity. For a subset of 10x10 m plots in each study area, we determined the observed vascular plant species and estimated the species most likely belonging to the dark diversity using species co-occurrences in neighboring plots. We then compared taxonomic, phylogenetic and functional species diversity in these sets of species belonging to observed or dark diversity. Although taxonomic observed diversity is consistently about three times lower than dark diversity, phylogenetic and functional diversity tend to be similar in both groups. Local soil conditions are more important in determining observed diversity patterns, whereas dark diversity is influenced by a multitude of factors. To prevent local species loss or restore impoverished communities, it is important to consider how regional and local environmental factors influence taxonomic, phylogenetic and functional community assembly.

1063. Large-scale deviations between realized and fundamental thermal niches in global seaweed distributions

Philipp Laeseke, *Justus Liebig University Giessen, Germany; Brezo Martinez, Rey Juan Carlos University; Kai Bischof, Marine Botany, University of Bremen*

Temperature is a primary explanatory variable of biogeographic distributions of organisms, and global warming significantly impacts species' ranges. For realistic estimates of future range shifts and extinctions under rising temperatures it is crucial to understand how well physiological limits predict distribution patterns. Seaweeds, important foundation species in global coastal ecosystems, show pronounced distributional changes in response to increasing temperatures. We tested the hypothesis that, unlike other marine ectotherms, physiological knowledge of temperature niches serves as a weak predictor for seaweed distributions. Using linear and generalized linear mixed models, we analyzed the predictive power of physiological temperature limits for the real-world distributions of 126 globally distributed seaweed species. In 72% of these species, there was a difference of ≥|2|°C

between physiological and realized thermal limits, including both thermal underfilling and overfilling. Only 28% of the species showed correspondence between physiological and distributional limits. While heat tolerance is a significant predictor for upper distributional temperature limits, cold tolerance showed no relationship with lower limits. Our findings suggest that seaweed species' responses to climate change may be highly variable and difficult to predict. Further, nearly 60% of the investigated species have populations close to or beyond their reported upper survival limits, making them likely threatened by rising sea surface temperatures.

1064. Community completeness illuminates global change effects on fungi

Mats Ittonen, *University of Tartu; Tanel Vahter, University of Tartu; Martin Zobel, University of Tartu; Meelis Pärtel, University of Tartu*

Climate change and habitat degradation reshape global biodiversity, and species' ability to track warming can be complicated when interacting species respond differently. For example, plant redistribution could be facilitated or inhibited depending on the relative colonization success of mutualistic and pathogenic fungi. However, subtle signals of biodiversity change are often difficult to detect with traditional biodiversity metrics. Such hidden patterns can be revealed by community completeness, the proportion of present species out of all species (present and absent) that could potentially inhabit an area. Community completeness is derived from observed species occurrences together with estimates of dark diversity, the set of species that could live in an area but are currently absent. We examined patterns of dark diversity (estimated with established co-occurrence–based methods) and community completeness in plant pathogenic, arbuscular mycorrhizal, ectomycorrhizal, and saprotrophic fungi. We used global datasets of fungal DNA sequences matched with approximately species-level taxa. Across all four fungal groups, community completeness declined polewards. This might reflect lags in colonizing suitable habitats after postglacial or contemporary climate warming, yet there was little difference between mutualists and pathogens. This pattern contrasts with latitudinal patterns of observed species richness, which varied among fungal groups. Moreover, community completeness decreased with increased human footprint index values, suggesting that human activity has adverse effects on soil fungal diversity, although these effects are not detected from species richness alone, possibly due to extinction debt. Our results highlight the usefulness of considering dark diversity for better understanding the ecological consequences of global environmental change.

1065. Diversity patterns in vertebrates are governed by time, diversification, or energy limits, whose effects change across phylogenetic scales

Inigo Rubio Lopez, *Czech Academy of Sciences; Charles University; Maxime Quétin, Charles University, Prague, Czech Republic; Antonin Machac, IMIC Prague*

Three prominent explanations have been proposed for diversity patterns across regions: (1) time for species accumulation, (2) diversification rates, (3) energy limits. However, the interplay and a possible synthesis of these explanations remains elusive. Here, we test the hypothesis that the mechanisms invoked by the three explanations operate simultaneously but are differentially important across phylogenetic scales. Tetrapod vertebrates (35,000+ species) serve as our study system. We find that time and diversification rates explain diversity patterns in small and young clades. However, their effects decline with the age and the size of the studied clades. Interestingly, energy limits show the opposite trend, exerting strong effects in old and large clades. These findings held, independently, within each of the four tetrapod classes (mammals, birds, reptiles, amphibians). Together, they indicate that the historical effects of time and diversification rates are influential early in a clade's history, but their effects are overwritten by energy limits over time, as clades grow and accumulate species. Consequently, the three prominent explanations appear to be phylogenetic scale dependent, governing diversity patterns across clades of different ages and sizes. Recognizing this phylogenetic scale dependence might reconcile the seemingly conflicting explanations and many of the previous empirical results, as needed to achieve their synthesis, improve conservation and biodiversity management.

1066. The geography of present-day diversification

Maxime Quétin, *Charles University, Prague, Czech Republic; Inigo Rubio Lopez, Czech Academy of Sciences; Charles University; Antonin Machac, IMIC Prague*

Why species diversify faster in some regions than others remains unresolved. Classic theory suggests the species-rich tropics and mountains are global engines of diversification, yet recent work points to rapid diversification in temperate regions. We systematically examined this pattern across >30,000 species from five major vertebrate classes. We find that temperate regions harbor both hotspots and coldspots of diversification, whereas tropical regions show only moderate diversification. Classic and new patterns are equally common across clades, and even sister clades often show opposite patterns. Present-day diversification correlates strongly with both regional species richness and climate, but surprisingly little with topography, challenging long-held views of mountains as biodiversity engines. These results hold across diversification estimates, and under null models controlling for sampling. Our findings reveal a scale-invariant interplay of multiple causes and refine our understanding of how richness, climate, and geography together shape global patterns of diversification.

1067. Feast or Famine: Using trophic networks to better predict predator range shifts

Maximiliane Jousse, *McGill University; Laura J. Pollock, McGill University*

In Canada, we expect vertebrate species ranges to shift northwards to track a rapidly warming climate. Theory predicts that the establishment and persistence of species depends mostly on species' environmental niches, but recent literature emphasizes the importance of community composition and species interactions on range limits. However, current methods to investigate potential range shifts typically rely on species distribution model predictions, both present and future, using only environmental co-variates. In this study, we explicitly integrate the idea that trophic interactions shape species distributions into predictions of species' range shifts. We use a predicted meta web along with validated food webs of predator-prey interactions to estimate changes in prey availability and restrict predator colonisation based on existing and future prey distributions. We find that predator and prey species' future ranges are tightly bound together, though network rewiring could rescue some species from extirpation. Going forward, it is critical to integrate trophic interactions into species range shift predictions to understand and monitor changes in the distribution of biodiversity.

1068. Quantifying functionally equivalent species and ecological network dissimilarity with optimal transport distances

Lydia Beaudrot, *Michigan State University; Kai Hung, MIT; Ann Finneran, Rice University; Alex Zalles, Rice University; Cesar Uribe, Rice University*

Quantifying the structure and dynamics of species interactions in ecological communities is fundamental to studying ecology and evolution. While there are numerous approaches to analysing ecological networks, there is not yet an approach that can (1) quantify dissimilarity in the global structure of ecological networks that range from identical species and interaction composition to zero shared species or interactions and (2) map species between such networks while incorporating additional ecological information, such as species traits or abundances. Therefore, we introduce the use of optimal transport (OT) distances to quantify ecological network dissimilarity and functionally equivalent species between networks. We apply optimal transport methods to synthetic and empirical data to identify the most functionally similar species between food webs, incorporate additional trait information into network comparisons and quantify food web dissimilarity among geographic regions. Our results demonstrate that OT distances can effectively differentiate ecological networks based on their topological structure while identifying functionally equivalent species, even when networks have different species. OT methods can be harnessed to analyse ecological networks at large spatial scales and compare networks among ecosystems, realms or taxa.

1069. Mapping temporal dynamics of vertebrate distribution records: A recurrent-event approach to biodiversity knowledge gaps

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Gaps in species occurrence documentation hinder our ability to understand biodiversity patterns and limit the effectiveness of conservation planning. Here, we used recurrent-event models to estimate how long it takes for species to be recorded in new areas and to identify factors influencing the pace of distributional knowledge accumulation. We considered the first record of a species in a new political-administrative unit as an event, with the final state defined by three thresholds: 50%, 75%, or 100% of expected units based on known range maps. We fitted Aalen's additive models to calculate documentation rates separately for each taxonomic class, including body size, nocturnality, and verticality as covariates. We found that temporal patterns varied across classes and thresholds. Larger mammals, birds, and reptiles exhibited higher documentation rates and took longer to attain complete distribution. Nocturnality lowered documentation rates in reptiles but increased them in mammals. Verticality increased documentation rates in mammals and reptiles while reducing distributional completeness in mammals, birds, and reptiles. No covariate predicted the documentation rate or completeness scenarios for amphibians. Under the time-to-full-representation threshold, documentation rate did not differ across taxonomic classes, although birds and mammals appeared to accumulate records more rapidly. In all thresholds, reptiles showed the slowest documentation. Amphibians reached 50% representation faster than reptiles and mammals, but did so with fewer sampled units, probably reflecting restricted ranges. These patterns reflect both historical sampling effort and ecological traits. Our findings can inform the prioritization of regions and taxa that require further sampling to complete biodiversity mapping.

1070. What traits tell us: Who is threatened where and by what?

Sarah Weil, *University of Göttingen; Roberto Rodríguez-Caro, Universidad de Alicante; Laure Gallien, Univ. Grenoble Alpes, Univ. Savoie Mont Blanc, CNRS, LECA; William Allen, Department of Biosciences, Swansea University; Holger Kreft, Univ. of Göttingen; Roberto Salguero-Gómez, University of Oxford*

Determining the drivers of species' extinction risk remains a significant challenge. In particular, the relationships between extinction risk and frequently proposed predictors, such as body size and life history traits, are often clade- and region-specific, possibly because species do not react in the same way to different threats, which also vary geographically. Knowing which threats species face and how they are likely to respond is therefore crucial to improve predictions of species' overall extinction risk, and for effective conservation action.

Here, we investigate geographic and taxonomic nuances in trait-threat relationships using a global dataset of 4,814 reptile species. Across regions, body size was generally better than life history strategies at predicting five key threats: direct exploitation, habitat modification, alien species, pollution, and climate change. Altogether, we found great variability in existence and shapes of trait-threat relationships. Only direct exploitation was consistently associated with large body size across regions, and habitat modification was exclusively associated with a slow life history strategy, but only significantly in two regions: Central Africa and East Asia. Taking into account region- and clade-specific relationships, we then propose an initial estimate of the probability of being threatened by a specific threat for 4,759 currently unassessed reptile species. Our approach can be extended to other clades to complete the large-scale extinction threat assessments needed for effective conservation actions.

1071. Effect of biome area variation on the diversification dynamics of Carnivora

Gustavo Burin, *University of Gothenburg; Tiago Bosisio Quental, Universidade de São Paulo*

Biodiversity has undergone different configurations throughout the history of life, caused by abrupt and gradual environmental changes driven by biotic and abiotic factors. Its dynamics can be investigated using historical approaches using molecular phylogenies, and the development of statistical methods allows these dynamics to be investigated for much of the biota through estimates of diversification rates. These studies at global scales are challenging, especially when investigating the eco-evolutionary mechanisms behind changes in biodiversity, partly due to the difficulty in determining and isolating the relevant environmental factors and evolutionary pressures. Characterizing an organism's "environment" is not trivial, but one way to do so is through the biome to which it belongs. Biomes represent combinations of abiotic (e.g., temperature) and biotic (e.g., ecological interactions) characteristics, whose areas have varied considerably over the past 50 million years. To understand how gradual environmental changes can alter diversification dynamics, we examined how variations in biome area have affected diversification rates of a terrestrial mammal lineage (Carnivora) in different biomes across the planet. In particular, we compared the dynamics of lineages associated with biomes that have undergone area expansion with those associated with biomes that have undergone area contraction, using molecular phylogenies, geographical distribution maps, and comparative phylogenetic methods. Carnivoran lineages in contracting biomes (such as tropical rainforests) or increased (such as grasslands) showed distinct diversification dynamics, with expanding biomes serving as source of species to contracting biomes caused by higher net diversification rates and transition rates from expanding to contracting biomes (also via widespread species).

1072. Evaluating Rare-edge and Abundance SDM Models for Estimating Ecological Marginalization of Species under Current Protected Areas

Eli Taub, *University of Copenhagen; Trevor Fristoe, University of Puerto Rico - Río Piedras; Nina Karnovsky, Pomona College*

In conserving the most vulnerable and largest number of species, the planning of future protected areas will ideally target habitats that represent core regions of species niches where abundances are highest. Unfortunately, conflicts between conservation priorities and alternative interests can result in ecological marginalization – where remaining refugia relegate species to suboptimal habitats. The potential for ecological marginalization in the current and future networks of protected areas, however, remains largely unexplored. Conventional conservation planning uses either occurrence-based methods, where all areas of a species distribution are given equal priority, or data intensive abundance-based Species Distribution Models (SDMs), necessitating new approaches that rely on easier to acquire data. Here, we evaluate a macroecological SDM based on the rare-edge effect, which assumes that species are more likely to have greater abundance at areas away from the edge of their climactic range. We then measure this model against a purely occurrence-based model and a SDM using abundance values from the North American Breeding Bird Survey. To estimate how sufficiently species are protected using the current regime of protected areas, we calculate conservation gaps between current protected areas and scenarios of random and of best-case protection. Our results indicate that occurrence-based conservation planning overestimates protection status for North American birds compared to the rare-edge and abundance SDM models, putting species at risk of being less adequately protected than currently perceived. Our findings highlight the viability of using biogeographic and macroecological relationships for improving conservation planning efforts, especially for understudied and data deficient species.

From paleo-ecosystems to rewilding and human biogeography

2000. Subterranean biodiversity patterns change along a Late Pleistocene glaciation gradient

Mara Knüsel, *Eawag and UZH; Marjorie Couton, Eawag and Université de Lyon; Roman Alther, Eawag and UZH; Florian Altermatt, EAWAG - Swiss Federal Institute of Aquatic Science and Technology*

Past climatic shifts have inherently shaped today's biodiversity. A better understanding of the mechanisms and effects can be valuable in the face of current climatic change. Compared to aboveground taxa, subterranean species might respond differently to changing climates.

Thought knowledge on the geographically large-scale effects of historic climate extremes on subterranean fauna is limited, it is assumed that they generally respond with much lower dispersal and recolonization potential. Here, we investigated how the Last Glacial Maximum has shaped present-day biodiversity patterns of groundwater amphipods. We used an unprecedented dataset of 1000 systematically sampled sites across Switzerland and computed biodiversity indices using a sliding window approach along a distance gradient from ice-covered to ice-free sites. Our results revealed a clear legacy of glaciation on present-day assemblages, with pronounced species turnover and individual species' occurrence in spatial envelopes of formerly ice-covered, transitional, or ice-free zones. Local richness remained uniformly low along the glaciation gradient. Yet, communities within formerly glaciated areas were more homogeneous, had lower gamma diversity and reduced occurrence probabilities. Molecular data suggests that karstic habitats in particular may have provided important refugia for groundwater organisms during glaciation periods, enabling some species to even survive within glaciated areas under the ice cover. Together, our results emphasize that Pleistocene glaciation has shaped both the ecological assembly and genetic legacy of groundwater amphipods, leaving signatures still visible in present-day biodiversity patterns. Understanding these legacies is essential for predicting how subterranean ecosystems may respond to ongoing and future climate change.

2001. Quantitative assessment of how well climatic niches might be represented in the fossil record

Katherine Magoulick, *University of California, Berkeley; Mac Borozan, University of Arizona; Charles Marshall, University of California, Berkeley*

Paleoecological niche models (paleoENMs) provide information about the ecology of extinct species and have been used to improve niche estimates for extant species. However, they may be unable to capture the full extent of a species' niche due to the spatial incompleteness of the fossil record. Here we assess how well the fossil record might preserve climatic niches by analyzing 103 terrestrial mammal species in the contiguous United States. We approximated the future fossil record of a species by taking the subset of its present-day occurrences that overlap with areas of potential fossilization (based on two different assessments of the regions with active sedimentation) and then asked what proportion of their current niche was captured in these simulated fossil records. We found that an overestimate of the future fossil record captured on average ~80% of the present day niches (from 44% to 95%), while an underestimate captured on average a ~47% (from 7% to 84%). We also found significant differences in the inferred values for three of the four climatic variables assessed. This raises concerns about modeling niches in the past, especially given that our approach is a best-case scenario because we assumed that any overlap in the current ranges and areas of active sedimentation would be reflected in the future fossil record. Nonetheless, previous work has shown that the fossil record can be used to make

meaningful inferences about the niches of extinct taxa, so the implications of this study for the use of paleoENMs need further exploration.

2002. Spatio-Temporal Dynamics and Drivers of Plant Diversity in the European Alps: Differentiation and Homogenisation Over 8,000 Years

Franka Gaiser, *University of Bayreuth; Sandra Garcés-Pastor, Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona & Institute of Marine Sciences,; Barcelona; Manuel J. Steinbauer, Bayreuth University; Inger Greve Alsos, The Arctic University Museum of Norway*

Global biodiversity results from regional dissimilarity in species composition. Contributing considerably to global diversity, the European Alps are a hotspot of endemic plant species. After the Last Glacial Maximum, rapidly changing climate and the glacial retreat created new environments, which may have facilitated colonisation and landscape differentiation in the Alps. With advancing time and stabilising climate, species likely dispersed more widely, leading to the homogenisation of alpine habitats. In recent millennia, humans introduced livestock farming that may have increased local diversity while also promoting similar species and homogenising flora across the Alps. It is, thus, unclear how the increase in local floristic richness scales to regional diversity as increasing local richness may be accompanied by regional homogenisation. Using sedimentary ancient DNA data from 14 lakes in the European Alps, we demonstrate that pairwise similarity of floral assemblages has remained stable during the past 8,000 years but shows a marginal increase in the past 500 years. While richness has distinctly increased, individual plant taxa have on average constantly occupied a fourth of the lake catchments. Lake catchments experiencing none or the same land use practices tend to be more similar than pairs of catchments of which only one is used. Past increases in richness do not consistently correlate with changes in floristic similarity. Temporary appearances and disappearances of plants resulted in both, increases and decreases, of pairwise similarity. While livestock farming may benefit local floristic richness, it is not as beneficial for biodiversity in the landscape when considering similarity of assemblages.

