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SCHEDULE OVERVIEW

2-JUNE	3-JUNE	4-JUNE	5-JUNE	6-JUNE
08:30 am WORKSHOPS & FIELD TRIPS	08:30 am Welcome MacArthur & Wilson Award Talk	08:30 am Wallace Award Talk	08:30 am Dissertation Award talk	08:30 am FIELD TRIPS
	09:20 am Innovation Biogeography Symposium	09:00 am Changing Ocean Ecology and Biogeography Symposium	09:00 am Conservation & Restoration Biogeography Symposium	
	10:40 am Break	10:45 am Break	10:45 am Break	
	11:10 am Innovation Biogeography Symposium	11:10 am Changing Ocean Ecology and Biogeography Symposium	11:10 am Conservation & Restoration Symposium	
	12:45 pm Lunch Break	12:45 pm Lunch Break	12:45 pm Lunch Break	
	02:00 pm Concurrent Sessions 1-4	02:00 pm Concurrent Sessions 9-12	02:00 pm Concurrent Sessions 17-20	
	03:30 pm Break	03:30 pm Break	04:00 pm Break	
	04:00 pm Concurrent Sessions 5-8	04:00 pm Concurrent Sessions 13-16	04:30 pm Business Meeting/ Closing/Awards	
	06:00 pm Mentor Session/ Social	06:00 pm Break		
		06:00 pm Poster session		

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KEYNOTE/AWARD SPEAKERS

June 3rd 8:50 am PT

Keynote - MacArthur & Wilson Awardee – Jason Weir

Speciation, extinction and the origins of the latitudinal diversity gradient

Jason Weir[1],

[1] University of Toronto

The tropics possess exceptional numbers of species when compared to high latitude regions. My research investigates the factors that drove the excess of high tropical species richness. Leading hypotheses link high tropical richness to a faster rate at which tropical species form or to a slower rate at which they go extinct. Alternatively, greater ecological niche differentiation may allow more species to coexist in the tropics. Here I harness large comparative datasets to investigate latitudinal variation in speciation, extinction, and niche differentiation in birds. I quantify latitudinal differences in the rate of evolution of traits important to premating reproductive isolation and to ecological niche differentiation and compare rates of speciation and extinction across latitudinal gradients. My research arrives at several conclusions. First, speciation appears to be slower, rather than faster, in tropical taxa, suggesting that very low rates of extinction may be key to high tropical species richness. Second, while tropical species evolve reproductive isolation slowly and take longer to come into sympatric overlap with close relatives, once in sympatry, they more readily undergo ecological character displacement into a diversity of specialized forms. Ecology-driven evolutionary divergence that operates after speciation is complete may therefore be fundamental to long-term biodiversity accumulation in tropical regions.

June 4th 8:30 am PT

Keynote – Alfred Russel Wallace Awardee - Petr_Pyšek

Biogeography and macroecology of biological invasions: state of the art

Petr Pyšek[1]
[1]Czech Academy of Sciences

Biological invasions are a global consequence of an increasingly connected world and the rise in human population size. The numbers of invasive species (the subset of alien species that spread widely in areas where they are not native, affecting the environment or human livelihoods) in all taxonomic groups are rapidly increasing. Synergies with other global changes exacerbate current invasions and facilitate new ones, thereby escalating the extent and impacts of invaders. Invasive alien species break down biogeographic realms, affect native species richness and abundance, increase the risk of native species extinction, alter phylogenetic diversity across communities, and modify trophic networks. Many invasive alien species also change ecosystem functioning and the delivery of ecosystem services by altering nutrient and contaminant cycling, hydrology, habitat structure, and disturbance regimes. These biodiversity and ecosystem impacts are accelerating and will increase further in the future. The awareness is growing of how serious problem biological invasions are – invasions have become a topic in the Scientists warning initiative and a subject of the ongoing IPBES assessment. Still, in many countries, invasions receive little attention, and improved international cooperation is crucial to reducing invasive alien species' impacts on biodiversity, ecosystem services, and human livelihoods.