2003. Post-glacial demographic history of Alpine flora for a better evaluation of its migration abilities in the current and future global changes

Jules Sougnier, *University of Liege; Antonia Salces-Castellano, Instituto de Productos Naturales y Agrobiología; Patrick Mardulyn, Free University of Brussels; Antoine Guisan, University of Lausanne; Pascal Vittoz, Institute of Earth Surface Dynamics, University of Lausanne; Flavien Collart, University of Lausanne; Alain Vanderpoorten, University of Liège*

Current biodiversity patterns in the northern hemisphere have primarily been shaped by past glaciations (e.g. Pleistocene). Hence the identification of glacial refugia and back colonisation of the Alpine area has long been a major focus in historical biogeography and appeared as a striking puzzle. This question leads to our understanding of the speed at which organisms migrated which is particularly timely given the current velocity of climate change. Using RAD sequencing data for bryophytes, pteridophytes and spermatophytes species, we determine whether current distribution patterns result from the in-situ persistence of populations under the ice or migrations from ice-free refugia. We further assess the rate at which migrations effectively occurred, and its taxa-dependent variations using coalescence simulations. Taxa exhibited contrasted patterns of genetic structure, consistent with their dispersal capacities. Although the analyses revealed different biogeographic origins for species currently distributed across the Alps, observed genetic structure and diversity were globally largely consistent across taxa with simulations under a scenario of persistence within the Alps. Spatially explicit models of coalescence which consider movements of individuals and genes, while attempting to connect current patterns of genetic variation with the evolution of the species range over time. This framework pointed to different recolonization scenario across species. Some species could have migrated to ice-free refugia at the southern limit of the mountain range while other survived under the ice sheet and back colonized the Alps lower than thought, raising concerns about their ability to track the velocity of climate change.

2004. A peak into the future: predicting Alpine species responses to environmental changes with eco-evolutionary models

Elisabetta Canteri, *University of Copenhagen*

Accurately predicting how species will respond to human-driven environmental changes is essential to address the ongoing biodiversity crisis. Doing so requires a deeper understanding of eco-evolutionary processes and their interactions with global change drivers. Spatiotemporally, these processes include behavioural plasticity, dispersal, and genomic adaptations. When these processes fail, population and range sizes decline, genomic diversity decreases, and species may ultimately go extinct. In addition to abiotic factors, biotic interactions play an important role in shaping species' spatiotemporal distribution and ability to respond to threats. However, their importance has often been overlooked compared

to anthropogenic impacts. I aim to fill this gap by explicitly modelling competition between the red deer (Cervus elaphus) and the Alpine ibex (Capra ibex) across the Alps, two species competing for the same food resources in an area expected to be deeply affected by climatic warming. With ibex already suffering from low genetic diversity and with its suitable habitat expected to decline in coming years, interspecific competition could have detrimental effects. I want to use environmental data, animal observations, mechanistic models, and hunting records to 1) investigate variations in both species' movement behaviour under competitive interactions; 2) reconstruct their range dynamics over the last 400 years, in response to climatic changes, human hunting, land-use change, and competition; and 3) use validated models of the past to generate genomic simulations projecting forward in time, under different climate change scenarios. This approach will uncover the processes determining species' vulnerability to extinction, and ultimately advise strategic conservation plans.

2005. Functional Vegetation Paleoecology: Mitigate the impact of climate change with data-driven insight from past vegetation

Natálie Hanusová, *Charles University, Faculty of Science; Ondřej Mottl, Charles University*

Understanding how ecosystems respond to global climate change requires an interdisciplinary approach due to the complexity of the challenge. This project involves integrating global palaeoecological pollen data with contemporary plant functional traits in order to reconstruct long-term changes in functional vegetation patterns and ecosystem properties. This synthesis advances our understanding of how ecosystems vary in space and time, providing new insights into the resilience and vulnerability of ecological communities in the face of environmental change.

This poster serves as an overview of my PhD project's plans, methodology, expected outcomes, and project's objective: to link global fossil pollen records with contemporary plant functional trait databases in order to investigate how ecosystem functions have shifted since the Last Glacial Maximum. Specifically, the project's main goals are: (A) connecting global fossil pollen assemblages with key contemporary plant traits related to growth, survival and reproduction; (B) estimating Community Weighted Means (CWM) for each spatial and temporal sample; (C) quantifying ecosystem dynamics at multiple spatial scales, from local biomes to the global level; and (D) moving beyond species-based reconstructions by exploring links between community-level trait composition and climatic variability and anthropogenic impact. This project also aims to pursue several methodological innovations to address long-standing challenges in palaeoecological synthesis, such as better incorporation of taxonomic uncertainty between contemporary plant and fossil pollen types and it's propagation into quantification of spatio-temporal ecosystem dynamics.

2006. A Comparative Analysis of Methodological Frameworks for Reconstructing Continental Diversity Trends of Vegetation: Case of the Northern Hemisphere during the Holocene

Bryan Valladolid Novio, *Charles University; Ondřej Mottl, Charles University*

With the progress and advances of quantitative methods in paleoecology, the estimation of vegetation diversity through the analyses of fossil pollen has significantly improved. However, differences in data processing, method of diversity estimation, and usage of statistical modelling to summarise the temporal patterns on a continental scale can produce different results. To our knowledge, no effort has been made to explicitly quantify the effects of such choices on the estimated continental trends of past vegetation. This study aimed to first test the reproducibility of four previously published studies of continental diversity trends in the Northern Hemisphere since the Last Glacial Maximum using publicly available fossil pollen data. Next, we created a methodological framework to determine the potential impacts of various data preparation steps (age binning, rarefaction), selection of a specific index in estimation on pollen diversity estimates and trends, and selection statistical model (e.g. a hierarchical generalised additive model) on the observed patterns. This comparative study provides insights that can potentially lead to an improved interpretation of past vegetation diversity, which may serve as a baseline for predicting plant diversity amidst global environmental changes.

2007. Understanding the colonisation, establishment and impacts of dingoes in Australia

Nathan Michielsen, *University of Copenhagen, University of Adelaide; Carsten Rahbek, Center for Macroecology, Evolution and Climate, University of Copenhagen; Damien Fordham, University of Adelaide; Anna Brüniche-Olsen, University of Copenhagen*

Dingoes were likely introduced to the Australian continent by seafarers during the Late Holocene. However, the precise timing of their arrival and other aspects of their historical biogeography remain uncertain. Outstanding questions include: How many founding events took place? How rapidly did dingoes establish themselves across the continent? And did humans facilitate their dispersal? With my poster, I will present the outline and initial results of my PhD project, which is reconstructing the colonisation, establishment and ecological impacts of dingoes in Australia from their arrival until European colonisation. By combining spatially explicit population genomic analyses with process-based ecological models, my project aims to gain a more detailed understanding of dingoes' origin, history and impact. It is expected that the results will deepen our understanding of Australia's natural history and provide valuable insights for the conservation and management of dingoes.

2008. Assessing biodiversity restoration potential considering species distributions under multiple anthropogenic threats

Conor Waldock, *University of Bern, Switzerland*

Recognising the spatial drivers of biodiversity and determining how to optimally recover lost biodiversity are major aims of conservation biogeography. Before regions can be identified as having high biodiversity recovery potential, we must first know how potential anthropogenic threats impact species across the geographical areas they could naturally occur. The multidimensionality of factors influencing species' geographical distributions, combined with differences in the sensitivity of species to different threats, is a challenge to optimising restoration and conservation efforts. We present our progress on a case study addressing these challenges in a highly impacted riverine system in Switzerland. For each of the 9 anthropogenic threats considered here, we first assessed the support for a threat's impact on the spatial distribution of 45 riverine fish species using causal forests. We highlight the challenge of modelling multiple threats for conservation decision making in data-limited situations. For threats supported by causal forests, we then explain their contribution to habitat suitability loss at specific locations within a species' natural distribution using explainable AI tools (SHAP). Next, we applied systematic conservation planning algorithms to identify priority regions for restoration - areas where complementary sets of species could naturally occur but are spatially restricted due to negative anthropogenic impacts. Our approach also allows us to assess where trade-offs exist among different restoration actions, such as floodplain restoration and longitudinal re-connectivity of river networks. Overall, our findings suggest that focusing on areas that are currently biodiversity priorities risks overlooking historical biodiversity hotspots that have been depleted by human impacts.

2009. Vegetation resilience to climate change under rising biosphere novelty

Shuyu Deng, *Aarhus University; Robert Buitenwerf, Aarhus University; Elizabeth le Roux, Aarhus University; Jens-Christian Svenning, Aarhus University*

The relationship between biodiversity and ecosystem stability has been a central question in ecology since the late 20th century. Although results remain inconsistent due to variation in resilience metrics, biodiversity measurements and perturbation types, greater biodiversity and community complexity are generally thought to enhance ecosystem resilience and temporal stability. With the growing prevalence of novel ecosystems, driven by climate change and altered community composition, a pressing question is whether these ecosystems can maintain their resilience under new conditions. To address this, we integrated remote sensing data from Landsat, TerraClimate and MODIS for the past 35 years with 49,787 global on-site biodiversity sampling data from sPlotOpen, together with assessments of ecosystem novelty based on multiple drivers, to examine how novelty gradients modulate diversity, resilience and their relationship. We hypothesise that the

positive diversity-resilience relationship persists in novel ecosystems and that higher novelty amplifies this effect. These insights are crucial for strengthening ecosystem resilience in the face of accelerating novelty, thereby supporting strategies for climate change mitigation.

2010. Nature, humans, and management areas all exposed to highly novel conditions

Matthew R. Kerr, *Aarhus Universitet; Celina Aznarez, Aarhus Universitet; Alejandro Ordonez, Aarhus University; Felix Riede, Aarhus University; Jonas Trepel, Center for Ecological Dynamics in a Novel Biosphere (ECONOVO), Department of Biology, Aarhus University; Jens-Christian Svenning, Aarhus University*

Novel ecosystems are a key outcome of the Anthropocene, widespread across natural and semi-natural areas. Although some work exists testing the broad ecological dynamics within novel ecosystems, their impact on both nature and human-nature interactions is poorly understood. Here we explore multiple types of potential vulnerabilities to rising ecological novelty across the nature and human spectrum. We draw on recently published data on ecologically novel conditions, covering abiotic and biotic sources of novelty, and use them in conjunction with three key interaction datasets. We first explore the exposure of highly at-risk animal species, identifying hotspots of high novelty and vulnerable populations. Secondly, we analyse human populations, focusing on those with high dependence on nature and on natural areas with high value for humans. We finally explore the exposure within protected areas and key biodiversity areas, which are equally exposed to highly novel conditions. Our results paint a spatial picture on how ecological novelty could influence ecosystems globally, highlighting areas of importance which may be at risk to unpredictable ecological dynamics. We finish by offering perspectives on how rising ecological novelty impacts different vulnerabilities, both from a the nature and human dimensions, and how these could be included in future research and management.

2011. Modelling global effects of potential natural densities of large herbivores

William Tejler, *University of Gothenburg; Thomas Hickler, Senckenberg Biodiversity and Climate Research Centre (BiK-F); Paul Miller, Lund University; Søren Faurby, University of Gothenburg*

Large herbivorous mammals may play a powerful role in shaping ecosystems, sometimes transforming vegetation from one state to another. Yet, their influence has probably been significantly reduced due to human-driven extinctions and extirpations. As a result, most vegetation today interacts with greatly diminished herbivore populations—an altered baseline with profound consequences for biodiversity and ecosystem management. In this study, we investigate how global vegetation might appear under present-natural herbivore dynamics i.e. if all mammals had the same abundance and distribution as they would have given current

climate but without any human influences. To do so, we integrated grazing and browsing into the dynamic global vegetation model LPJ-GUESS and incorporated previous estimates of present-natural abundance and distribution of all mammalian herbivores above 10 kg. Our findings reveal that, in a world with intact herbivore communities, vegetation would be more open, with savannahs and grasslands prevailing in some regions now dominated by closed-canopy forests, such as in some parts of temperate Europe and North America. Furthermore, we observed large-scale biome shifts compared to simulations with current herbivory pressure, along with notable changes in overall ecosystem functioning, including nutrient cycling, carbon pools, and fire regimes. These shifts suggest that the absence of megaherbivores has not only altered vegetation structure but also fundamentally changed key ecological processes. Our results highlight the important role of large herbivores in shaping ecosystems, reveal the biomes most sensitive to herbivory, and offer a valuable potential baseline for how natural vegetation might appear across the globe.

2012. Seeing the mountains for the trees: herbivore body mass ecometrics and altitude

Oscar Edward Wilson, *Department of Geosciences and Geography, University of Helsinki; Abigail K. Parker, University of Helsinki; Juha Saarinen, Department of Geosciences and Geography, University of Helsinki*

Body mass is a universal functional trait which shows significant variation across space on intraspecific and community levels. For example, larger mammals are generally found in cooler climates than smaller relatives. Elevation, as a key factor controlling environment, has previously been found to relate to community body mass distributions. Therefore, mammal body mass distributions at a community level can be used as an ecometric trait to estimate elevation (and other aspects of environment). One method of community composition analysis is generalised linear latent variable models (GLLVMs) using species counts in different body mass bins. Body mass ecometrics, including GLLVMs, have potential utility in palaeoenvironmental reconstructions. In central South America, a ~30-million-year record of Andean fossil mammal assemblages is available. We fitted GLLVMs with a single latent variable (LV1) for 6843 modern South American large herbivore (>2 kg) communities with ranges of extinct megafauna included and found that LV1 was negatively correlated with various environmental variables, including mean annual precipitation (MAP), temperature (MAT), net primary productivity (NPP) and tree cover. We applied these models to 12 fossil assemblages from the early Oligocene (Tinguiririca) to the late Pliocene (Inchasi) and recorded a linear decline in LV1 across this period, reflecting habitat cooling, drying, canopy opening, and Andean uplift. This is consistent with other proxies like mesowear in toxodontid notoungulates, which shows expansion of grassy habitats. The successful application of GLLVMs to Andean palaeohabitats suggests that they may have utility in other regions for quantitatively reconstructing faunal responses to altitudinal changes.

2013. Using Ecometric Models to Predict Future Ecological Disruptions

Ankit Raj, *Georgia Institute of Technology; Daniel Avery Lauer, Georgia Institute of Technology; Jenny McGuire, Georgia Institute of Technology; Michelle Lawing, Texas A&M University*

Ecometrics, the study of trait–environment relationships at the community level, has been widely applied in paleoecology and conservation paleobiology to infer past environments and ecological function. However, its potential to forecast community-level responses under future climate change remains largely unexplored. Here, we present the first continent-wide application of ecometrics to project how trait–environment relationships may be disrupted under future climate scenarios.

We modelled ecometric relationships for 9,168 communities of African large herbivorous mammals using two key traits: body mass, which correlates with temperature via thermoregulatory constraints, and hypsodonty (tooth crown height), which reflects dietary adaptation to precipitation-driven vegetation structure. Maximum-likelihood estimates from both models strongly correlated with modern climate data, confirming robust baseline trait–environment relationships. We then quantified future anomalies as the difference between projected climate and ecometric-based estimates. Our results indicate substantial disruption of trait–environment relationships, with >50% of communities projected to show weakened or persistently weak relationships under all future scenarios. Disruptions are especially pronounced in northeastern Ethiopia (~10°N) and Morocco (~32°N, 5°W). To assess potential for re-establishing functional relationships, we integrated ecometrics with landscape connectivity modeling in Omniscape, incorporating human modification as resistance. Connectivity outcomes reveal barriers to movement across the Sahel and northwestern Morocco, but more diffuse flow in the central Sahara, suggesting spatial variation in opportunities for adaptation. Our study demonstrates the novel use of ecometrics to forecast future ecological disruption and highlights its value for linking paleoecological methods with conservation biogeography in the context of ongoing climate change.

2014. Carnivores increase use of anthropogenic resources in human-modified landscapes Nerea

Nerea Fernandez-Arrieta, *University of the Basque Country (UPV/EHU); Luc Bussière, University of Gothenburg; Francisco Javier Zabala, University of the Basque Country (UPV/EHU); Søren Faurby, University of Gothenburg; Ferran Sayol, Beta Tech Centre - UVic-UCC*

In the face of global change, understanding how wildlife responds to anthropogenic pressures is a key research priority. Here, we used a dataset of diet content for 74 carnivore species across 451 sites to analyze whether and how their diets varied with human footprint, human population density, or the proportion of croplands and pastures in a region, focusing

specifically on the fraction of anthropogenic food and mean prey size. We used Bayesian regressions to incorporate spatial and phylogenetic autocorrelation into the analyses, as well as climatic factors as nuisance predictors. We found that the consumption of anthropogenic food increased with both human footprint and population density, with medium-sized carnivores being the most frequent consumers of anthropogenic resources. We also found that larger carnivores eat larger prey, and that the increase in prey size with carnivore mass was steeper in areas with higher human footprint and human population, but only when domestic species were considered as prey. In agricultural landscapes, high human impact further accentuated the differences in prey size among small, medium, and large carnivores. Our results highlight that dietary flexibility may help carnivores persist in human-dominated landscapes and can give insights for the coexistence of carnivores and humans in these ecosystems.

2015. Better Modeling of Paleodistributions of Species Using Diachronic Data

Peter Yaworsky, *Aarhus University & Copenhagen University; Fernando Racimo, University of Copenhagen*

To understand how a species is impacted by changes in climate, we first need to understand the range of climatic conditions suitable for its survival and reproduction. Generally, the climatic space that a species can exist in is estimated from observations of its members in present-day habitats, but such an approach likely underestimates the range of climates in which a species can survive. This limits our ability to model past distributions of species and, more importantly, accurately predict the effects that human-driven climate change will have on a species' persistence in the future. A potential remedy for the issue is to use observations from the past, like fossil observations and ancient sedimentary DNA observations (sedaDNA), to better approximate the range of climatic conditions suitable for a species with a wider temporal sampling. Here, using present-day, fossil, and sedaDNA observations of reindeer (Rangifer tarandus), paleoclimate data, and ecological niche theory, we provide a framework constructed around an under-sampled MaxEnt model from which to better estimate the fundamental niche space of species from diachronic observations of a species' realized niche space over millennia. We find that estimates of the fundamental niche space derived solely from present-day observations results in a narrower estimation of the fundamental niche space for reindeer but is still capable of capturing general trends in changes in the projected potential niche space. The estimates derived from diachronic observations allow for a better estimation of the effects of climate change on species throughout the Pleistocene, Holocene, and incipient Anthropocene.

2016. Did Neanderthals Reach Scandinavia?

Peter Yaworsky, *Aarhus University & Copenhagen University; Trine Kellberg Nielsen, Moesgaard Museum*

Neanderthals occupied western Eurasia between 350-40ka ago, roaming an ever-changing landscape through multiple cycles of extreme climate change. Based on the distribution of Middle paleolithic sites, the geographic range of Neanderthals generally expanded during warm phases and contracted during cold phases. A key issue in Neanderthal research is to what extent Neanderthal populations expanded into northern latitudes, particularly those above 55°N, and what conditions facilitated such range expansions. The Eemian Interglacial (MIS 5e/c. 130-116ka ago) is often identified as a period of peak Neanderthal range expansion, however, the land-altering nature of more recent glacial expansion, such as the LGM, has erased much of the already sparse archaeological material evidence of Neanderthal occupation in the northern latitudes. To fully understand the climatic niche space of Neanderthal's, we need a spatiotemporal species distribution model with an unconstrained sample of observations derived from across Eurasia and the Middle Paleolithic. Here, using dated Neanderthal sites from across western Eurasia, paleoclimate reconstructions, and a new implementation of a spatiotemporal species distribution model using the machine learning method, Maximum Entropy, we a) infer the climatic niche space of Neanderthals from 130-50ka ago, b) test the impact of climate on Neanderthal niche size and distribution, and c) estimate the northern extent of Neanderthal occupation. The results have important implications for how we understand the climates that Neanderthals lived in and can tell us how Neanderthal populations reacted to the volatile climate of Pleistocene Eurasia, in both periods of expansion and con traction (i.e., extinction).

2017. Neanderthal Hunting Patterns: Understanding the Spatiotemporal Variation in Zooarchaeological Assemblages

Konstantinos Dardavesis, *University of Copenhagen; Peter Yaworsky, Aarhus University & Copenhagen University*

Neanderthals (*Homo neanderthalensis*) occupied regions of Eurasia for at least the last 350ka hunting and foraging. This hunter-gatherer life comes to us in the form of archaeological material, like faunal assemblages at archaeological sites representative of a portion of the diet. These faunal assemblages indicate that Neanderthal diet varied both spatially and temporally. Understanding this variability has been challenging, and is structured primarily by two factors. First, the presence or absence of specific species in local ecologies. Second, human behavioral decisions about which prey species to pursue within their local ecology. Here, using faunal assemblages from dated archaeological contexts and Prey Choice Model, we derive preliminary expectations about the relative species abundances within zooarchaeological contexts as a function of their profitability within a Prey

Choice framework. We expect a general pattern of diet expansion with the incorporation of lower ranked prey species when encounters with higher ranked prey species decline, either as a function of climate-driven habitat shifts, or human-induced resource depression. With this information, we make predictions about the spatial and temporal variation in zooarchaeological assemblages as a product of human decision making and interaction with local environments. Preliminary results suggest that the presence of reindeer in zooarchaeological assemblages supports the idea that their relative abundance in the zooarchaeological record are a product of their abundance in the local ecology and their rank relative to other species present. The next step in this project is to pair these data with estimate relative species abundances derived from Ecological Niche Models.

2018. Black Death land abandonment drove European diversity losses

Jonathan Gordon, *University of York*

The current prevailing perception is that human impacts on the biological realm have been overwhelmingly negative. Here, we test this narrative by considering the consequences for biodiversity of the 'Black Death era' (1300–1400 CE), where one third of Europe's population died within half a decade. Based on evidence from 111 European pollen records spanning the Common Era, we find increasing floristic diversity from 0 CE to ~1300 CE as human populations increased, followed by rapid and substantial diversity reductions during the famine- and disease-driven human mortality events of the 'Black Death era'. As human populations recovered following the mortality shock, diversity recovered as well. Strikingly, it was landscapes characterised by cereal cultivation that generated both the overall Common Era increases and the Black Death era declines in diversity. The highest diversity levels were achieved in human-generated, mosaic landscapes, highlighting the integral part of human action in biodiverse European landscapes.

2019. Language biogeography: using analytical tools from macroecology to understand processes shaping linguistic diversity

Lindell Bromham, *Australian National University (ANU); Xia Hua, ANU*

Patterns of global linguistic diversity broadly resemble patterns of biodiversity, yet the underlying causes of these spatial patterns might not be the same for languages and species. We can adapt methods from macroevolution and macroecology to explore the causes of spatial variation in language diversity, and to predict future patterns of loss of linguistic diversity. Importantly, methods developed in biology provide a platform for incorporating relationships between languages, distribution in space and covariation among environmental and socioeconomic variables. We have shown that features of the environment that support high year-round productivity lead to more languages, supporting human cultural groups with

smaller distributions, and that these ecological factors are a stronger correlate of language diversity than landscape features that could influence language isolation, such as altitudinal range. Physical separation does play a role in language diversification, but in ways that are unique to humans, and not necessarily as we expect for species (for example, island biogeography of languages may be influenced by human technology and knowledge). We also need to consider the social environment, for example when we predict patterns of language endangerment, we need to account for not only environmental change but also social factors such as education.

2020. Delineating the radius of urban influence: a new approach for the macroecology of cities

Paul Savary, *Université Marie et Louis Pasteur; Riikka Kinnunen, Concordia University; Gabriel Muñoz, Concordia University; Natalie Dupont, Concordia University; Jordi Vilanova, Concordia University; Eric Pedersen, Concordia University; Chloe Schmidt, Dalhousie University; Colin Garroway, University of Manitoba; Carly Ziter, Concordia University; Jean-Philippe Lessard, Concordia University*

Urban areas have become quintessential ecosystems of the Anthropocene, yet the macroecological study of cities is still in its infancy. A central challenge to urban macroecology is the definition and delineation of urban areas. Although common, delineations based on anthropogenic criteria (e.g., built-up areas, administrative limits) do not necessarily match the radius around city centers until which urbanization shapes species communities. Estimating it with biological data could shed light on the shape and determinants of urban-rural ecological gradients. Here, we defined the radius of urbanization influence as the radius at which the species composition turnover among communities located inside and around cities peaks at a maximum. We estimated it for 812 cities from 34 countries, using bird communities observed within and around them (complete checklists from the eBird database 2016-2021), considering radius up to 45 km, with a GAM-based peak detection method. We then modeled this radius with land cover and socio-economic factors to identify its drivers. In parallel, we simulated communities influenced or not (control) by urbanization to test the reliability of this method. Simulations confirmed that the composition turnover peaks at a radius reflecting the relative scale of urbanization influence on biodiversity. Although the radius of influence could not be detected in small cities, empirical analyses revealed that urban features such as city size, urban sprawl, and pollution levels had a significant influence on the spatial extent at which urbanization reshapes species communities. Our results could guide global efforts to limit the impact of urbanization on biodiversity.

Documenting and inferring effects of ongoing climate change

2021. The costs of global environmental change in the Amazonian Forest

Vitor Hugo Freitas Gomes, *University of Turku; Hanna Tuomisto, Aarhus University and University of Turku; Hans ter Steege, Naturalis Biodiversity Center; Rafael de Paiva Salomão, Museu Paraense Emilio Goeldi; Jesús Aguirre Gutiérrez, University of Oxford; Tereza Cristina Giannini, Instituto Tecnológico Vale*

The conservation of tropical forests is vital to mitigate global environmental change and to sustain biodiversity-based livelihoods. Amazonia, the largest contiguous tropical forest on Earth, has undergone a sharp increase in deforestation over the past decade, with climate change projected to intensify its impacts. Yet, the combined effects of deforestation and climate change on ecosystem services and biodiversity use in the region remain underexplored. Here, we integrate species distribution modelling, projected deforestation scenarios, and a comprehensive dataset on over 10,000 Amazonian tree species, including 12 categories of human use, to assess the impacts of global change on species richness, composition, and ecosystem service values. We found that forest loss between 2000 and 2023 led to a 12% reduction in forest cover, with predicted losses reaching up to 40.2% by 2050 under business-as-usual scenarios. These changes drive substantial reductions in species richness and composition, particularly in Central and Eastern Amazonia, threatening tree species of nutritional, medicinal, and cultural importance. Consequently, we estimate that the total value of Amazonian ecosystem services, initially US$3.01 trillion per year, could decline by up to 66.7% under future scenarios. Our findings underscore the urgent need for coordinated conservation and sustainable management strategies to safeguard the biodiversity and critical ecosystem services upon which millions depend.

2022. High-resolution climate data for biogeographic research at your fingertips: The new CHELSA data portal, R package, and datasets

Franziska Zilker, *Swiss Federal Institute WSL; Dirk Nikolaus Karger, Swiss Federal Institute for Forest, Snow and Landscape Research WSL*

Since their introduction in 2017, the CHELSA (Climatologies at High Resolution for the Earth's Land Surface Areas) datasets have become among the most widely used high-resolution climate resources in biogeographical research. Recent advances in the CHELSA downscaling model now allow virtually any Earth System Model or reanalysis product to be downscaled to a broad range of spatial and temporal resolutions. This flexibility has substantially expanded the range of applications, leading to an unprecedented increase in the volume and diversity of climate information available to the research community. Earlier CHELSA

versions focused on long-term climatic means at kilometer resolution. The current CHELSA products cover extended time periods (from millions of years ago, through the Last Glacial Maximum, to projections up to 2100), finer temporal resolutions ranging from long-term means to monthly and daily time series, and a wider array of climatic variables. These advances not only refine our ability to map and predict species distributions but also deepen our understanding of how climatic variability and temporal dynamics shape ecosystems and their responses to climate change. With the expansion to several terabytes of data, accessibility and searchability have become priorities. To meet these needs, the CHELSA data portal and storage infrastructure have been completely redesigned to deliver faster and more convenient access. Here, we present an overview of the CHELSA datasets, the new online platform, and tools such as an R package that simplify integration into research workflows.

2023. Feeling the heat: the role of microclimates in amplifying versus mitigating extreme temperatures under climate change

Esme Ashe-Jepson, *Global Change Ecology, University of Würzburg; Edgar C Turner, University of Cambridge; Andrew J Bladon, University of Reading*

Climate change is a threat to global biodiversity, with changes to mean temperatures and increasing frequency and intensity of extreme weather events. Heatwaves pose a threat to species' persistence, as temperatures may rise above physiological tolerance. However, individuals rarely experience temperatures measured at the macroclimatic scale: topographical or vegetation differences can result in microclimates that can provide cool refugia during heatwaves. However, little is known about the stability of microclimates through a period of regional warming. In this study, we recorded microclimate temperatures across different microhabitats within a calcareous grassland nature reserve in Bedfordshire, UK, in 2018, 2019 and 2022. During this time, six heatwave events occurred, including the highest air temperatures ever recorded in the UK. We found that the ability of microhabitats to offset air temperatures varied with topographic aspect, slope, amount of bare ground, shelter, vegetation height, and vegetation type, with encroaching scrub and north-facing slopes showing the strongest abilities to maintain relatively stable microclimate temperatures with increasing air temperatures. No combinations of environmental structures consistently maintained cool refugia during heatwaves. Microclimate temperatures were amplified close to the ground, whereas at 50 cm height temperatures were more stable and similar to the macroclimate temperature, therefore ground-dwelling species may be particularly vulnerable to extreme heat. We identified a breakdown in the ability of microhabitats to maintain cool refugia above 7°C, implying cool refugia become increasing rare with increasing temperatures. Our results indicate that the majority of microhabitats will amplify the effects of climate change rather than mitigate them.

2024. Vegetation-Informed Statistical Models for Scalable Microclimate Mapping

Benjamin Deneu, *Swiss Federal Institute for Forest, Snow and Landscape Research WSL; Florian Zellweger, WSL; Dirk Nikolaus Karger, Swiss Federal Institute for Forest, Snow and Landscape Research WSL; Katrin Di Bella Meusburger, Swiss Federal Institute for Forest, Snow and Landscape Research WSL; Catherine Graham, Swiss Federal Research Institute WSL; Pincelli M. Hull, Yale University*

Accurately assessing climate impacts on biodiversity requires microclimate data at the spatial and temporal scales experienced by organisms. However, most available climate datasets describe coarse-scale macroclimate conditions that miss fine-scale heterogeneity driven by local conditions. Mechanistic models can accurately simulate microclimate dynamics but are computationally demanding and difficult to scale globally. Statistical approaches offer a scalable alternative, especially when informed by high-resolution remote sensing and ecological data. In this study, we evaluate whether vegetation-related predictors, either explicit (canopy height estimated from Sentinel-2 imagery) or implicit (from a deep species distribution model, Deep-SDM), can enhance statistical microclimate predictions. Using a nationwide network of temperature loggers in Switzerland, we benchmark different statistical models using the vegetation derived information to predict daily maximum minimum and average near ground temperature against a semi-mechanistic state of the art model (radiative transfer model). Our results show that a simple model using globally available high-resolution variables can achieve performance comparable to the semi-mechanistic baseline. We conclude that statistical models informed by remote sensing and vegetation information provide an efficient, scalable, and globally applicable alternative for microclimate mapping. Our workflow opens roads to fast and easy microclimate predictions for integration into ecological distribution models without the need for intensive computational resources or region-specific input data, helping ecological monitoring under climate change.

2025. Changing phenology of zoonotic diseases under climate and land use change

Valén Holle, *University of Potsdam; Raphaëlle Klitting, Aix-Marseille University; Damaris Zurell, University of Potsdam*

Tick-borne encephalitis (TBE) and West Nile virus (WNV) are zoonotic, vector-borne diseases of growing concern in Europe, marked by rising case numbers and new infection areas. Their transmission risk follows characteristic seasonal patterns, largely driven by the weather-dependent activity of their arthropod vectors. Consequently, climatic warming - particularly alongside land-use changes - may significantly alter the phenology and seasonal dynamics of TBE and WNV by shifting the geographic and temporal distribution of vectors and viruses. In this study, we assess the impacts of climate and land-use changes on the seasonal transmission dynamics of TBE and WNV in Europe, both historically and under future

scenarios. Specifically, we focus on phenological shifts in the intensity of infection risk and the length of the transmission season throughout the year. To achieve this, we developed spatiotemporal species distribution models (SDMs) for both viruses and their primary vector species, generating monthly habitat suitability predictions across Europe for past and projected future conditions. For virus modelling, we employed a nested approach incorporating vector habitat suitability as an additional predictor, capturing the dependence of virus occurrence on vector presence. By identifying temporal shifts in infection risk and highlighting emerging or intensifying future hotspots of prolonged transmission seasons across Europe, our results offer valuable insights into how TBE and WNV transmission patterns have responded to environmental change. Importantly, our results also provide a basis for anticipating future trends, thereby supporting more effective disease risk management through informed early warning systems, targeted surveillance, and adaptive public health strategies.

2026. Climate change favors African malaria vector mosquitoes

Tiem van der Deure, *University of Copenhagen; David Nogues Bravo, Center for Macroecology, Evolution and Climate; Lembris Laanyuni Njotto, University of Dar es Salaam; Anna-Sofie Stensgaard, University of Copenhagen*

Mosquitoes of the genus *Anopheles* are vectors of multiple diseases, including malaria. The *Anopheles* genus has hundreds of members species globally; dozens of these are involved in malaria transmission. Despite an extensive literature on the climate change impacts on malaria, there has been little research on how climate change might affect the distributions of the various *Anopheles* vectors and how this in turn could affect transmission. In this study, we focus on six African *Anopheles* species that together are responsible for the majority of malaria transmission in Africa. Drawing on a continent-wide dataset of mosquito occurrences, we investigate the climatic niches of each species and use species distribution models to predict their current and future suitability. Our projections reveal divergent responses to environmental change, with *Anopheles gambiae, An. coluzzii, and An. nili sensu lato* poised for substantial range expansions. When intersected with demographic forecasts, these shifts suggest that up to 200 million additional people could be exposed to high-risk vector habitats by 2100. These findings highlight that *Anopheles* species are likely to respond to climate change in a highly species-specific way. We thereby add nuance to earlier epidemiological modelling studies that focused on the malaria parasite, but ignored differences between *Anopheles* species, and predicted climate change would reduce malaria risk. As vector distributions are reshaped by climate and land-use change, adaptive strategies for malaria control must be grounded in a nuanced understanding of vector biogeography.

2027. Environmental Constraints on Dispersal: Using Landscape Resistance Surfaces and Mark-Release-Recapture to Identify Movement Barriers

Brett Morgan, *UC Davis, United States*

Understanding how environmental features constrain or facilitate mosquito movement is critical for effective vector control, yet few studies have empirically linked dispersal behavior to landscape structure. To address this gap, we conducted the first study to integrate Mark–Release–Recapture (MRR) experiments with resistance surface modeling. We used this approach to investigate how environmental conditions influence the dispersal of the malaria vector, *Anopheles coluzzii*, on São Tomé and Príncipe islands. We generated three classes of conductance-based resistance surfaces from terrain, vegetation density, and river data, from which we calculated cost-weighted distances as predictors of recapture counts in negative binomial generalized linear models. Resistance surface-informed distances frequently outperformed geographic distance across four spatially and temporally replicated MRR experiments. Uphill terrain limited dispersal in most experiments, pointing to slope as a key constraint on mosquito movement. Vegetation-based resistance effects varied more across sites and seasons, while rivers consistently acted as barriers in Príncipe. Despite limitations in sample size and resistance surface optimization, our study demonstrates the value of integrating resistance surfaces with MRR data to identify movement barriers to dispersing organisms. These results can inform spatial planning for vector control interventions, such as targeted releases of genetically modified mosquitoes, and underscore the need for resistance surface modeling approaches tailored to short-term dispersal data.

2028. Mountain biodiversity along elevational gradients in China: Shifts and transitions

Jian Zhang, *Sun Yat-sen University, Guangzhou, China*

Mountains cover about a quarter of all land area on Earth, and contribute disproportionately to the terrestrial biodiversity. Due to complex topography, climate, and geologic history, mountains exhibit striking biodiversity variation along elevational gradients. Inspired by the early works by Alexander van Humboldt and other following studies in elevational gradients, we initialed a regional research network BEST (Biodiversity along Elevational gradients: Shifts and Transitions) in 2017, to monitor long-term biodiversity dynamics of multiple taxa under climate change and land use. By collaborating with over 20 research teams with different backgrounds, we have set up 20 elevational transects across a large research area in China. In this poster, I will present some results based on the data we collected in last eight years.

2029. From Tropics to Temperate: Latitudinal Vulnerability of Seed-Dispersal Networks under Climate Change

Baltazar González Chávez, *University of California, Merced; Paulo R Jr Guimarães, Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil; Marilia Palumbo Gaiarsa, University of California, Merced*

Climate change is reshaping biodiversity patterns and species interactions worldwide, with profound implications for conservation and human well-being. The Atlantic Forest—a global biodiversity hotspot—harbors exceptional richness and supports diverse ecological functions. Among these, animal-mediated seed dispersal is especially critical: it enables plant regeneration, connects fragmented habitats, and sustains food webs. Yet, the extent to which climate instability threatens the robustness of seed-dispersal networks remains poorly understood. Here, we integrated functional, phylogenetic, and geographic data to model 1,022 taxa engaged in seed dispersal across the Atlantic Forest. We then assessed how the robustness of different plant-seed dispersal communities responds to gradients of climatic stability and extremes, under current and different projected future scenarios. Our analyses revealed that communities in climatically unstable regions consistently exhibit lower robustness. We also identified a strong latitudinal signal: austral communities were more vulnerable to instability than their tropical counterparts, revealing geographic asymmetries in their resilience. These findings demonstrate that the Atlantic Forest, often treated as a single ecological unit, harbors internal biogeographical contrasts that mediate responses to the same climatic drivers. Recognizing these differences of vulnerability is essential to anticipate future biodiversity trajectories and changes in ecological interactions, to inform effective conservation strategies that maintain critical ecosystem functions such as seed dispersal.