June 5th 8:30 am PT

Keynote – IBS Dissertation Awardee – Antonia Salces Castellano (virtual presentation)

Spatial structure of biodiversity: local and regional patterns in an insular ecosystem

Antonia Salces Castellano[1,]

[1] University of Liège and Free University of Brussels

What forces drive the origin and maintenance of biodiversity? This is a central question in biology, and an important challenge, particularly in oceanic islands, which harbour singular but also threatened biodiversity. Within island biodiversity, arthropods are an ecologically important group but typically with only limited biological data. The present PhD research contributes to our understanding of insect biodiversity in oceanic islands through two core objectives: (i) describe spatial and temporal patterns of relatedness and similarity, from the level of genetic diversity through to community assemblages, and (ii) identify the variables and processes that shape diversity, focusing on non-adaptive evolutionary pathways to speciation. Using an integrative approach combining standardised single-locus (mitochondrial) community sampling with high resolution genomic (ddRAD-seq), geographical, ecological and historical data, we have been able to explore important drivers of species diversification in an insular context, such as dispersal limitation, topography, climatic variation, and niche conservatism, acting at multiple spatial scales: from regional (i.e. archipelago) to local (i.e. small scale within island). This research underlies the importance of climate, history and spatial scale for the beetle community assembly in the oceanic islands, and also points to flightless and hydrophilic species of beetles as potential indicators of how past climate change has influenced the distribution of habitat, potentially offering the possibility to predict future responses to global warming.

SYMPOSIA

Symposium 1: Innovation Biogeography
June 3rd 9:20 am – 12:40 pm PT

Biogeography everywhere, all the time: remote sensing as a source of technological innovation

James Kellner[1],

[1] Brown University

Advances in remote sensing are revolutionizing how we observe and understand the surface of our planet, and the role of life within it. It is now possible to quantify flows of energy and material, some of which are biologically regulated, and to characterize the physical environment at scales that are clearly aligned with decades of understanding in the biological sciences. New sensors mounted on airborne and spaceborne platforms can observe individual plants and animals, populations, ecosystems, entire species ranges and the whole planetary surface. Some of these instruments measure the entire surface of our planet at high spatial resolution every day. Others collect samples over diurnal cycles. Some provide information about ecosystem structure and condition, including temperature, chemical properties, pigments, and water, while others distinguish individuals or characterize the environment in three dimensions. The integration of these measurements with high-performance computing can catalyze a sea change in the study of the spatial distribution of life on earth. By linking the biological and the physical at high-resolution, technological innovation promises not just quantitative improvement, but a conceptual shift to biologically-driven remote sensing, opening the door to biogeography everywhere, all the time.

Drone ecology reveals the landscape context of Arctic global change

Isla Myers-Smith[1],

[1] University of Edinburgh

As the Arctic warms at three times the rate of the rest of the planet, the snow and ice-free period is becoming longer, giving plants more time to grow. From space, forty years of satellite observations suggest a greening of the Arctic, thought to indicate an increase in plant productivity. However, tundra greenness trends observed by satellites are not just a result of increases in plant productivity, but represent complex land-surface dynamics at high latitudes. Imagery from longer time series of satellite data have pixels hundreds of metres to kilometres in extent, much larger than the spatial mosaic of changing tundra landscapes. From the ground, field studies indicate that plants are coming into leaf earlier in spring, bare ground is becoming vegetated, and tundra plant communities are growing taller with an increase in tundra shrubs. Although satellite greening and in-situ vegetation data have been collected for decades, we lack the landscape-level data to bridge from plots to satellites. New field data from drones, time lapse photography (phenocams) and microclimate monitoring are capturing variation in Arctic vegetation change across landscape scales. Synthesis of these data addresses critical research gaps about the responses of Arctic ecosystems to global change. In this talk, I will discuss how drones and other technology are reshaping our understanding of biogeography in a rapidly warming Arctic.

Historical ecology of sea otters from Alaska to California: a case study in the use of compound-specific stable isotope analysis for paleoecology and conservation.

Emma Elliott Smith[1,]

[1] Smithsonian Institution

Stable isotope analysis has been a powerful tool in the arsenal of historical ecologists, allowing reconstruction of pre-industrial food web structure and providing insights into the impacts of people on animal communities across space and through time. However, the inferences that can be drawn from traditional bulk tissue analyses are limited by spatiotemporal isotopic variation and uncertainties in trophic discrimination. Compound-specific stable isotope analysis, a technique which focuses on individual monomers, such as amino or fatty acids, has the potential to resolve many of these issues. Notably, isotopic analysis of essential amino acids can shed light on the importance of primary producer groups and habitats to animal communities, allowing quantification of energy flow in past ecosystems. In this talk, I will explore the insights that can be gained from essential amino acid d 13 C analysis through a case study of archaeological remains of an endangered marine mammal, the sea otter (*Enhydra lutris*). Hunted to near extinction during the fur trade, sea otters are now found only in portions of their historical geographic range across the northern Pacific. However, their remains are abundant in coastal archaeological sites. We conducted isotopic analysis on over 100 specimens from southeastern Alaska to southern California and from the mid-Holocene to 500ybp. Our study localities span a gradient of modern sea otter population recovery trajectories, and include regions (e.g., Oregon) where sea otters existed historically but have not yet successfully recolonized. We infer the trophic role and intraspecific dietary patterns of pre-fur trade sea otters from bulk bone collagen d 13 C and d 15 N data. Through essential amino acid d 13 C fingerprinting we characterize the sources of primary production that supported sea otter populations in the past, which provides a high resolution proxy for habitat use. Through this work we provide important baseline ecological data for conservation efforts of a keystone species.

Environmental and ecological variation in ancient sharks: coupling stable isotope analysis with other quantitative approaches

Sora Kim[1,]

[1] UC Merced

Shark teeth are the most abundant vertebrate fossil and contain ecological information in their morphology and chemistry. However, most studies featuring the stable isotope analysis of fossil shark teeth are limited to an environmental reconstruction. How can we leverage the rich fossil record of sharks to elucidate macroecological patterns and processes? The sand tiger shark *Striatolamia macrota* had a global distribution during the Eocene that spanned the Arctic and Southern Oceans as well as Gulf of Mexico. The stable isotope composition and body size distribution in these localities indicate environmental and ecological variation. For example, the Eureka Sound Formation (Fm.) in Arctic Canada had reduced salinity with smaller sharks, which likely represented a nursery. In contrast, the La Meseta Fm. in Antarctica was a fully marine habitat with a mixture of juveniles and adults. The oxygen isotope composition from localities can also be compared to global climate model outputs to offer empirical comparisons of conditions or hypothesize possible migration localities. A dynamic demographic model emphasizes the role of movement; there is ontogenetic segregation of sand tiger sharks with strong size selection and seasonal migration. The temporal and spatial abundance of fossil shark teeth provides a unique system to combine empirical, theoretical, and analytical approaches to probe ecological patterns and processes.

HumBug - an acoustic mosquito monitoring tool using budget smartphones

Marianne Sinka[1],

[1] University of Oxford

There are over 3500 species of mosquito across the world but only a small proportion are vectors of human disease, yet those few species are responsible for more death and misery than any other animal. To adequately control these disease vectors, we need to conduct mosquitoes surveys to pin point and target the most dangerous species. Yet mosquito surveys are time consuming, expensive and, common to all field surveys, are biased towards more accessible locations and may not always accurately represent the occurrence of the mosquitoes.
I will present HumBug, an interdisciplinary project developing an acoustic sensor that exploits the distinct flight tone of mosquitoes and, by simply downloading an app, allows any Android smartphone to become a mosquito sensor. Our HumBug sensor has the potential to significantly increase the quantity of mosquito occurrence data needed for ongoing mosquito control, as well as access locations that are more difficult to survey by traditional means.