2030. Species network centrality varies within their climatic niches

Fabricio Villalobos, *Instituto de Ecologia, A.C. (INECOL), Xalapa, Mexico*

Species interactions can vary depending on the location where these occur. Thus, the importance (centrality) of a species across the interaction networks where it participates can be expected to vary within their geographic ranges and climatic niches. Understanding such variation can help revealing the drivers of interaction networks organization. Here, I'll present two case studies, one for birds in seed-dispersal networks at the global scale and one for bats in frugivory networks at the continental scale, introducing a novel integration between interaction network theory and ecological niche theory under a macroecological perspective. These studies evaluated the variation of species' centrality across networks along their occupied climatic conditions (niches) based on a compilation of local-scale, georeferenced network studies and ecological niche modeling from their complete geographic distributions. In the case of birds in seed-dispersal networks, around half (102) of the evaluated species (239) showed a negative relationship between network centrality and climatic niche

suitability (higher centrality towards their niche centroid), whereas the other half (122) showed a positive relationship (higher centrality away from their niche centroid). In the case of bats in frugivory networks, only five out of 20 evaluated species showed a relationship between network centrality and climatic niche suitability. Overall, both case studies provide evidence on the variation of species' network centrality within climatic niches, regardless of the interaction type, taxa and spatial scale, suggesting the existence of climatically suitable areas where species can achieve high network importance and which could determine evolutionary and ecological dynamics.

2031. Truncated niche edges, novel climates, and anticipating ecological surprises in North American tree species

Nora Schlenker, *University of Wisconsin Madison; John W. Williams, University of Wisconsin*

Novel climates and ecosystems continue to emerge as environmental conditions move beyond the range experienced by species in the recent past. These changes are expected to produce ecological surprises resulting from unanticipated species range expansions and community reshuffling, especially in places where climate changes reveal previously unknown portions of species fundamental niches. To better understand where these ecological surprises may occur, we map truncated niche edges for 501 tree species in North America and intersect these distributions with projected and downscaled assessments of climate novelty and shifts in climate prevalence. The spatial patterns of truncated niche edges in North America are complex and do not simply correspond to geographic range edges. Rather, truncated niche edges are concentrated in temperate mountainous and coastal areas with wetter climates and lower temperature seasonality relative to other portions of North America climate space. Many truncated niche edges are located in regions projected to experience future novel climates and declining prevalence of local climates; in these areas there is increased risk for the loss of current communities, with high uncertainty of which species will replace them. Some truncated niche edges are located in regions with future novel climates and increasing prevalence of local climates; these areas are more likely to experience unexpected expansion of species into these newly available climates and the emergence of novel communities. This work thus begins to sharpen our understanding of where ecological surprises may emerge in the future.

Island Biogeography

3000. Identifying potential establishment hotspots of non-native plant species on the Pacific Islands

Anna Rönnfeldt, *University of Potsdam; Valén Holle, University of Potsdam; Katrin Schifferle, University of Potsdam; Laure Gallien, Stellenbosch University; Tiffany Marie Knight, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; Patrick Weigelt, Radboud University; Dylan Craven; Juliano Sarmento Cabral, Ecosystem Modeling, Center for Computational and Theoretical Biology (CCTB), University of Würzburg; Damaris Zurell, University of Potsdam*

Biological invasions threaten biodiversity worldwide, with island systems being particularly vulnerable to their impacts. The prevention of the initial establishment of non-native species is essential for the successful management of biological invasions, but resources are limited. Here, we use species distribution models to map environmentally suitable areas for the establishment of multiple non-native plant species across the Pacific Islands. We combine regional and global models to identify hotspots of unrealised colonisation potential. These hotspots make for ideal focal points for targeted screening and prevention measures, aiming to maximise the effective use of the resources available for the management of biological invasions.

3001. Invasive terrestrial arthropods on Pacific Islands: DNA observatories and AI classification tools

George Roderick, *University of California, Berkeley, Natalie Graham, University of Hawaii at Hilo; Rosemary Gillespie, University of California Berkeley; Henrik Krehenwinkel, University of Trier; Sven Weber, UC Berkeley; Pritam Banerjee, UC Berkeley; Susan Kennedy, Okinawa Institute of Science and Technology; Jeremy Andersen, U Mass Amherst; Evan Economo, U Maryland College Park; Ken Puliafico, Guam, Colorado State Univ., Haldre Rogers, Virginia Tech; Paul Krushelnycky, Unviersity of Hawaii, Manoa*

We describe a collaboration of DNA inventories and genomic observatories across the Pacific to detect, identify, and monitor, invasive terrestrial arthropods. Island groups include, Hawaiian Islands, Guam and Mariana Islands, Society Islands, French Polynesia, Federated States of Micronesia and Okinawa, Japan. The work builds on a set of multi-national projects, including the Moorea BioCode, Hawaii NSF-Dimensions, and SERDP-Pacific Next Generation DNA Biomonitoring. We are developing and using a set of tools for detecting and monitoring invasive species using DNA meta-barcoding and eDNA and managing DNA data and associated information (using GEOME). The data are useful for detecting emerging invasive species (i.e., “horizon scans”, pathway analyses, targets for eDNA), as well as in

understanding the function and impact of introduced species in biological communities and for encouraging citizen science.

3002. Extending the Theory of Island Biogeography: Niche Dynamics on Islands

Maria del Rosario Miranda, *Institut de Biologie de l'Ecole Normale Superieure (IBENS) - École normale supérieure - Université PSL*

The theory of island biogeography (TIB) describes biodiversity as a balance between colonization, speciation, and extinction, linked to island area and isolation. Given the assumed importance of ecological niches in shaping biodiversity, we expanded TIB by examining how niche filling unfolds on islands and how island area, isolation, and age influence these dynamics. We also tested whether niche dynamics reflect specific characteristics of species that gradually accumulate on islands, or instead follow expectations under a null model. We integrated phylogenetic and morphological data with community assembly information to reconstruct occupied niche space through time in bird communities across 25 archipelagos worldwide. We fitted a logistic model to estimate the initial rate of niche filling, the inflection point at which this rate slows, and the equilibrium niche space. Our results show that isolation, as well as its interaction with island area, influence niche filling dynamics. Equilibrium niche space is higher on larger islands and lower on more isolated islands. The initial rate of niche filling is higher on islands that are both larger and more isolated, and the time required to reach equilibrium is correspondingly lower compared to smaller, more connected islands. The simulations indicate that niche filling dynamics can be largely explained by a null model of random species assembly, suggesting that island species richness, rather than species-specific traits, is the primary driver of niche filling. Overall, our findings suggest that species richness alone shapes niche filling, offering a simple yet powerful extension to TIB.

3003. Separating the drivers of endemic occurrence and richness for vascular plants on islands worldwide

Osanna Chu, *University of Birmingham; Tom Matthews, University of Birmingham; Julian Schrader, Macquarie University; Holger Kreft, University of Göttingen; Francois Rigal, Université de Pau et des; Pays de l'Adour; Laura Jane Graham, University of Birmingham; Adriane Esquivel-Muelber, University of Birmingham, Birmingham, UK; Jon Sadler, University of Birmingham; Liam Trethowan, Royal Botanic Gardens, Kew*

Islands hold a significant proportion of global vascular plant biodiversity. However, hundreds of millions of years of evolution, including c. 17 families and c. 1,700 genera of island endemics, are at risk of extinction. Even though islands are hotspots of biodiversity and endemism, most global studies have focused on total native richness, and our understanding

of the patterns and drivers of plant endemism remain less clear. To address this, we used a mixed-effects hurdle model spanning 1,288 islands worldwide to separate endemism into the processes of occurrence and accumulation. We found that island area is a very strong driver of both, as is mean annual temperature, while higher precipitation is associated with accumulation only. Additionally, area during the Last Glacial Maximum (a proxy for past mainland connectivity) is linked to a higher probability of zero endemics. Another hurdle model focusing on 321 oceanic islands and including island age as an additional predictor variable also supported these results. Furthermore, random intercepts for archipelago captured substantial inter-archipelago differences in both models, indicating biogeographical structure beyond measured environment. Overall, our results frame island endemism as a two-step process shaped by area, climate, and biogeographical history. Improving our understanding of the processes determining where endemics occur and accumulate is imperative to the conservation of island floras.

3004. Trait space remains constant during succession despite shifts from secondary to ancestral woodiness

Simon Biedermann, *University of Bayreuth; Carl Beierkuhnlein, University of Bayreuth*

Oceanic islands are cradles for biodiversity, giving rise to distinct life forms, like insular woodiness in plants. Multiple hypothesis emerged trying to explain the evolution of woodiness on islands. A recent hypothesis links frequent volcanic activity and subsequent burial of vegetation through tephra depositions as a selecting force for (insular) woodiness. Ancient tephra fields are model systems to study this selection process. We use a chronosequence of five ancient tephra fields on the island of La Palma to find evidence for the selection towards (insular) woodiness. These tephra fields display unique plant communities and are dominated by woody species irrespective of age. Insular woody species almost exclusively occur on young fields, whereas a shift towards ancestral woodiness occurs with age. The occupied functional trait space remains constant during succession. These findings highlight the strong selection and filtering of tephra depositions for woody species and their traits. Only certain, woody species can pass the abiotic filter posed by tephra depositions. The dominance of secondary woody species in early succession may be due to increased survival and colonization ability after volcanic eruptions in comparison to ancestral woody species. Understanding which environmental filters limit certain species and their traits to establish on these fields and why secondary woody species are dominant on initial tephra fields may be crucial to understand the drivers of the evolution of insular woodiness.

3005. Continental patterns in bat-associated virus diversity

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The species-rich mammalian order of bats hosts a highly diverse virome. Bat-associated viruses have spilled over to infect livestock and humans, causing zoonotic diseases. Here, we analyse the diversity and biogeography of bat-associated viruses to identify global hotspots and patterns by combining phylogenetic data of bat-associated viruses with global bat species ranges. For this, we use over 8,000 publicly available virus sequences from six major virus families. Viral diversity patterns for Coronaviridae, Rhabdoviridae, Paramyxoviridae, Astroviridae, Adenoviridae and Herpesviridaehave distinct hotspots in tropical regions of the Old World and the Americas. These viral diversity patterns are mainly influenced by continental barriers rather than global biomes or bat diversity, suggesting that bats share viruses throughout continents but are confined by geography. Bat diversity is highest in tropical regions, however data on their associated viruses is often lacking, suggesting that bat viruses are insufficiently studied, especially in their global hot spots. Increasing human pressure on ecosystems with high viral diversity may increase the risk of zoonotic virus spillover. This requires joint healthcare and nature conservation policies to raise awareness about zoonotic risks and implement preventative measures to reduce potential spillover events.

3006. Disentangling the relative importance of deterministic, stochastic, and human effects on beta diversity of plant species across multiple islands

Keonhak Lee, *Seoul National University; Daehyun Kim, Seoul National University*

In biogeography, deterministic factors and stochastic processes have been intensively investigated separately and synthetically. In addition, human impacts on the biogeography are getting more attention these days. Taking the three perspectives into a single account with equal importance would yield a holistic interpretation of species distribution. For this purpose, we performed a variation partitioning analysis to statistically show how much each biogeographic perspective explains the plant species composition of 180 islands in South Korea. Three habitat diversity proxies, including geomorphic variations, were chosen as deterministic factors. The spatial structure of the islands, representing stochastic processes, was indicated by the PCNM. The degree of human impact was quantified by four variables: species richness of invasive plants and cultivated plants, and distance from the nearest inhabited island and regular sea route. The result demonstrated that 10%, 15%, and 5% of variance were explained by pure deterministic, stochastic, and human effects, respectively.

The total variance explained was 45%. The fundamentals of island biogeography have been laid on stochastic approaches, and the result also supports their importance with the highest variance explained. Meanwhile, deterministic and human effects, being widely acknowledged for their biogeographical significance, further explained the spatial distribution of plants on islands. It should be mentioned that jointly-explained variances also exist, although additional analyses are required for interpretation. As illustrated in this research, an archipelago would be an adequate system to compare the relative importance of deterministic and stochastic approaches, with additional consideration of quantifying the impacts of humans on a vegetation community.

3007. Seed dispersion mechanism influences Gymnosperm colonization of the Caribbean

Natalia Ruiz Vargas, *Memorial University of Newfoundland; Víctor Pérez-Calle, Memorial University of Newfoundland; Julissa Roncal, Memorial University of Newfoundland*

The assembly of island floras is a complex and dynamic process that results from the interaction of migration, speciation, and extinction. The islands' geomorphological features and geology, as well as natural history components of possible colonizing taxa play a role in migration and successful establishment of island biotas. The Caribbean islands are home to approximately 11,000 indigenous plant taxa of which over 70% are endemic to the region. There are 19 recognized taxa of Gymnosperms on the islands belonging to the genera *Juniperus, Microcycas, Pinus, Podocarpus,* and *Zamia*. In this project we use the R program DAISIE to test: 1) if seed dispersal mode (animal vs. wind) and 2) the period of increased land connectivity during the Oligocene had an impact in the rates of colonization and speciation of these plants to the Caribbean Islands. Our results indicate that wind dispersed taxa have a lower colonization rate to the islands and that increased land connectivity had no impact in species assembly.

3008. Testing the dispersal role of a Paleogene land connection to the Caribbean via a meta-analysis and modeling approach

Víctor Pérez-Calle, *Memorial University of Newfoundland; Julissa Roncal, Memorial University of Newfoundland*

The geographic origin and assembly mechanisms behind the rich and unique flora of the Caribbean biodiversity hotspot are still under debate. A long-standing controversy is whether ancestral lineages colonized the archipelago via long-distance overwater dispersal or via emerged lands in the past (e.g., GAARlandia and GrANoLA). During the last decade, an increasing number of phylogenetic trees sampling Caribbean plants has been available. However, scant research has merged these data in search of general colonisation and

speciation patterns in the Caribbean. To address this, we compiled 59 publications of molecular plant phylogenies that sample 124 Caribbean endemic and native lineages to estimate the accumulation of speciation and colonization events through time. Our analysis showed that ~87% of the colonisation events from continental America occurred in the last 20 million years, after the subsidence of all hypothesized land connections, suggesting that most plant colonisation of the Caribbean was not land mediated. Our results showed two speciation peaks: one around the Oligocene-Miocene boundary, matching the end of the GrANoLA connection, and the second over the last ten million years. We used DAISIE to test for differences in speciation and colonization rates during and after the presence of GrANoLA using palms (Arecaceae) as a model group. Results suggested that the colonisation rate has been constant through time, corroborating the negligible effect of transient land bridges. The speciation rate has been constant or increased in the last 20 million years, suggesting a constant replacement of old species by recent ones.

3009. An updated subsidence map for the Sunda Shelf and its implication for southeast Asian Biogeography

Nina de Munck, *University of Amsterdam, Netherlands*

We present an updated and harmonized subsidence map for the Sunda Shelf. We reviewed the literature and compiled subsidence rates from existing, mainly petrochemical sources. We also designed a quality label for each subsidence data point based on criteria related to transparency and degree of reproducibility. We found that the data is scarce and heterogeneous. The data quality is variable ranging from anecdotal evidence for subsidence to very well recorded radiometrically dated records. A key result is that the data points of heterogeneous rates of subsidence across the shelf, are related to active tectonic structures, fault lines, and paleo-basins. Striking is that the inner shelf is only represented by a few data points located outside known paleo-basins, these estimates yield relatively high subsidence rates from cores not extending past the Holocene. Our work indicates that paleogeographic models based on a heterogenically subsiding Sunda Shelf will yield different paleo-geographies as those based on a single uniform subsidence rate and will have implications for our understanding of the biogeography of the region.

3010. Area threshold of abrupt increase in biological invasion risks on islands

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Biological invasions are a major threat to global biodiversity and social sustainability especially on islands. Identifying the threshold of area at which non-native species begin to

increase abruptly is crucial for early prevention strategies. The small-island effect (SIE) was proposed to quantify the nonlinear relationship between native species richness/abundance and area but has not yet been applied to non-native species and thus to predict the key breakpoints at which established non-native species start to increase rapidly. Using a global dataset of established non-native terrestrial vertebrates, we found that approximately 50% of islands have reached the threshold area according to the SIE and thus may be undergoing a rapid increase in biological invasions, especially for those archipelagos with higher introduction pressure, lower habitat diversity, more established historical non-native species, and wider area ranges. Based on field surveys of established populations of the American bullfrog (*Lithobates catesbeianus* = *Rana catesbeiana*) across 92 permanent water bodies on 31 islands in the Zhoushan Archipelago, China, we did not detect the non-linear increase of bullfrog abundance with island area but found a piecewise trend of the bullfrog abundance with the area of invaded waters. Overall, bullfrogs were more abundant on larger, less isolated islands and in waters with fewer native frogs. By linking global species–area relationship and local abundance–area data, our studies demonstrated that SIE provides a promising avenue to reveal the golden window for early detection and prevention of non-native species invasions on islands.

3011. Disparate patterns of genetic divergence in parallel evolution of the island syndrome

Michal Tomasz Jezierski, *University of Birmingham; Jenny C Dunn, Keele University; Carolina RF Chagas, Nature Research Centre; William J Smith, University of Nottingham*

The island syndrome is the macroevolutionary pattern of convergent biology in island organisms, thought to arise in response to shared ecological conditions across islands worldwide. The island syndrome is a potentially powerful driver of speciation, particularly when parallel colonisations lead to the divergence of multiple independent lineages. However, the extent and pace of island syndrome evolution have rarely been investigated in such microevolutionary contexts. We examined the evolution of the island syndrome in an apparent case of parallel island colonisation by the Eurasian Wren (*Troglodytes troglodytes*). In the British Isles, this small passerine is thought to occur as five or six subspecies, with four restricted to smaller Scottish archipelagos/islands, and one or two on mainland Great Britain. We confirmed the distinctiveness of the four Scottish subspecies, all of which originated from Great Britain. Furthermore, we found that the Shetland and St Kilda subspecies have diverged significantly at the genetic level from their ancestor, with no evidence of gene flow from the mainland. Morphologically, both have evolved island gigantism, but their songs have diverged from one another. The two subspecies do not share highly divergent genomic regions, suggesting different genetic mechanisms underlie their parallel morphological evolution. Our findings reinforce recent evidence for the idiosyncratic genetic basis of the island syndrome, despite similar island environments and near-simultaneous colonisation of islands from a

common ancestral population. This study also confirms that the British Isles harbour genetically and phenotypically divergent Wren populations, which have evolved in apparent isolation over the past 17,000 years.

3012. Reconstructing the Origins and Diversification of Madagascar's Biomes through Time

Friederike Johanna Rosa Wölke, *Stockholm University; Jan Hackel, Stockholm University*

Biomes are large ecological and evolutionary units that have shifted repeatedly with climatic change, tectonics and edaphic changes through Earth's history. Recent studies emphasise their importance for conservation, as biomes often overlap with regions experiencing severe environmental pressure. Understanding the history of biomes is thus useful for linking biodiversity to long-term environmental dynamics. Madagascar, a continental island with exceptional species richness, offers a unique setting to study biome origins and diversification. Its isolation for more than 80 million years, together with strong contrasts in rainfall, topography, and soils, has fostered extraordinary endemism, with up to 90% of species found nowhere else. While many Malagasy lineages likely arrived by transoceanic dispersal and subsequently radiated in situ, the ages and assembly pathways of Madagascar's biomes remain unclear. Which biome arose first, and how did colonising lineages adapt and diversify within novel environments?

3013. Brain evolution in extinct dwarf hippopotamuses from Madagascar and Cyprus

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Islands are renowned for driving distinctive evolutionary trajectories, yet the influence of insularity on neuroanatomy in large mammals remains poorly understood. Based on 19 virtual cranial endocasts, we investigated brain evolution in three extinct insular dwarf hippopotamuses: *Hippopotamus madagascariensis* and *H. lemerlei* from Madagascar, and *H. minor* from Cyprus. We described their endocranial morphology and quantified changes in brain size and shape using encephalization quotient (EQ) estimates, 3D geometric morphometrics, and relative proportions of olfactory bulbs. Our comparative sample includes the mainland relatives *H. amphibius*, a semi-aquatic species, and *Choeropsis liberiensis*, a forest-dweller with a higher degree of terrestriality. To account for differences in lifestyle among species, we included in our analyses an index of semi-aquatic habits based on the disposition of sensory organs. We found that EQ values do not differ significantly among taxa in our sample, indicating conserved brain-to-body scaling and no detectable island effect on brain size. Nevertheless, we recorded a significant endocranial shape

variation among focal taxa and significant pairwise differences in shape between island species and *H. amphibius*. Notably, the extremely dwarfed *H. minor* shows smaller olfactory bulbs than H. *amphibius*. Differences in brain structure between Madagascan and Cypriot dwarf hippopotamuses likely reflect different lifestyles —that is, retained semi-aquatic habits in Madagascar versus a higher degree of terrestriality in Cyprus— and island-specific selective pressures, suggesting that even closely related island taxa can follow distinct neuroanatomical trajectories.

3014. Virtual endocast of Duboisia santeng (Artiodactyla, Bovidae) from the Early-Middle Pleistocene of Java and brain evolution in insular bovids

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Mammals on islands often undergo remarkable evolutionary changes, including changes in body size and in the morphology of their skull, brain, teeth and limbs. A reduction in relative brain size has been recorded in a few extinct insular large mammals, with the most extreme case being the Balearian mouse goat *Myotragus balearicus*, a dwarf caprin (Bovidae, Caprini) whose brain was up to 52.1% smaller than that of its extant mainland relatives. However, relatively little is currently known about the generality and magnitude of this pattern in island bovids. Here, we report the first digital endocast of *Duboisia santeng*, an Early-Middle Pleistocene endemic boselaphin (Bovidae, Boselaphini) from Java. We compared its endocranial morphology with that of extant and extinct relatives — including its putative ancestor, *Boselaphus namadicus* from the Late Pliocene-Middle Pleistocene of India and Pakistan; the only two living *Boselaphini, B. tragocamelus* and *Tetracerus quadricornis; and M. balearicus* — and investigated brain size variation in our sample. We recorded a moderate brain size reduction in D. *santeng*, which shows a lower encephalization quotient than *B. namadicus* and a brain that is approximately 20% smaller than expected for a Boselaphini with the same mean body mass. The absence of a strongly reduced brain size in this Javanese bovid may result at least in part from the lack of reduction of its olfactory bulbs and occipital cortex, which is instead well-documented in *M. balearicus*, and likely reflects distinct selective pressures on their respective islands.

3015. Spatiotemporal data integration for marine megafauna SDMs in dynamic environments: A point process approach

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Species distribution models (SDMs) for cetaceans traditionally use occurrence data from scientific surveys. These surveys follow standardized protocols and provide spatially structured data, making them a reliable source of information on distributions. However, they are costly, and temporally limited, offering only a snapshot of distributions in time. Because cetaceans track changing oceanographic features, models built on survey data alone often lack temporal transferability. In contrast, commercial whale-watching (an opportunistic platform), generates occurrence data with high temporal resolution and near-daily sampling. These data are restricted to small coastal areas and subject to spatial bias yet remain informative through time. Given the complementary nature of these two data sources, we use an integrated species distribution modelling framework that combines survey and opportunistic data, leveraging their complementary strengths: broad spatial coverage structure from surveys, and fine-scale temporal resolution from citizen science. We implement the model using the Integrated Nested Laplace Approximation (INLA). Both sources are modelled as inhomogeneous Poisson point processes (IPPs) with a shared latent structure: a spatial random field (Matérn via SPDE) and flexible covariate responses as 1D SPDE smoothers. Simulations show that survey data primarily informs the spatial structure, whereas opportunistic data improves temporal predictions. We apply the approach to common dolphins (*Delphinus delphis*) in mainland Portuguese waters, combining line-transect surveys with whale-watching records, and obtain results consistent with simulations: improved estimation of dynamic effects and better temporal transferability. In data-sparse marine systems, this joint-likelihood, point process framework maximizes the utility of heterogeneous datasets, enhancing the robustness of ecological predictions.

3016. Ancient Beluga Genomes: Unraveling the Historical Biogeography of Arctic Marine Mammals

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The global environment has changed dramatically over the past few decades, especially in the Arctic, and Arctic sea ice is predicted to decline by up to 94% by 2050. By losing their

habitats, ice- associated marine mammals are highly vulnerable to changes in sea ice conditions. Historically, Arctic ecosystems have experienced dramatic shifts in sea levels and sea ice cover during the Late Quaternary. Yet, how climate change has affected Arctic marine mammals on a long-term scale is still not well understood. In this ongoing study, we employ whole-genome shotgun sequencing and mitogenome capture to recover genomic data from more than 50 ancient beluga whale (*Delphinapterus leucas*) specimens dating from the Late Pleistocene to Holocene. Most of the specimens are from far south of their contemporary distribution ranges, e.g., south Scandinavia and the ancient Champlain Sea, and thus they may represent lost populations. By integrating their genomic data with isotopic analyses, we aim to investigate how the diversity and distribution of the beluga whale populations have changed after the Holocene. This work provides one of the few ancient studies of the Arctic marine mammals, and may provide valuable insights for understanding how global warming and diminishing Arctic sea ice might impact future marine mammal conservation efforts.

3017. The impairment of juvenile survival under global warming in temperate oceans

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Temperate oceans are characterized by distinct intra-annual changes in environmental conditions (i.e. seasonality), wherein organisms synchronize the timing of distinct ontogenetic stages. Larval recruitment usually peaks in spring when water temperatures and food availability increase, and juveniles grow into adults under the more benign environmental summer conditions. Anthropogenic ocean warming may represent a bottleneck for the development of juveniles, as elevated summer temperatures could impair juvenile survival. We explore this process along a biogeographic gradient in the eastern Mediterranean Sea, which is experiencing high rates of temperature increase and has sectors where conditions already proved unsuitable for its native species. To quantify the potential juvenile mortality after summer heat peaks, we compiled a large dataset that captures both native and nonindigenous species abundance and richness in spring and fall (i.e. before and after summer heat peaks). Further, we targeted both fishes and molluscs to assess the difference between two major components of marine ecosystems. As per our expectation, locations along our gradient with higher summer temperatures had native molluscs less abundant in autumn, whereas nonindigenous molluscs were unaffected. Nonetheless, native molluscs displayed higher summer mortality in Northern Cyprus compared to Israel. Further, native fishes' abundance increased towards autumn compared to a decrease in native molluscs. Overall, our results suggest that the increasingly high summer temperatures will be a bottleneck for juvenile development of the poorly mobile molluscs; in contrast, mobile species like fishes probably have different coping mechanisms (e.g. seasonal migrations) that buffer against the impairment of juvenile survival.

3018. Exploring Marine Biogeographic Connectivity through New Deep-Water Corals in the Indian Ocean

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The Indian Ocean serves as a critical bridge between the Atlantic and Pacific Oceans in shaping marine species distributions. It is characterized by strong endemism in the shallow waters of the western Red Sea and Arabian region, while at its eastern edge it overlaps with the Coral Triangle, the global center of coral diversity. The principal pathway for water entering the Indian Ocean from the Pacific is the Indonesian Throughflow (ITF). Despite this biogeographic significance, most studies have focused on shallow-water reef fauna, whereas deep-water communities remain poorly known and largely undocumented. In 2022, the Ocean Census expedition to the Maldives employed ROV surveys and collected specimens from depths exceeding 100 m. This survey revealed several previously undocumented deep-water corals. Among them, the octocoral genus *Imbricacis*—a tree-like, sessile, azooxanthellate coral inhabiting depths of 80–500 m—was identified. Formerly included in *Paracis* (now *Neoacis* Matsumoto & Ofwegen, 2023), the genus *Imbricacis* has been represented in the Indian Ocean only by *Imbricacis foliata* Matsumoto & Ofwegen, 2023. Here, we report multiple new species of *Imbricacis* from the Maldives, expanding the known diversity of this genus in the Indian Ocean. These discoveries provide new insights into marine biogeographic connectivity, suggesting that the distribution of deep-water corals in the region has been shaped, at least in part, by Indo-Pacific faunal exchanges linked to the Coral Triangle and the pathways of the ITF.

3019. The historical biogeography of marine ray-finned fishes (Actinopterygii) in the Southwest Pacific: species richness and endemism patterns

André Philippe Samayoa, *Massey University; Libby Liggins, University of Auckland*

Understanding how biodiversity is generated and how it responded to past events is fundamental to infer how marine resources will respond to future changes. As the largest taxonomic group among marine vertebrates, ray-finned fishes (Actinopterygii) facilitate our understanding of biodiversity generation and the processes that shaped contemporary marine biogeographic patterns. In the Pacific Ocean, evidence shows that hotspots of marine fish richness and endemism do not overlap, where the former concentrate in the tropical western region, and the latter in peripheral oceanic islands. Although the evolutionary setting for marine fish endemism in parts of the Central Pacific has been described, processes that generate and maintain biodiversity in other peripheral regions remain unknown. The Southwest Pacific (20°S-55°S and 150°E-165°W) spans subtropical, temperate, and subantarctic climates, containing major landmasses such as eastern Australia and New Zealand, as well as oceanic islands. Due to this configuration, the unique regional

biogeographic patterns can improve our understanding of marine biodiversity evolution. In our recent work, we have reviewed the latest biogeographic investigations that examine the origin, evolution, and processes shaping patterns of marine fish richness and endemism in the Southwest Pacific. We propose a biogeographic scenario where the subtropical islands of the Southwest Pacific act as biodiversity cradles, with mainland Australia representing the main source of endemic lineages. Empirical data highlight the significance of both rare colonisation events and vicariance within formerly widely distributed lineages in shaping endemism patterns, and reveal that the processes shaping patterns of endemism and richness differ at local scales.

3020. The paleontological perspective of skeletal marine tropical fossil fishes throughout the Paleogene and Neogene of the Indo-West Pacific

Hadeel Hassen Saad, *University of Michigan; Matt Friedman, University of Michigan*

The Indo-West Pacific (IWP) region spans two-thirds of the equatorial globe, from the eastern coast of Africa to the islands of Polynesia and from the coasts of Japan to the southern tip of Africa. This biodiversity hotspot is currently home to over 6,000 species of fishes, but its current diversity is a snapshot of today's conditions. Species richness and locations of biodiversity hotspots are thought to have changed throughout geological time. The marine invertebrate fossil record suggests a transition from the West Tethys (modern-day Mediterranean Sea) in the Eocene to the Arabian Peninsula during the Oligocene and finally to the modern-day Indo-Australian Archipelago by the Miocene. The fish fossil record is particularly patchy, with the rich European record dominating past discussions. To date, there is no broad overview of the marine fish record of the IWP and adjacent areas, creating a major gap in our understanding of modern vertebrate biodiversity. Here, we review the fish skeletal record of this region from the Paleogene to the Neogene (~66–2.6 Ma), drawing on a combination of museum collections, published data, and new fossils to create a data set that includes over 30 localities and 400 specimens. Although the skeletal record is too patchily distributed to test the predictions of hotspot migration, we were able to quantitatively compare faunas to examine the relative paleoecology, paleogeographic, and stratigraphic controls on ancient fish communities in and around the IWP.

3021. Pleistocene legacy effects of past shallow-sea positions on current stony reef-coral diversity patterns

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Deglacial changes in shallow marine environments left a lasting imprint on the diversity of present-day marine biodiversity. This study analyzes the relationship between stony coral species diversity and current physical and chemical environmental factors, as well as changes in shallow-water areas from the Last Glacial period to the present across subtropical and tropical zones (30°S–30°N). We assessed variations at 1-degree grid-cell resolution using stacked-range maps and modeled paleo-shallow area changes (less than 40 meters in depth) based on 52 global raster datasets at 500-year intervals from 26 thousand years before present (kyr BP). The results reveal that shallow marine configurations shifted nonlinearly, reaching their maximum extent between 12 and 10 thousand years before present, and then contracting to their current levels. The highest shallow-marine area change rates occurred at 14 kyr BP and were controlled by the local rates of sea level rise. Today's shallow-water environment predominantly overlaps with those from up to 12 kyr BP. Importantly, shallow-water areas after 12 kyr BP exhibit a significant positive correlation with current coral diversity. The 11.5 kyr BP configuration emerges as the strongest predictor among all tested factors. In contrast, pre-12 kyr BP configurations demonstrate no link to the current shallow-water areas and less explanatory power. Understanding the marine species response to the spatiotemporal evolution of the shallow-marine environment is relevant in area-based conservation measures.

3022. How would estimation of geographic range shifts of marine fishes be different when using occurrence and abundance data?

Yin Zheng Lai; Chia-Ying Ko; Ying-Chung Jimmy Lin, all at National Taiwan University

Climate change is reshaping global marine ecosystems, with range shifts of fishes representing one of the most direct ecological responses. While most studies rely on occurrence data to infer species distributions, recent evidence suggests that occurrence-only approaches may underestimate or misrepresent distributional changes, highlighting the importance of abundance data. Yet, systematic comparisons of these two data types across long timescales and major ecosystems remain scarce. In this study, we evaluated whether occurrence versus abundance data yield divergent predictions of fish range shifts. Using bottom-trawl surveys since 1968, we estimated annual species range centroids from both data types and applied linear regressions to detect temporal trends in latitude and longitude, classifying shifts into four directional categories. Across three ecosystems—the Northeast

US Continental Shelf, North Sea, and East Bering Sea—between 38.5% and 45.9% of species showed inconsistent movement directions depending on the data type used. Notably, many of these inconsistently shifting species were of high commercial value. Our results demonstrate that projections of fish distributions, particularly for economically important species, are highly sensitive to data choice. Misinterpretation of distributional trends risks misguided management and underestimation of climate threats. We recommend systematically incorporating abundance data into biogeographic analyses and resource assessments to strengthen the scientific foundation for biodiversity conservation, fisheries management, and climate adaptation strategies. More broadly, enhancing data quality and integrating multiple data streams are critical for improving monitoring and prediction of marine ecosystem responses under accelerating global change.

3023. Behavioural Bias in Global Biodiversity Records: Sociality and Detectability in Reef Fishes

Victoria Marchment, *Lancaster University, UK*

Macrobehaviour, the study of behavioural traits at broad spatial and taxonomic scales, offers new opportunities to link animal behaviour with ecological and evolutionary processes. However, it remains unclear whether species' behaviour influences how they are represented in biodiversity databases such as the Ocean Biodiversity Information System (OBIS). In this study, I will test whether sociality, measured as schooling behaviour, affects patterns of reef fish occurrence in OBIS. Using a trait-matched dataset of over 6,000 reef-associated species, I will map the global distribution of sociality, identify latitudinal trends, and examine variation among families. I will also compare geographic patterns of behavioural knowledge with observation density, assessing where gaps in sociality data coincide with high or low sampling effort. Finally, I will evaluate whether schooling rank predicts observation frequency, alongside other ecological and life-history traits. By situating reef fish sociality within a macroecological framework, this project will map large-scale patterns of behaviour in marine systems and test how sociality relates to data coverage and detectability. In doing so, it will extend the scope of macrobehavioural research to the ocean, provide new insights into the geography of behavioural knowledge, and highlight the opportunities and limitations of using biodiversity databases to study behaviour at scale.

3024. Environment and spatial constraints shape riverine fish biodiversity

Ana Berenice Garcia-Andrade, *CASUS/HZDR; Justin M. Calabrese, CASUS/HZDR*

Biodiversity patterns, including species richness and beta diversity, are shaped by the structural connectivity of the habitat and environmental conditions. In river systems, the dendritic structure of networks makes connectivity a fundamental regulator of biodiversity

through dispersal processes. However, studies combining network structure and environmental factors have returned conflicting and context-dependent results. This lack of clarity underscores the need for large-scale comparative analyses across rivers with diverse features. Here, we evaluated the effect of river network connectivity and environmental factors on fish biodiversity patterns across rivers spanning broad environmental and spatial gradients. Using a comprehensive dataset and applying a cross-landscape approach, we quantified both local species richness and beta diversity across the 81 largest rivers worldwide, which collectively represent 8,815 fish species. To determine the drivers of diversity patterns, we evaluated two groups of predictors: river network connectivity and environmental factors, and used variance partitioning analyses to quantify the variance explained by each group. Then, to determine if the explanatory power of predictors varied with the river features, generalized linear models were fitted. Our results show that environmental factors predominated in explaining both richness and beta diversity, while network connectivity played a secondary role. Also, weak or non-significant trends emerged between the variance explained by each group of predictors and environmental or spatial gradients. Overall, our results indicate that riverine biodiversity is mainly determined by environmental filtering rather than dispersal processes, but without consistent shifts across ecological or spatial gradients.