Pathogeography - recent advances in biogeographical study of human infectious diseases (virtual presentation)

Kris Murray[1],

[1] Imperial College of London

Pathogeography is a term resurrected from the botanical literature that is shorthand for the “biogeography of disease”. We observe that theory and analytical approaches drawn from biogeography have already helped improve our understanding of individual human infectious disease distributions and the processes that shape them in space and time. More critically, we have argued that the application of biogeographic approaches to human diseases could become an important and novel source of management-relevant information with which to combat existing and anticipate future disease outbreaks, emerging and even pandemic diseases. Here, in the wake of the SARS-COV2 pandemic, we review some of the most recent and important advances in pathogeography and put these expectations to the test. We conclude that although by no means a crystal ball, biogeographic approaches are continuing to provide surprising insights into current and future infectious disease risks and are providing novel added value to more conventional methods from medical geography and spatial epidemiology in this rapidly changing world.

Symposium 2: Changing Ocean Ecology & Biogeography
Organizer: Mary O'Connor
June 4th 9:00 am – 12:45 pm PT

Global drivers of marine predator diversity

John Grady[1,]

[1] National Great Rivers Research & Education Center

Large predatory sharks, bony fish, mammals and birds show strikingly different patterns of global diversity, but the origins of these differences have only recently received attention. I synthesize species distributions from 824 large-bodied predators occupying shallow water habitats, and present a theoretical framework for spatial patterns of richness due to metabolic and foraging strategy. Fast- metabolizing and fast-moving mesotherms and endotherms progressively dominate richness in open waters away from the coast and at higher latitudes, where metabolic advantages are greatest. In warmer and more open waters — where kinetic constraints on foraging are higher — cooperative-foraging dolphins and aerial-foraging birds systematically increase in richness and abundance relative to other endotherms. Observed patterns point toward a general mapping of biological power with temperature and habitat openness over space.

Thermal safety, environmental variability, and biodiversity change

Amanda Bates[1,]

[1] University of Victoria

Determining the vulnerability of species in an era of global change remains a priority in order to make accurate predictions, prioritize future research, and advise conservation and management practices. The identification of mechanisms enabling species to cope with temperature change underpins our capacity to predict biotic responses to climate variability and develop reliable ecological indicators for accurate and meaningful tracking of threats. Global data sets of thermal niche data can thus help define patterns in thermal physiology of ectotherms across a wide range of habitats and latitudes. While the magnitude of experienced temperature is clearly important, environmental variability is also a key determinant of physiological response that will influence species survival if variability also becomes more extreme. Considering environmental variability in combination with thermal physiology can inform predictions of species and community vulnerability, range shifts and change in the functional traits of communities.

Conservation biogeography and genomic restoration in the sunflower sea star

Lauren Schiebelhut[1,] Michael Dawson[1,]

[1] University of California, Merced

The increased frequency of marine heat waves and mass mortality events are changing species' distributions, perhaps irrevocably. In 2013, the sunflower sea star (Pycnopodia helianthoides) experienced 88–100% mortality from all but the northern-most portion of its range due to sea star wasting (SSW) disease and elevated water temperatures. Eight years later, this very high dispersal species is yet to return. Once abundant and widespread from Baja California Mexico to Alaska USA, the recent sharp decline and related ecosystem change led *P. helianthoides* to be listed as critically endangered by the IUCN in 2021 and initiated the development of recovery plans. However, there were no data on the geographic distribution of genetic diversity, population structure, or local adaptation collected before the rapid loss of the species from the southern half of its range. Thus, the information necessary to inform potential conservation interventions is largely lacking. With Revive & Restore, we are working to uncover genomic associations with wasting and temperature stress and contextualize this genomic diversity with historical museum samples, live samples from the extirpated range (preserved in aquaria), and wild contemporary samples. These results will provide the genomic insights needed to map the geographic-genomic seascape to help inform conservation decisions and increase success along two conservation trajectories: (1) captive breeding for potential out-planting and (2) assessing wild populations for potential translocation, both taking into consideration the historical and potential future geographic distributions of genomic diversity.

Beyond temperature and range shifts: Coastal ecosystems along the Southeastern Pacific are being transformed by changes in pelagic productivity

Sergio Navarrete[1]

[1] Pontificia Universidad Católica de Chile

Studies on the impact of Climate Change in marine ecosystems have largely focused on the effect of temperature on geographic range shifts of species. But climate change can alter the vital rates that control population dynamics, persistence and overall productivity of harested and non-harvested populations, which in turn can bring up wholesale changes in geographic patterns of functional structure and composition. Along the Humboldt Upwelling Ecosystem, climate change has intensified and pushed southward the Southeastern Pacific Anticyclone, forcing diverging regions of increasing, and decreasing coastal phytoplankton productivity equatorward and southward of 31-32°S. Using a 20 years dataset of barnacle larval recruitment we show striking increases in larval arrival in the region of higher productivity, while slower but significantly negative trends dominate poleward of 30°S, where years of recruitment failure are now common. Rapid increases in benthic adults result from fast recruitment-stock feedbacks following increased recruitment. Slower population declines in the decreased productivity region may result from aging but still reproducing adults that provide temporary insurance against population collapses. Since the 30°S is a region of major biogeographic shifts in community functional abundance, invertebrate and algal gene flows, and species ranges, this slow bottom up changes may transform biogeographic patterns in the next decades.

Temporal analysis of warming-driven distributional changes in macroalgae

Rosa Chefaoui[1,] Rosa M. Viejo1, Francisco Arenas, Brezo Martínez[1]

[1] Universidad Rey Juan Carlos

The amplitude and frequency of marine heatwaves is increasing with climate change. Several European coastal regions have reached record sea surface temperatures during the past decades and marine macrophytes have started to shift their ranges. Understanding how patterns of extreme events intensification and/or gradual warming set the scene for future species redistributions becomes crucial. We analyze a set of descriptors of marine heatwaves events and time series of seawater temperature in the Northern Spanish coast, encompassing the same time frames as observations of macroalgae changes in this coast. Shifts in the southern distributional limits of cold-temperate macroalgae species are evidenced by recent field surveys and historical data. This research aims to identify the patterns of sea surface temperature variation affecting macroalgae species differently, depending on their life cycles and thermic tolerance. Our work will provide an analytical workflow in the framework of the project MarHot, reproducible in other coastal regions.

The role of species interactions in mediating biogeographic responses to a changing climate

Chris Harley[1,]

[1] University of British Columbia

Patterns in the distribution and abundance of species across spatial and temporal scales depends on the relationship between prevailing environmental conditions, the survival and fitness of individual organisms, and the dynamics of local populations. However, the biology of organisms and ecology of populations depends on more than just the physical environment; sufficient resources must be available in the form of nutrients and food, and threats from predators and competitors must be overcome. These ecological inter-relationships also change over space and through time due to individualistic responses among species in their population size and per capita effects. For example, disproportionally strong effects of warming on either predators or prey can drive shifts in range edges that would not be predictable based on ecophysiology alone. Positive interactions including biogenic habitat provision and stress amelioration can also affect the vulnerability of many species to environmental extremes. The relative importance of interspecific interactions varies at a variety of intermediate scales depending on species mobility, the presence of refugia from abiotic stress, and the sources and identity of novel species in local ecosystems. Species interactions and community ecology represent a vital bridge between the proximate mechanisms of the ecophysiologist to the ultimate patterns of the biogeographer, and small-scale interspecific interactions require better integration into our understanding of larger-scale ecological patterns.