3025. River Network Topography Shapes Intra- and Interspecific Diversity of Freshwater Fish in Northern Taiwan: Insights from eDNA Metabarcoding

Carolin Krug, *ETH Zürich; Ing Chen, National Taiwan Normal University; Loïc Pellissier, WSL; Sean Willett, ETH Zurich*

Mountain regions are globally recognized as biodiversity hotspots. However, the links between mountain-building processes and the emergence of biodiversity remain underexplored. During orogeny, tectonic uplift and deformation, as well as surface erosion, act on the landscape, generating dynamic, transient landscapes with reorganizing drainage networks and changing topography. Because aquatic habitats are tightly coupled with river topography, freshwater species are particularly insightful to study how landscape evolution influences biodiversity.

In this study, we investigated freshwater fish diversity in northern Taiwan, a tectonically active hotspot with high island endemism. Our study area spans both sides of two hypothesized dispersal barriers—the main drainage divide and the Qing-Shui Cliff, a coastal highland—as well as the highly dynamic Lanyang River basin, which is forming along a young, active fault. We collected environmental DNA (eDNA) from 22 riverine sites across the study area. We amplified a 420 bp fragment of the cytochrome B (cytB) gene, and denoised the sequences to retrieve amplicon sequence variants (ASVs). We then examined variation in assemblage composition and phylogenetic turnover among sites (interspecific), as well as genetic differentiation within selected species (intraspecific). Our results reveal clear geographic

patterns, indicating the existence of geographic barriers to gene flow, as well as identifying water divides that allow gene flow. These biogeographic patterns can be further tested for correspondence with geomorphic metrics that capture drainage divide stability, highlighting how tectonic processes and river network reorganization shape biodiversity at both inter- and intraspecific levels.

3026. Effects of the above- and below-ground life history strategy on ecosystem functions in Yellow River Delta

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Environmental stress reshapes the relationships between biodiversity and multiple ecosystem functions. However, the specific contributions of both above-ground and below-ground biodiversity to ecosystem multifunctionality under natural environmental stresses remain poorly understood. To address it, we employed extensive sampling, metagenomic barcoding, and trait dimension partitioning to assess the biodiversity and life history strategies of plant, fungal, and bacterial communities, and their relationships with ecosystem multifunctionality along a natural stress gradient. In stressful environments, plant diversity was negatively correlated with ecosystem multifunctionality, potentially due to diminish both the light complementarity and the relative abundance of functional species as plant diversity increases. However, environmental stress inhibited positive relationships between soil bacterial diversity and ecosystem multifunctionality, potentially by reducing network complexity and increasing the importance of low-functioning keystone species in the networks. Furthermore, both plant and microbial communities shifted towards stress-tolerant strategies, moving away from fast-growing competitors under heightened stress. Environmental stress also weakened the correlation between taxonomic composition and ecosystem functioning composition, while strengthening the correlation between ecological strategies and ecosystem functioning composition. Our findings reveal the critical role of community functional composition, particularly shifts in life history strategies, as a reliable and complementary predictor to predict changes in ecosystem functions under stress.

Avian Biogeography

3027. Spatial scale shapes the effects of intraspecific trait variation on Avian functional diversity

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Intraspecific trait variation (ITV) is recognized as an important facet of functional ecology, with emerging evidence suggesting that ITV can significantly alter measurements of functional diversity. This evidence remains fragmented across taxa and contexts, leaving

major gaps in our understanding of the circumstances under which ITV meaningfully shapes ecological patterns. Incorporating ITV into functional diversity studies requires significant time and resources, yet there is no clear guidance on where such investment is warranted, perpetuating these gaps. Spatial scale is likely one of the most critical but least resolved factors mediating ITV's effects, highlighting the need for systematic investigation of how spatial scale affects the contribution of ITV to functional diversity. We take a simulation approach to explore how spatial grain (resolution) influences the effect of ITV on a core set of functional diversity metrics (richness, evenness, divergence). Using distributional data from eBird Status and Trends, we simulate populations of 588 bird species across the contiguous United States. We aggregate populations into communities of different sizes by progressively coarsening spatial grains from 3x3km cells to a single country-wide community. Morphological trait measurements are assigned either at the species level (excluding ITV) or the individual level (including ITV), and functional diversity metrics are calculated separately for each grain. Finally, we assess how ITV alters functional diversity metrics in each context. Preliminary results indicate that ITV's effect size is trait-specific but generally greater at intermediate grains, reflecting a scale- and trait-dependent relationship between ITV and other sources of trait variation (e.g., species turnover).

3028. Trait-mediated responses of Danish bird communities to five decades of global change

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Avian communities in Denmark have undergone substantial turnover over the past five decades, with species differing in migratory strategy and ecology showing markedly different trends. Long-distance migrants have declined significantly in their distributions, while insectivorous and granivorous species show similar downward trends in population size. These patterns suggest a specific influence of the environment these species are exposed to, yet the interaction between species traits and the environment remains putative. I investigate the processes shaping avian community assembly across Denmark over five decades, using comprehensive bird atlas data from 1971–1974, 1993–1996, and 2014–2017. These datasets provide high-resolution, nationwide coverage of breeding bird distributions at a 5×5 km scale, with consistent survey methodologies through time. I apply a spatiotemporally explicit joint species distribution modelling framework that quantifies the roles of environmental covariates and species characteristics in shaping community composition. Focusing on approximately 200 Danish breeding bird species, I assess how seasonal climate variables and aggregated land-use metrics influence avian communities. I group species by their migratory strategy and dietary habits enabling identification of trait-mediated responses to environmental change. This approach provides insight into whether specific taxa or ecological types exhibit consistent responses, and to what extent they interact with global

change drivers to restructure avian communities. The integration of rich, historical occurrence data, trait information, and robust statistical tools offers an insight into the processes underlying biodiversity change in Denmark and contributes to broader efforts in forecasting and managing biodiversity under global change.

3029. Effectiveness of agri-environment measures in enhancing farmland bird diversity

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Global biodiversity loss is one of the main challenges of the 21st century. Farmland birds are among the most rapidly declining species, with their loss leading to reduced ecosystem services and negative consequences for humans. A major driver of their decline is agricultural intensification. To address the intensification, the EU Biodiversity Strategy for 2030 proposes increasing space for nature within agricultural landscapes. In this study, we use farmland birds as indicator species to evaluate the effectiveness of current Biodiversity Strategy 2030 and Common Agricultural Policy targets. To quantify how land cover and land use practices affect bird occurrence, we applied a nested species distribution model (SDM) approach that accounts for environmental drivers acting at different spatial scales while avoiding niche truncation. At the European scale, we modeled species distributions based on climate variables and at the finer German scale, we incorporated climate suitability, land use, soil moisture, mowing intensity, and topographic data. The resulting models allow assessing preference and avoidance patterns of farmland birds in relation to different land uses. We further simulated policy scenarios to assess their impact on habitat suitability for farmland birds, identifying potential trade-offs between species and measures. These insights can inform both policy and agricultural practice, supporting more targeted, region-specific agri-environmental measures.

3030. Most solar photovoltaic facilities are affecting highly favourable areas for threatened steppe birds in Andalusia (S Spain)

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We analysed the distribution during the 21st century of three steppe bird species in Andalusia: the Great Bustard *Otis tarda*, the Little Bustard *Tetrax tetrax* and Montagu's Harrier *Circus pygargus*. These species are threatened by the loss and fragmentation of their

habitat due to the expansion of human infrastructures, including solar photovoltaic facilities. In the last two decades, the energy transition towards non-fossil sources, particularly solar and wind, has intensified in Spain to reduce greenhouse gas emissions. Andalusia, due to its topographical and climatic conditions, is presented as a strategic area for the expansion of solar plants, with a remarkable projected increase in the area allocated to this industry. We analysed census data from the last two decades to determine to what degree the favourable areas for these species are affected by photovoltaic facilities and to assess the possible impact of the installation of solar panels on their distribution. Resulting favourability maps reveal that more than half the surface area covered by photovoltaic facilities up to 2020 are affecting highly favourable areas for any of these species. This highlights the need to apply strategic planning in the expansion of solar photovoltaic facilities to reconcile biodiversity conservation with energy transition in areas of high ecological sensitivity.

3031. Reconstructing the species tree in the face of incomplete lineage sorting and gene flow in three clades within the Avian family Paridae

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Phylogenetic conflict among gene trees is frequently attributed to incomplete lineage sorting (ILS), which is further exacerbated by interspecific gene flow. Although genomic data can effectively take into account the impact of ILS, the phylogenetic topology inferred from genome-wide data may not necessarily represent the species tree topology (species branching order) due to gene flow. Here, we investigated the phylogenetic relationships within three clades comprising a total of 13 species in the songbird family Paridae (tits) using one de novo genome assembly and 82 re-sequenced genomes. Despite the influences of gene flow and ILS, the most frequent gene tree topology that emerged on autosomes for all three clades was identical to the most likely species tree topology. However, due to gene flow, the species tree reconstructed from genome-wide loci using multi-species coalescent methods inaccurately reflected the most likely species tree topology for one clade. Gene trees topologically concordant with the most likely species tree were significantly enriched on large chromosomes, the Z chromosome, and genomic regions with low recombination rates, nucleotide diversity, and GC content in one of the clades. However, in another clade, this enrichment effect was observed only in a subset of these genomic regions, and in the third clade, no such enrichment was observed. These results highlight the confounding effects of large chromosomes, sex chromosomes, recombination rates, nucleotide diversity and GC content on species tree prediction in the face of ILS and gene flow.

Theoretical and practical approaches to species range dynamics

4000. Abiotic factors shape plants' co-occurrences network: methodological perspectives

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Co-occurrence affinity refers to the non-random association of plant species within ecological communities. It's well-known that certain species coexist spatially or temporally more frequently than expected by chance. This phenomenon can manifest across various spatial scales, from local habitats to global biomes encompassing a multitude of ecological interactions. Co-occurrence affinity emerges as a key principle, shedding light on the underlying mechanisms driving community assembly over space and time. This intricate interplay of species associations is essential to understanding community structure over space and time. We propose a new method to investigate how plant species co-occurrence affinity is shaped by abiotic factors. To test this method, we used the European Vegetation Archive database of plant-community data, and we calculated all the existing combinations among pairs of species (more than 4,500,000). Then, all the plots (about 1 million) were associated with a specific abiotic condition (in this case, we used only climatic variables) and grouped by similarity, thus creating a climatic grid where plots belong to specific climatic cells. After that, for each pair, we calculated different indices (e.g. Jaccard) to quantify co-occurrence affinity in each climatic cell. Then, the obtained co-occurrence affinity for each pair was modelled as a function of climatic conditions using a GLM to assess how climate shapes co-occurrence affinity. This approach opens new opportunities to study the effect of abiotic factors in shaping association, facilitation and competition among species and to provide an innovative and reproducible workflow to investigate mechanisms of underlying community assembly.

4001. Quantifying niche overlap and transgression in allopolyploid hybrids: Case study of Sorbus subgenus Aria

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Seed reproduction without recombination (apomixis) in combination with hybrid speciation is increasingly recognized as a developmental trait rather than an evolutionary dead end. In this study, we investigate whether apomicts of the genus *Sorbus* can conserve adaptations at the edges of parental capabilities. To analyze niche differences among apomictic entities of hybrid origin, we examined *Sorbus* subgenus *Aria* in the Franconian Jura. We calculated two-dimensional hypervolumes to infer the niche space of triploid entities and their di- and tetraploid parents, *Sorbus aria* and *S. collina*. For the analysis of niche overlaps, we used four

environmental variables with the highest importance in PCA analyses to construct two-dimensional hypervolumes. Across a total of 762 occurrences, observation numbers per entity ranged from 11 to 452 individual trees. Hypervolume differences were significant between nearly all triploid entities and single genotypes and their parental taxa. However, the environmental niche space of triploid entities did not significantly drift toward the margins of the parental hypervolumes. Niche space extending beyond the parental ranges accounted for 5–21% among the triploid entities. Niche transgression exceeding 10% was detected in four entities, yet most observations still fell within the 95% confidence interval derived from random sampling within the parental populations. Although variation in adaptive strategies among the polyploid entities may exist, it could not be detected using weather data (1×1 km resolution) combined with fine-scale topographic indices.

4002. Latitudinal Patterns in Seed Defences and Nutrition

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Seed defences and nutrition are critical for plant regeneration, influencing the interactions between plant species and their mutualists (seed dispersers) and antagonists (seed predators). It is hypothesised that seed defences and nutrition may be shaped by latitudinal gradients in biotic interactions, yet empirical evidence remains scarce and large-scale patterns of related seed traits are still poorly understood. Here, we collected seeds for 268 dominant woody species across 31 natural forest communities in China (18.68°N–52.36°N), encompassing 453 unique species-site combinations. We measured ten traits related to seed defences and nutrition, and applied Bayesian phylogenetic multilevel models to quantify latitudinal patterns in these traits. We found that seed defences showed a decreasing tendency towards higher latitudes, consistent with the hypothesised weaker seed predation in temperate regions. Seed nutritional contents (e.g. soluble sugars, starch, proteins) tend to increase with latitude, likely reflecting adaptations to harsher environments and resource limitations. Our findings demonstrate contrasting latitudinal patterns in seed defences and nutrition, suggesting the essential roles of both biotic interactions and environmental conditions. These results advance our understanding of how key plant functional traits related to biotic interactions evolve in response to biogeographic gradients, offering critical insights for predicting plant community dynamics under global changes.

4003. Geometric causes of species rarity

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Geographic range size is a key species attribute, closely tied to extinction risk and biodiversity patterns. While variation in range size has often been attributed to ecological traits, environmental gradients, or historical biogeography, the fundamental role of spatial geometry remains underexplored. We present a spatially explicit geometric null model that predicts both observed geographical patterns and the characteristic right-skewed frequency distribution of range sizes, without invoking ecological or evolutionary processes or preassigned range parameters. The model depends on a single parameter, the density of inner barriers that delineate species' distributions, and is implemented on a real spherical world and continental boundaries. Analytical and simulation results show that smaller ranges occur along continental margins and massifs, and that most species occupy small ranges, simply as a geometric consequence of random barrier placement and their relative position with external boundaries. These findings highlight the ability of geometry alone to generate large-scale macroecological patterns and provide a rigorous null baseline against which ecological and evolutionary explanations must be evaluated.

4004. One metric to rule them all? A global assessment of the importance of shape complexity for the environmental heterogeneity of protected areas

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Protected areas (PAs) are often designed as single, large, and compact patches, with area as a fundamental attribute. While the importance of area is strongly supported by the species-area relationship, much less is known about other geometric attributes. For instance, based on the distance-decay of similarity, PAs composed of multiple, dispersed, non-circular patches could encompass a broader range of habitats. From a spatial-geometry perspective, in addition to location and size, shape is a fundamental property that could be adjusted to enhance nature protection.

Here we evaluated how geometric attributes of PAs—specifically area, shape (e.g., fractal dimension, elongation), fragmentation (polygon count), and northerness alignment— and their interactions affect environmental heterogeneity, a key proxy for biodiversity. We analyzed 108,957 terrestrial PAs from the World Database of Protected Areas using Random

Forest, with heterogeneity quantified through the coefficient of variation of NDVI and elevation, and the indices Shannon, Simpson evenness and number of classes representing diversity of climate and landcover.

Area ranked consistently among the top predictors of environmental heterogeneity. However, shape descriptors such as fractal dimension also contribute meaningfully, while circularity, northernness, elongation, and fragmentation have weaker effects. Furthermore, the importance of size and shape depended on the geographic location. Our findings highlight the generally overlooked roles of shape in contributing to environmental heterogeneity within PAs. By complementing the role of area considering the shape and spatial configuration, conservation strategies could be refined to maximise habitat heterogeneity, potentially supporting greater species diversity.

4005. Compiling data on contemporary biodiversity change at meso-scales

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We need to know how much, where, and why has biodiversity been changing. However, assessments of biodiversity change during the past decades focus on spatially disconnected local assemblages, or on global extinctions. We lack data on biodiversity dynamics at biogeographic extents and intermediate spatial resolutions, i.e. the “meso” scales (1x1km-100x100km). Here, we introduce two projects in which we have been compiling such data: 1. National species loss data - the RegRed project (https://preprints.arphahub.com/article/160483/). Countries publish assessments called national red lists, which contain data on species threats and extirpations. In RegRed we are building an open database of these red lists. We have identified 2,093 regional red lists from 170 countries and 483 taxonomic groups. We are digitising these data using a semi-automated workflow, including large language models. RegRed expands on the existing National Red List database by ZSL (https://www.nationalredlist.org/), in collaboration with its authors. RegRed will create a standardised and open database which can be used in global conservation and in studies of biodiversity dynamics. We are looking for collaborators! 2. Temporally replicated gridded atlases. Some countries have produced atlases, where distribution of every species was systematically surveyed over a continuous grid over multiple time periods. These are valuable presence-absence meso-scale data. We have built a spatial database of about a dozen of these (11,360,339 records), and we have been using them to address key questions concerning contemporary dynamics of species distributions and biodiversity.

4006. Recasting the Heterogeneity-Diversity Relationship: A Trade-Off Triad with Applications to the Geodiversity-Biodiversity Relationship

Kyle Reilly Turchick, *Cornell University; Steven M. Grodsky, Cornell University*

Spatial environmental heterogeneity is a fundamental driver of biodiversity, yet more heterogeneity does not inevitably support more species because of the area-heterogeneity trade-off (AHTO). The AHTO bridges niche and island biogeography theory by positing that niche gains from added heterogeneity are constrained when partitioning a fixed area reduces habitat area available per niche, elevating extirpation risk. We recast the heterogeneity-diversity relationship (HDR) as having three meaningful AHTO trajectories across a previously identified spectrum of possibilities, delineating the weak trade-off (monotonically increasing), moderate trade-off (increasing then plateauing), and strong trade-off (unimodal, hump-shaped) – each with distinct implications when heterogeneity is high. We then identify mediating factors that shift systems among these forms and provide a diagnostic workflow that pits models against one another to classify curve shape. In an illustrative reanalysis, we show richness climbed and plateaued with heterogeneity at fine spatial scales (moderate AHTO) but peaked and declined at the broadest scale (strong AHTO). Finally, knowledge gaps are outlined, and future directions are suggested. For example, we point out that the geodiversity-biodiversity relationship (GBR) is a domain specific instance of the HDR and must be interpreted through the AHTO triad lens. Our ongoing work refines and unifies the HDR, AHTO, and GBR across spatial scales, trophic levels, and disturbance agents. Our empirical tests include multitrophic analyses linking >40,000 vegetation-soil plots with continental bird richness across seven nested spatial tiers, and a comparison of solar facility and debris flow chronosequences to quantify how mediators shift the HDR form and identify thresholds.