The functional consequences of extinctions: from giant sharks to small mollusks (virtual presentation)

Catalina Pimiento[1,]

[1] Palaeontology Institute and Museum, University of Zurich

The fossil record of the marine megafauna, the largest animals in the oceans, has revealed that in the Pliocene (~3Ma), habitat loss driven by sea-level oscillations caused the extinction of one third of their genera. Trait-based analyses further showed that this extinction resulted in the erosion of nearly one fifth of their functional diversity. Such a level of ecological loss contrasts with the almost negligible changes after the (mass) extinction of benthic invertebrates around the same time. Unlike the marine megafauna, small invertebrates can share similar ecological traits and thus be highly redundant and ecologically resilient in the face of extinction. The much larger marine megafauna, on the other hand, tends to be functionally unique and therefore highly vulnerable. Given that the Pliocene extinction left the marine megafauna functionally depleted, how will they respond to the current extinction crisis? Forty percent of marine megafaunal species are currently threatened. Simulated extinction scenarios forecast this could result in the loss of up to half of their ecological functions. Sharks, in particular, show greater-than-expected losses of functional diversity. Biogeographic analyses further indicate that megafauna functional richness is globally greatest along the tropical continental shelf and oceanic island environments. Meanwhile, high latitudes harbour the most functionally unique species. The protection of these areas could therefore help safeguard the key ecological functions these organisms play in marine ecosystems.

Symposium 3: Conservation & Restoration Biogeography
June 5th 9:00 am – 12:45 pm PT

The biogeography of useful plants: reconciling biodiversity and humanity

Samuel Pironen[1],

[1] Royal Botanic Gardens, Kew

Plant diversity sustains global ecosystems and humanity. The geographic distribution of multiple intrinsic facets of plant diversity (e.g., taxonomic, phylogenetic, functional) has long been investigated. However, surprisingly little is known about the distribution of the fraction of plant diversity directly contributing to people's subsistence and well-being. This ultimately impedes our fundamental understanding of the interaction between people and nature, in addition to the implementation of evidence-based conservation, restoration and sustainable use strategies. In this presentation I will revisit several important biogeographical concepts, including biodiversity hotspots, rarity-commonness patterns, and resilience to environmental change, all seen through the lens of the interaction between plants and people. Matches and mismatches between total plant diversity and useful plant diversity will be discussed for different plant uses (including food, medicine, and gene sources for plant breeding), at global to national scales, across multiple regions of the world such as Sub-Saharan Africa and South-East Asia. I will highlight how these biogeographical patterns can inform both in- and ex-situ conservation strategies, laying the groundwork for the selection of candidate species with potential for future use in activities such as the diversification of food systems, ecosystem restoration, and resilience to climate change. Plants underpin all life on Earth. Therefore, concurrently protecting their diversity and contributions to people is crucial for the future of both nature and humanity.

Integrated macroecological-paleoecological perspectives on large-herbivore effects on ecosystems – implications for conservation and restoration

Jens-Christian Svenning[1], Camilla Fløjgaard[2], Rasmus Østergaard Pedersen, Emilio Berti[3], Søren Faurby[4], Rasmus Ejrnæs[2], Pil B.M. Pedersen[5], Christopher Sandom[6],

[1] Department of Biology, Aarhus University
[2] Department of Ecoscience, Aarhus University
[3] German Centre for Integrative Biodiversity Research (iDiv)
[4] University of Gothenburg, Department of Biological and Environmental Sciences
[5] Centre for Landscape and Climate,University of Leicester
[6] University of Sussex