4007. Comparing landscape heterogeneity metrics for explaining biodiversity variation in space and time

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Landscape heterogeneity (LH), which describes the diversity and spatial arrangement of land cover, influences species diversity via controlling ecological processes such as movement, predation, pollination, or pest control. Interest in LH has been growing over the last decades, and a wide range of metrics has been developed to quantify LH. However, the effectiveness of these metrics for explaining biodiversity variation in space and time remains unclear. In this study, we aim to quantify LH using spaceborne remote sensing data across the German federal state of Bavaria. Furthermore, we aim to compare the effectiveness of different LH metrics for explaining insect biodiversity trends. To quantify LH, we will use two data sources:

(1) ready-to-use land cover classification maps, like CORINE, and (2) classifications of satellite imagery, to achieve a tighter temporal coverage. To avoid categorization through human interpretation, also raw spectral indices like the Normalized Difference Vegetation Index (NDVI) will be used. To compare LH changes at different geographical scales and assess how it has changed over time, we will calculate LH over multiple spatial and temporal scales. To assess the practical applicability of the previously developed methods and data, we then apply them to a long-term monitoring dataset of insect biodiversity. We hypothesize that LH is positively correlated with insect occupancy trends, i.e. we expect more stable or increasing trends in areas of higher LH. By improving our understanding of the influence of LH on biodiversity, this research may support the development of informed conservation and land management strategies.

4008. Monitoring in Focus: Using Citizen Science and State-Owned Data to Enhance Interpretation and Close Gaps

Christian Zehner, *Global Change Ecology, University of Wuerzburg; Eva Katharina Engelhardt, Julius-Maximilians-Universität Würzburg; Christian Hof, Global Change Ecology, University of Würzburg*

Monitoring programs covering large spatial and temporal scales provide valuable data on species occurrences. However, designing and implementing such programs is resource-intensive, and historical data cannot be retroactively collected once a reliable and structured monitoring program is initiated. Citizen science initiatives, in particular, can yield large-scale data across space and time, offering unique insights into species occurrences. These data are not without shortcomings: observations tend to cluster in areas where people live or travel and focus on species of conservation concern. While statistical methods can correct some biases, understanding data quality and coverage remains critical for robust results. In this study, we analyse insect occurrence records collected over several decades in a typical Central European region, based on a state-owned dataset and publicly available citizen science data. We investigate observation behaviour to identify spatial and temporal hotspots and their predictors. Guided by the gaps left by citizen observations, professionals could be strategically deployed in a resource-efficient way to undersampled regions or time periods. Our results indicate that occurrences of conservation-related species have a stronger impact than human population density. In highly populated areas, citizen science provides the majority of records, whereas in rural areas, state data becomes more relevant. For long-term trend analyses, state databases remain most important, while citizen science contributes additional value due to the recent increase in records. This assessment of monitoring efforts can offer valuable guidance for optimising current and future biodiversity monitoring in a resource-efficient manner.

4009. Trees in the Eastern U.S. are even more dispersal-limited than previously feared: A field study and modeling analysis

Aryan Jakhar, *Brown University; Dov Sax, Brown University*

Despite pronounced regional warming, range boundaries of Eastern U.S. tree species have largely been reported to be stationary. Previous large-scale studies, utilizing forest-inventory datasets, have not provided the detail needed to fully evaluate the dispersal limitation of trees. Here we use a novel approach to estimate spread rates in the field and pair this with species-specific models of dispersal capacity. Our field work leveraged naturalized populations of 8 tree species that have escaped from horticulture northwards of their native ranges. At 40 such sites, we measured the spatial extent of the population and cored the largest trees to determine its age of establishment, allowing us to estimate the spread rate. We found that the mean spread rate, across all sites and species is only 0.33km/century (max = 2.3km/century). Our species-specific models of potential range shifts, which included factors like key dispersal agents and age of first reproduction, indicated that by the end of century, only 1 of 8 modeled species has any possibility of tracking climate change. Finally, to validate these models, we examined a group of 'control' species that are not commonly sold in horticulture and found that they rarely, if ever, naturalize polewards of the native range, suggesting that LDD events are not being realized either. Our work suggests that tree species are primarily shifting northwards through a slow process of diffusion, rather than through LDD events, with range-shift velocities of less than 1% of the pace of climate change in portions of the Eastern U.S.

4010. A methodology for explicitly accounting for temporally dynamic landscapes when training niche models

Connor Hughes, *Virginia Polytechnic Institute and State University; Luis E Escobar, Virginia Tech*

The fields of ecological niche modeling and species distribution modeling are rapidly evolving, yet one area which has received relatively little attention is the temporally dynamic environment. Species occurrence data used to train niche and distribution models are typically collected over many years or decades. During that time frame, the environmental conditions of a region may change, either due to natural processes or stochastic events (as with forest succession or hurricane damage), or anthropogenic influence (as with urban development and other land use changes). Despite this, during model training many niche modeling practices consider only a snapshot of modern-day environmental conditions, potentially misrepresenting suitable conditions for the species. We present a workflow for temporally explicit niche modeling practices, which account for this changing environment in their training data. Additionally, explicitly considering the temporal environment when modeling allows for year-specific estimates of habitat suitability in geographic space,

allowing for an exploration of where and when habitat is lost, gained, and where stable patches occur.

4011. The influence of range properties on regional patterns of alpha and beta diversity

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The complex interplay of eco-evolutionary processes in relatively small areas makes the world's mountains key to understanding the origins and maintenance of biodiversity. Assessing the drivers of montane diversity can be difficult, given that each region often has its own unique evolutionary trajectory. Using the framework of geometric models, which show that the distribution of geographic ranges in a bounded domain can yield surprisingly diverse richness patterns, we offer a fresh perspective to assessing regional montane endemic diversity. With the Western Ghats as a study system, we model alpha and beta diversity patterns by spreading and overlaying ranges of varying size and continuity within an environmentally heterogenous gridded domain. We compare our predictions to empirical estimates from comprehensive primary occurrence data for endemic frogs, birds and woody plants. The model results show that diversity patterns can differ between clades with different range properties, even if they respond similarly to the environment. This is exemplified by our three study taxa, which despite being primarily adapted to wet evergreen forests, vary in range size and continuity, presumably due to differences in dispersal ability. Our study highlights the influence of range attributes – the outcome of historical niche-dispersal dynamics of a taxon within a landscape – on contemporary regional diversity patterns. It also offers a template for assessing such patterns in other hotspots where fine-scale data is available.

4012. Modeling boreal forest understory vegetation change and drivers across latitude

Sarah Rettie Naughtin, *University of British Columbia; Isla Myers-Smith, University of British Columbia*

Shrub species are rapidly expanding across high-latitude ecosystems, but while Arctic shrubification has been widely documented, the dynamics of understory shrub vegetation within the North American boreal forest remain understudied. This knowledge gap is particularly pronounced in the Yukon Territory, a climatically diverse region spanning from dense boreal forest to open tundra. In the context of accelerating climate change, understanding the controls on boreal shrub distribution is critical for predicting future

vegetation patterns and associated ecosystem impacts. This research will use species distribution models (SDMs) to investigate the spatial drivers of 17 dominant shrub species across a latitudinal gradient in the Yukon. Based on an extensive 2025 summer field season across 50 sites—from Asì Keyi to Ddhäl Ch'èl Cha Nän—I will integrate presence/absence observations with high-resolution moisture and canopy data, alongside global biodiversity and climate datasets. A combination of modeling approaches will be used to evaluate the relative influence of temperature, moisture, and disturbance on shrub habitat suitability. Future projections under climate change scenarios will test whether moisture availability acts as a critical constraint on northward and upslope expansion. By focusing on the understory vegetation of boreal forests—an often overlooked yet ecologically essential component—this study addresses a pressing biogeographic blind spot. The findings will inform predictions of vegetation change and contribute to a more complete understanding of boreal ecosystem responses in a warming world.

4013. When Data Are Scarce and Ranges Are Small: Modelling Trade-offs in Fine-Scale Insular Species

Eva Benavides Rios, *Anglia Ruskin University, United Kingdom*

Fitting Species Distribution Models (SDMs) for range-restricted species presents unique challenges, as occurrence data are often limited and spatially imprecise. These issues are especially pronounced in island ecosystems, which host many geographically rare species of conservation concern. Fine-resolution environmental variables may better capture the ecological scales at which range-restricted species respond to environmental heterogeneity, but their use requires careful consideration. We identify three key challenges. 1)Finer-resolution grids capture more specific environmental variation but reduce the likelihood that small datasets represent the full range of suitable conditions, making minimum sample size critical. 2)Occurrence precision must align with predictor resolution. Excluding imprecise records reduces sample size and model performance, while including them risks introducing noise, particularly on islands where sharp gradients and narrow habitat preferences increase mismatches. 3)Because presence-only records are often the only available data, selecting modelling approaches and pseudo-absence or background (PsA/BG) strategies suited to restricted ranges is essential. Current guidelines, developed mainly for wide-ranging species, rarely accommodate narrow ranges and can bias validation metrics. To explore these issues, we combined simulated data with high-quality empirical records from insular plant species. We systematically varied sample size, spatial accuracy, range size, and PsA/BG ratios to assess potentially suitable modelling approaches. Despite sparse and uncertain data, reliable predictions were achievable. Smaller-ranged species required relatively more occurrences, and some methods tolerated spatial imprecision when larger datasets were retained, showing that over-cleaning can be detrimental. Optimising PsA/BG sampling further

improved performance and validation. Findings are broadly relevant to other restricted-range cases requiring accurate high-resolution predictions.

4014. Modelling species distribution at the boundaries of the Earth's climate

Chiara Serafini, *La Sapienza University of Rome; Francesca Cosentino, University of Rome; Giovanni Amori, National Research Council (CNR); Luigi Maiorano, Department of Biology and Biotechnologies "Charles Darwin*"

Correlative species distribution models (SDMs) are widely used to project species' responses to global changes. The climatic niche of a species is calibrated under current climate conditions and then projected in space and/or time, making model extrapolation an important concern. This issue is particularly relevant when considering species that live simultaneously at the boundaries of the current Earth's climate and at the edges of their physiological tolerance, such as desert-adapted species. Modelling approaches alternatives to SDMs have been proposed as a better solution to tackle extrapolation. These models should explicitly consider the species' thermal tolerance, producing outputs closer to the species' ecology. We compared correlative SDMs with different extrapolation options and hybrid SDMs incorporating thermal tolerances of mammals of the Arabian Peninsula. We projected all models under current and future climate scenarios and measured the differences between the outcomes. We found important differences between model outcomes at least in future projections, especially for species physiologically adapted to the extreme climate conditions of the desert. Correlative SDMs not allowing for extrapolation led to more conservative projections, while SDMs allowing for extrapolation were more flexible. Hybrid SDMs produced intermediate results, with up to 93% of the species losing parts of their suitable ranges under future climate scenarios. Our findings highlight that correlative SDMs cannot track the true thermal tolerances of desert species. Hybrid SDMs hold the premise for a better understanding of the impact of global changes on such species, turning on a spotlight on a neglected but endangered component of biodiversity.

4015. CISO: Species Distribution Modeling Conditioned on Incomplete Species Observations

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Species distribution models (SDMs) are widely used to predict species' geographic distributions, serving as critical tools for ecological research and conservation planning.

Typically, SDMs relate species occurrences to environmental variables representing abiotic factors, such as temperature, precipitation, and soil properties. However, species distributions are also strongly influenced by biotic interactions with other species, which are often overlooked. While some methods partially address this limitation by incorporating biotic interactions, they often assume symmetrical pairwise relationships between species and require consistent co-occurrence data. In practice, species observations are sparse, and the availability of information about the presence or absence of other species varies significantly across locations. To address these challenges, we propose CISO, a deep learning-based method for species distribution modeling conditioned on incomplete species observations. CISO enables predictions to be conditioned on a flexible number of species observations alongside environmental variables, accommodating the variability and incompleteness of available biotic data. We demonstrate our approach using three datasets representing different species groups: sPlotOpen for plants, SatBird for birds, and a new dataset, SatButterfly, for butterflies. Our results show that including partial biotic information improves predictive performance on spatially separate test sets. When conditioned on a subset of species within the same dataset, CISO outperforms alternative methods in predicting the distribution of the remaining species. Furthermore, we show that combining observations from multiple datasets can improve performance. CISO is a promising ecological tool, capable of incorporating incomplete biotic information and identifying potential interactions between species from disparate taxa.

4016. Beyond static SDMs: A dynamic and nested framework for transferable distribution modelling

Camila Rocabado, *University of Aberdeen; Roslyn Henry, University of Aberdeen; Greta Bocedi, University of Aberdeen*

Species distribution models (SDMs) are widely used to assess biodiversity responses to environmental change, yet they remain limited by two issues. First, short- to medium-lived species respond rapidly to environmental change, making dynamic temporal matching critical to capture these responses. When static predictors are used instead, a temporal mismatch can arise—for example, when land-use transformations occur but models rely on outdated or averaged snapshots. Second, niche truncation occurs when regional models represent only a subset of the species' climatic space. Together, these can bias predictions and reduce model transferability. We present a dynamic and nested (DN) SDM pipeline designed to address both challenges. The framework is dynamic, with occurrences and predictors matched year by year, generating suitability layers from 1990 to the present and into future scenarios. It is also nested, with European-scale climatic SDMs incorporated as covariates in Denmark-focused models that integrate high-resolution land-use variables. We benchmark and compare this modelling strategy to static-regional (SR), static-nested (SN) and dynamic-regional (DR) using spatial block cross-validation, temporal holdouts, climatic-

space coverage and measures of temporal smoothness. A key strength of dynamic models is that they yield yearly, continuous layers of habitat suitability. These can be directly coupled with mechanistic models, which can benefit from inputs that evolve with habitat conditions rather than static snapshots. Although demonstrated on Danish butterflies, this framework advances SDM methodology towards more ecologically realistic and transferable biodiversity forecasts and provides a reproducible template for integrating multiscale climate information with land-use change.

4017. From Climate to Croplands: Dynamic and Nested Species Distribution Models Reveal Butterfly Responses to global changes

Camila Rocabado, *University of Aberdeen; Roslyn Henry, University of Aberdeen; Greta Bocedi, University of Aberdeen*

Insects are declining globally due to agricultural intensification and climate change. To address how these pressures shape butterfly distributions, we have developed a modelling framework that integrates climate- and land-use–driven scenarios. We applied a dynamic and nested species distribution modelling (SDM) pipeline to 30 Danish butterfly species with varying degrees of habitat specialization, diet breadth and dispersal ability. The approach combines global-scale climate SDMs with high-resolution, temporally matched land-use data for Denmark, producing habitat suitability maps from 1990 to the present and into future scenarios. The nested structure allows global climate niches to be incorporated into regional models, reducing the risk of environmental niche truncation. Crucially, the models are dynamic: they are calibrated with year-specific conditions, enabling detection of short-term responses, which is particularly relevant for butterflies as they have short generation times and respond rapidly to environmental change. By running three experiments—climate change only, land-use change only, and combined-change—we can disentangle the relative and interactive impacts of these drivers. Results show that species traits mediate responses, with low-dispersal species facing greater constraints across time. Beyond correlative predictions, this framework also links to individual-based simulations by incorporating biotic constraints on dispersal, such as density-dependent emigration from low-density patches. This behaviour, observed in butterflies, reflects ecological realities of mate-finding and habitat quality. Overall, this modelling framework provides ecologically meaningful insights into how abiotic and biotic processes interact to shape species' distributions. It advances our understanding of trait-mediated vulnerability under global change and supports the design of conservation strategies that can safeguard biodiversity

4018. A comparison between Static and Dynamic Species Distribution Models: case study of Romanian herpetofauna

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Biodiversity is not a stable entity and shifts toward suitable habitats in response to fluctuations in environmental conditions. Classical Species Distribution Models (SDMs) assumes climate stability and overlooks variability and trends, especially under anthropocentric climate change. Species, however, respond to climate change in diverse ways, such as moving toward higher latitudes or elevations, often constrained by their dispersal capabilities. In this study, we compared the performance of Static and Dynamic SDMs using optimized MaxEnt, to delineate the potential species ranges of the Romanian herpetofauna, a group susceptible to temperature and moisture due to their ectothermic physiology. We evaluated their performance using Principal Component Analysis and niche equivalency tests across the available climate space of Romania. Static SDMs achieved significantly higher predictive accuracy, yielding smaller, more compact niches nested within the broader Dynamic hypervolumes. Conversely, Dynamic SDMs outperformed Static models in capturing spatio-temporal variability of species ranges, reflected in broader realized hypervolumes and the ability to account for extreme weather events that Static models typically smooth out. The principal trade-off of Dynamic SDMs was its greater reliance on extrapolation, which increased variability and overpredicted suitable habitats, thereby reducing performance scores. Our findings show Static SDMs provide more conservative and precise estimates of core habitats, while Dynamic SDMs reveal the broader climatic tolerance and potential range shifts under variable conditions. We argue that integrating both approaches offers a more robust framework to delineate species distributions and guide effective conservation strategies under ongoing climate change.

4019. Migrating in a warming world: A deep learning approach to predict pan-American seasonal shifts in the monarch butterfly niche

Chiara Vanalli, *École Polytechnique Fédérale de Lausanne; Robin Zbinden, EPFL; Nina van Tiel, Ecole Polytechnique Fédérale de Lausanne; Devis Tuia, École Polytechnique Fédérale de Lausanne*

Climate change is profoundly reshaping global biogeography by driving biodiversity loss, altering species distributions, and disrupting ecosystem dynamics. Migratory species, whose ranges vary seasonally depending on specific climatic conditions, serve as sentinel species to study biogeographic responses to environmental change. However, traditional species distribution models (SDM) often overlook temporal dynamics, since they are often trained with time-static statistics. This limits their ability to predict future range shifts for migratory

species. In this study, we develop a time-aware deep learning SDM of the monarch butterfly (*Danaus plexippus*), an iconic migratory species. Using monthly climatic variables and occurrence data from scientific and citizen science sources, we model the monarch ecological niche across time and space. Compared to static models, our temporal model achieves higher predictive performance both in the present and historically. We show that climatic factors such as humidity, temperature and precipitation strongly influence the ecological niche of the monarch butterfly, with contrasting effects across seasons. Under projected climate change scenarios, our model predicts a marked northward shift in the monarch range, including expansion into Canada and contraction in overwintering regions of California and Central America. Using Shapley values, an explainable AI technique, we find that declining precipitation and humidity could mainly drive the described contractions in overwintering habitats that could severely compromise the species migratory cycle and population stability. By focusing on a species of high ecological relevance through a time-aware modeling approach, this work brings novel insights into the biogeography and conservation of migratory species in a changing climate.

4020. Beyond climatic constraints on species distributions: the role of lithology in determining the distribution of freshwater insects and its implication for climate change impacts

Pedro Abellán, *Department of Zoology. University of Seville*

While climate is typically regarded as the main determinant of species' range boundaries, additional abiotic factors may prevent the occupation of otherwise climatically suitable habitats. Incorporating substrate-related variables (e.g., soil properties or lithology) into species distribution models (SDMs) is common for plants but often overlooked for other organisms. Lithology, however, strongly influences continental aquatic habitats by shaping water chemistry, substrate structure, and hydrologic behavior, and may therefore constrain the distribution of freshwater organisms and limit future suitable habitats. In this study, I built two SDMs for each of 64 Iberian endemic water beetles—one using only climate predictors and another combining climate and lithology—across multiple algorithms, climate change scenarios, and general circulation models. The goal was to assess the relative importance of bedrock lithology in shaping freshwater insect distributions and forecasting range shifts under climate change. Results show that, although climate is the dominant driver of water beetle distributions, lithology-informed models outperformed climate-only models for about half of the species. Moreover, under future climate scenarios, models including lithology predicted often more pronounced distributional changes than those based solely on climate. These findings suggest that excluding lithology from forecasts may underestimate the magnitude of climate-driven range shifts, and they highlight the value of lithology data as a complementary predictor for assessing freshwater species distributions and projecting the impacts of global warming.

4021. How to measure compositional uniqueness and why it matters

Andrés Baselga, *Universidad de Santiago de Compostela; Carola Gómez-Rodríguez, Universidad de Santiago de Compostela*

Compositional uniqueness is the degree to which a community differs from all the others. Although rooted in dissimilarity metrics, this facet of biodiversity has been explored less than other more standard beta diversity patterns. However, the degree of uniqueness of a local community is a relevant attribute, both from ecological and conservation perspectives, as it indicates whether a community harbours species that are not found elsewhere. Because quantifying uniqueness requires relying on dissimilarity indices, we here (i) assess the performance of uniqueness measures based on different dissimilarity indices, and (ii) show how the concept of uniqueness requires that the dissimilarity index conforms to a specific set of properties. Once the appropriate dissimilarity index is selected, community uniqueness can be measured as the average dissimilarity between the focal cell and the remaining ones or as the Local Contribution to Beta Diversity (LCBD), which is a linear transformation of the former. Moreover, the spatial scaling of compositional uniqueness can be assessed by modelling the increase of dissimilarity with distance from the focal cell (uniqueness-increase models), analogous to distance-decay models but restricted to dissimilarities and distances involving the focal cell. These uniqueness-increase models inform about the degree of irreplaceability of the focal cell by assessing whether uniqueness derives from local or large-scale processes. These methods can be extended to phylogenetic and functional dissimilarity measures.

4022. Land use and climate: the diversity of native and alien urban floras are driven by different factors

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Multiple factors, including land use change, climate, socioeconomic conditions, and stochastic processes, influence urban floras. In this study, we examined whether land cover and local climate in the city of Brno, Czech Republic (population ~400,000, mean annual temperature ~10 °C, annual precipitation ~511 mm) shapes the spatial patterns of native and non-native species differently.

We analysed urban flora using vascular plant records in 102 grid cells of 1.3 km × 1.5 km. A total of 1,492 spontaneously occurring species were classified by origin (native, non-native), residence time (archaeophyte, neophyte), and status (naturalized, invasive), with their counts

recorded in each cell. Predictors included land cover area, land cover diversity (Shannon diversity index), and maximum air and land surface temperatures. We employed Random Forests and db-RDA to identify and compare the factors most associated with species diversity. Land cover had a stronger effect on native plant species diversity, while climate factors mainly influenced non-native species diversity. Native species diversity was mainly supported by large forests, green space areas, and higher land cover diversity. In contrast, non-native species diversity was positively associated with higher temperatures, larger residential areas, and exhibited more complex relationships with green space areas and land cover diversity. The ordination analysis revealed some specific patterns, such as invasive species' affinity to industrial areas, railways, and river surroundings. Our results indicate that different species groups are influenced by distinct combinations of factors, highlighting the importance of multivariable approaches for accurately identifying key environmental drivers of urban biodiversity.

4023. Do mountains share a common diversification history?

Saijing Liu, *Naturalis Biodiversity Center; Wen-Na Ding, Swiss Federal Research Institute WSL; Yago Barros-Souza, University of São Paulo; Kasper Hendriks, Naturalis Biodiversity Center; Frederic Lens, Naturalis Biodiversity Center, Leiden University; Renske E Onstein, Naturalis Biodiversity Center*

Mountains harbor disproportionately high biodiversity, yet the evolutionary mechanisms underlying disparity in species richness within and across mountain regions remain poorly understood. Here, we integrated phylogenetic and macroevolutionary analyses of five globally distributed plant lineages (*Draba, Primula, Saxifraga, Gentiana,* and *Potentilla*), comprising > 1800 species, to examine to which extent mechanisms leading to diversification across major mountain ranges (Rockies, Andes, Alps, Himalayas, and Caucasus) are similar. Here, we assembled and cleaned occurrence records, integrated these with phylogenetic trees. We inferred speciation and extinction dynamics using geographic state-dependent diversification models, and reconstructed ancestral ranges and colonisation times for each lineage. We found that diversification rates are clade-specific and vary across mountain systems, but are higher for montane than lowland taxa within the five genera. Particularly high diversification rates were found in Andean and Himalayan lineages. These findings indicate that high plant diversity in certain regions — Himalayas and Andes — is primarily explained by high net diversification rates, rather than by greater immigration or longer accumulation times. Colonisation times also differed among regions, with earlier establishment in the Himalayas and Caucasus, followed by later colonisation in the Rockies, Alps, and Andes. Furthermore, repeated dispersals from mid-latitude mountains outside the alpine zone into alpine and Arctic regions reveal a central role of montane systems as evolutionary sources. Taken together, this study highlights the importance of mountains in accelerating diversification and shaping large-scale patterns of plant diversity.

4024. Age, distribution and conservation of the world's oldest trees

Jiajia Liu, *Fudan University; Yumei Mu, Northwest A&F University*

Extremely old trees are irreplaceable natural resources that provide multifaceted benefits to humans, yet there has been limited work on their global distribution and conservation. Meanwhile, current conservation strategies focus primarily on large-sized trees that were often considered old. However, some studies have demonstrated that small trees can be more than thousands of years old, suggesting that conventional size-focused perceptions may hamper the efficiency of current conservation strategies for old trees. In this talk, I will assess the age of the world's oldest trees, identify the factors shaping their global distribution using data from 197,855 tree cores across 4,854 sites, and evaluate whether tree size reliably predicts age in old trees. This work will offer new insights into the ecology of the world's oldest trees and inform more effective approaches for their conservation.

4025. Ancient chloroplast genomes of large timber trees in late Holocene China reveal biodiversity loss at multiple levels

Xueting Zheng, *Nanjing University; Shuqing Teng, Nanjing University*

Despite accumulating support for Paleolithic and Neolithic causation of current defaunated and downsized biosphere, direct evidence for human-induced diversity loss of large-sized (> 20 m tall) timber trees is lacking. Taking advantage of well-preserved *Phoebe* (family Lauraceae) timber and log remains from ancient China over the past two millennia, we address this knowledge gap by analyzing chloroplast genome sequences extracted from 33 archeological wood samples that have been identified anatomically as Phoebe. Due to severe DNA degradation, only 11 complete plastid genomes from samples dated to the period of Little Ice Age were reconstructed successfully, with five by *de novo* assembly and six by mapping to optimal reference genomes. Including all high-quality *Phoebe* plastome sequences publicly accessible, both Bayesian Inference and Maximum Likelihood phylogenetic trees revealed an unrecognized monophyletic group where modern morphological misidentification occurs, suggesting potential evidence for richer traditional ecological knowledge about the taxonomical diversity of *Phoebe* timber species. In comparison with modern monophyletic plastome sequences, the ancient ones exhibit significantly higher genetic diversity, possibly due to either geographically specific harvesting in the past or incomplete sampling nowadays. Historical written records indicate that these 11 wood samples were likely sourced from Sichuan, Guizhou and Hunan provinces, approximately 800 to 1400 km west of Fujian and Zhejiang provinces where one matrilineal descendant has been reported. The underlying long-distance dispersal mechanisms are still unclear. Our study provides direct evidence that anthropogenic diversity loss of large timber trees may well be underestimated across genetic, taxonomical and ecosystem functional levels.

4026. The value of fine temporal scale monitoring in revealing insect diversity and population dynamics

Xiaolei Huang, *Fujian Agriculture and Forestry University; Chuan Liu, Fujian Agriculture and Forestry University; Xiaoyan Luo, Fujian Agriculture and Forestry University; Huizi Jia, Fujian Agriculture and Forestry University*

Most current studies on diversity dynamics of insects, the most diverse group of organisms on Earth, suffer from two main limitations. First, sampling effort is predominantly concentrated in the summer season, leading to complete omission of insect occurrences in cold season. Second, the temporal resolution of sampling is often coarse (e.g. bimonthly or even quarterly), making it difficult to capture the real insect community composition and occurrence patterns of rare taxa. To overcome these limitations, we have established an intensive insect monitoring network across multiple subtropical mountain ranges in China. Based on a once-every-two-weeks fine temporal scale sampling at different elevations of different mountains for at least one whole year, the dynamic patterns of insect occurrences and key environmental determinants across multiple temporal scales (biweekly, monthly, bimonthly and quarterly) and spatial scales (within a mountain and between mountains) have been investigated. Our analyses provide new evidence on the value of fine temporal scale monitoring in revealing rare insect taxa and insect community dynamics.

4027. Species diversity patterns of Cinara aphids in the mountains of southwest China and formation mechanisms

Jing Chen, *Institute of Zoology, Chinese Academy of Sciences; Shuang Xu, Institute of Zoology, Chinese Academy of Sciences; Li-Yun Jiang, Chinese Academy of Sciences; Ge-Xia Qiao, Institute of Zoology, Chinese Academy of Sciences*

The mountains of southwest China (MSWC) is one of the world's biodiversity hotspots. However, research on invertebrate diversity within this area remains limited. The genus *Cinara* Curtis, 1835 (Hemiptera: Aphididae: Lachninae) is the second largest genus of aphids, with over 260 species worldwide. It exhibits remarkable species diversity within MSWC. This study explores the species diversity patterns of Cinara both globally and specifically within MSWC using macroecological approaches. Our findings indicate that specific host plants, water availability, seasonal climate variations, and elevation play pivotal roles in shaping the distribution patterns of *Cinara*. Macroevolutionary analyses reveal that Cinara originated from eastern Palaearctic during the late Cretaceous and initially colonized the MSWC by the middle Paleocene, where it underwent long-term diversification and frequent dispersal events. Along with the mountain uplifts and climate shifts across different geological epochs, Cinara experienced rapid radiation through altitudinal and climate niche differentiation, host plant switches, and shifts in feeding sites. These processes have ultimately contributed to the high species diversity of *Cinara* within MSWC.

4028. Conservation Corridor Efficacy: They Work but Management Matters

Sydney Morgan Rosenkrantz, *University of North Texas; Reilly Elaine Neville, University of North Texas; Carmen Burkett, University of North Texas; Paul Beier, Center for Large Landscape Conservation; James M Bullock, UK Centre for Ecology and Hydrology; Richard K Broughton, UK Centre for Ecology & Hydrology; Emma Suzuki Spence, Cornell University; Justin Travis, University of Aberdeen; Andrew J Gregory, University of North TX, AERI*

Conservation corridors are among the most frequently proposed interventions to safeguard biodiversity from habitat loss and climate change. Rooted in Island Biogeography and Meta-population dynamics, the intuitiveness of corridors to protect biodiversity has led to their wide-scale adoption. However, empirical evidence for their efficacy in connecting populations and providing long-term stability and resilience remains largely equivocal. In a first-of-its-kind, multinational investigation, we studied the degree to which 16 long (>500m), old (>50 years in current configuration) corridors embedded in an anthropogenic matrix provided long-term connectivity (measured by gene flow) for multiple species (3-5/landscape). The selected focal species also represented a cross-section of natural and adaptive life-history strategies. Using an experimental design which allowed us to assess connectivity among isolated patches, corridor connected patches, and locations within intact natural areas, we evaluated if the presence of a corridor supported gene flow at levels near those observed across intact landscapes. Using a combination of Random Forest and Non-metric Multidimensional Scaling, we demonstrated that: 1) the presence of a corridor or an intact landscape is the single best predictor of gene flow, 2) straight corridors outperform more tortuous ones, and 3) minimizing habitat degradation within the corridor is instrumental for maintaining corridor success. We also found that edge-sensitive carnivores tend to benefit more from corridor presence than other species. These results provide some of the first empirical evidence that corridors work and form the basis for practical guidelines to better design and manage future corridors.

4029. Two Cheers for the Corridor Success Index (CSI) as a Measure of Connectivity and gene flow in Fragmented Landscapes

Reilly Elaine Neville, *University of North Texas, Northlake, United States*

Corridors are the primary conservation intervention proposed to preserve connectivity and genetic exchange, yet their long-term effectiveness is difficult to evaluate. Recently, Gregory and Beier (2014) proposed the use of a new metric based on gene flow (the Corridor Success Index; CSI) to assess the degree to which the presence of a corridor promotes dispersal and gene flow. We assessed the efficacy of the CSI by comparing it to more traditional population genetic measures of gene flow and dispersal on real landscapes. Our analysis included 12 mammal species across eight landscapes in six countries. Genetic analyses revealed complex population structures and variable differentiation among species. The CSI showed

only mediocre agreement with traditional metrics like Nei's Genetic Distance, the fixation index (FST), and Structure analysis, with consistent inferences in just 6 of 23 cases for each comparison. Contradictions between CSI and traditional metrics arose most often when its underlying landscape models were unrealistic, treating the land between habitat patches (the matrix) as a uniform barrier rather than a complex mosaic of features like roads and rivers that present varying resistance to movement. Despite these limitations, the CSI is a valuable method for scaling comparisons of gene flow. A key finding is the crucial role that even minimal connectivity plays in maintaining genetic diversity, which is essential for long-term species survival. We conclude that while CSI cannot replace traditional genetic analyses, it offers important insights into how species biology and landscape configuration interact to yield a complex mosaic of connectedness.

4030. How do species traits and biogeographical factors determine the fate of amphibians after long-term fragmentation?

Chuanwu Chen, *Nanjing Normal University, Yanping Wang, Nanjing Normal University*

Identifying key factors that render certain species more vulnerable to fragmentation is vital for elucidating processes underlying extinction and targeting conservation priorities. However, few studies have explored the delayed ecological responses of species following isolation. To bridge the gap, we conducted comprehensive analyses of correlates of extinction vulnerability and biogeographical variation in amphibians over long-term fragmentation. We found that species with low natural abundance, larger egg sizes, smaller clutch sizes, or restricted geographical distributions were more likely to experience higher population extinction rates and species nestedness rankings, while lower island occupancy frequencies across islands. Although most species were found on larger islands, we observed significant increases in the occurrence probabilities with island area for five species. Interestingly, the likelihood of occurrence of *Hyla chinensis* (treefrog) was negatively related to distance to the mainland after controlling for the effect of area. Our study highlights the variation in the fragmentation sensitivity of amphibians. Species distribution was primarily regulated by area-related extinction, particularly for those with 'slow' life-history strategies or restricted ranges. Overall, management efforts should focus on species with extinction-prone traits and landscape features that threaten the persistence of populations. Future studies should consider the sequential separation of island populations and the interaction of traits to reveal the fate of species to fragmentation.

4031. Do Protected Areas effectively preserve richness and rarity across taxa and diversity facets under future change?

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Most conservation strategies focus on taxonomic diversity, despite growing evidence that functional and phylogenetic dimensions are crucial for ecosystem resilience and long-term evolutionary potential. The current protected area (PA) network, covering 16% of terrestrial land, captures only a limited share of these diversity dimensions. As conservation resources remain constrained, evaluating whether current PAs will remain effective under future environmental change is critical. While scenario-based studies increasingly project biodiversity shifts, most focus on species richness, or on one dimension of functional and phylogenetic diversity for specific taxa, thus overlooking the multidimensional aspects of biodiversity. To date, no studies have focused on assessing the efficiency of PAs networks in protecting present-day and future biodiversity, for several dimensions of phylogenetic and functional facets of diversity and across various taxa. Using the Euro-Mediterranean forests as a case study, we focus on five key taxa of Mediterranean forests: trees, butterflies, reptiles, birds and mammals, and assess the efficiency of the current protected area network to safeguard their taxonomic, functional and phylogenetic richness and rarity under current and future conditions. To address these questions, we apply a randomisation approach to test whether IUCN-designated PAs protect more biodiversity than non-protected areas within each country. We then compare effect sizes across diversity facets, dimensions, and countries to provide a comprehensive assessment of PA efficiency under current conditions and two future land use and climate scenarios. This work is conducted within the INTEGRADIV consortium, supported by BIODIVERSA+.

4032. Terrestrial biodiversity monitoring using environmental DNA metabarcoding and temporal samples archived in environmental specimen banks

Shreya Pandey, *University of Oulu; Alexandra Schmidt, University of Konstanz; Majid Moradmand, University of Oulu; Till-Hendrik Macher, Trier University; Stefan Prost, University of Oulu*

Biodiversity is essential for ecosystem stability, productivity, and resilience but is increasingly threatened by anthropogenic pressures, including habitat destruction, climate change, pollution, and invasive species. Traditional biodiversity assessments based on morphological species identification are time-consuming, labor-intensive, and prone to misidentification, limiting their effectiveness for large-scale monitoring and historical reconstructions. Environmental DNA (eDNA) metabarcoding offers a non-invasive, high-throughput alternative, detecting species through genetic material shed into the environment. This study applies eDNA metabarcoding to samples obtained from the Finnish environmental specimen bank, specifically conifer-derived needle samples, to reconstruct past biodiversity, assess long-term ecological changes, and evaluate shifts in arthropod and fungal communities over several decades. The project focuses on conifer samples collected between 1962 and 1998 by the Natural Resources Institute, LUKE, Finland, aiming to uncover long-term biodiversity trends and ecological changes influenced by environmental pressures. We further compare Illumina and Oxford Nanopore sequencing technologies to analyze degraded eDNA over time, assessing their relative strengths and limitations for biodiversity monitoring. eDNA metabarcoding successfully detected diverse arthropod and fungal taxa, revealing temporal biodiversity patterns. Integrating both sequencing platforms enhances species detection and ecological monitoring, demonstrating the method's potential for reconstructing historical biodiversity from archived plant specimens. The findings emphasize the value of eDNA in long-term biodiversity assessments and provide a framework for future conservation applications and ecological research. This approach offers scalable, efficient, and robust solutions to monitor biodiversity shifts over time, supporting evidence-based management and informing strategies to protect natural systems in Finland and globally.