Large herbivores are potential ecosystem engineers via their vegetation feeding activities, non-trophic disturbances and movements of propagules and nutrients. Hereby, they promote key factors for biotic community assembly and the maintenance of species richness, namely environmental heterogeneity and dispersal. However, the importance of large herbivores for conservation and restoration is often underappreciated or misunderstood due to near-ubiquitous downgrading of large-herbivore assemblages worldwide across both recent decades and into recent prehistory. These losses have left natural and semi-natural ecosystem with large-herbivore assemblages that are highly down-sized and simplified relative to the mid- and late Cenozoic norm. Using macroecological approaches, traits, and allometry- and phylogeny-based modelling, we here assess the ecological consequences of these losses as well as restoration implications. Comparing large-herbivore biomass across natural ecosystems world-wide, we estimate that biomass levels are often much reduced, e.g., tenfold less or lower at medium productivity. Further, we find that that consumption rates by wild herbivores in current natural areas worldwide are only 56% (mean) of their level in the absence of late-Quaternary extinctions and extirpations, based on a conservative estimation procedure. We furthermore find that 74% of average movement capacity of mammal assemblages has been lost due to late-Quaternary extinctions and extirpations. Our results show that the past and current pressures on large-herbivore assemblages have affected the functioning of ecosystems throughout the world. These findings highlight the need for widely restoring large natural and semi-natural areas with higher densities and diversities of large herbivores than typically exist today and, more generally, careful reconsideration of assumptions and management goals for wild large herbivores in conservation and restoration efforts.

Restoring ecosystems and landscapes for multiple benefits

Robin Chazdon[1,]

[1] University of Connecticut

The restoration of ecosystems and landscapes unlocks the potential for multiple benefits for people and nature, including raising capacity for environmental stewardship within communities, enhancing human health and well-being, helping mitigate and adapt to climate change, improving water quality and flows, reducing soil erosion and flooding, regaining soil fertility and preventing species extinction. Different outcomes, benefits and costs of restoration actions become manifest over various temporal and spatial scales. Understanding the distribution of benefits and costs associated with restoration is critical as aggregate benefits can hide significant imbalances, with benefits skewed towards a few stakeholders and costs borne by others. Inclusive engagement in restoration planning may enable more equitable distribution of net benefits and increase the potential for long-term success. Trade-offs and synergies can be better understood and addressed through answering seven key questions related to the distribution of restoration costs and benefits in the planning process: 1) How do ecosystem goods and services change with degradation, conservation or restoration? 2) What are the causes and risks of ongoing ecosystem degradation and who gains and who loses? 3) What benefits, outcomes, and disbenefits are likely to be achieved with restoration, at what time scales, and what is their distribution? 4) What are the implications of identifying trade-offs for restoration priorities? 5) Which areas or types of restoration may maximize multiple benefits while minimizing costs? 6) Where and when should restoration actions be scheduled in space and time? 7) Where and how intensively should restoration actions be implemented?

Pining for home: assisted migration as a climate change adaptation strategy

Gregory O'Neill[1,]

[1] Ministry of Forests, Lands, Natural Resource Operations and Rural Development

The intention of this presentation is to make a case for "boldly going where no forester has gone before": for deconstructing the 100-year-old paradigm of reforesting with local seed sources. Numerous reports have already linked large-scale forest disturbance with 20th and 21st century climate change. As the rate of Anthropocenic climate change continues to outpace the ability of natural systems to respond through natural selection and migration, tree populations are becoming increasingly distanced from their climatic optimum, maladapted and susceptible to pests and disease. In forested ecosystems, where trees are often foundation species, the stability of ecosystems and the diversity of life that they support are jeopardized. Assisted migration – reforesting or afforesting with tree seed sources from climates that are slightly warmer than the planting site – is intended to mitigate forest maladaptation associated with evolutionary lag due to Anthropocenic climate change and climate change expected during the life of the planted forest. This presentation will discuss the rationale for assisted migration in forestry and British Columbia's new Climate Based Seed Transfer system through which assisted migration is being implemented across the province. What happens when trees are moved outside their current distribution? This question will also be addressed by examining the Assisted Migration Adaptation Trial, a large, long-term, multi-species field trial in western North America.

The relevance of historical perspectives to species recovery

Loren McClenachan[1],

[1] University of Victoria

Humans are fundamentally terrestrial animals, and as a result, change to underwater ecosystems has gone largely unobserved for much of human history. Consequently, baselines have shifted, with formerly productive fisheries, abundant marine animals, and widespread intact habitat frequently forgotten. This memory loss is relevant to modern recovery efforts because recovery of depleted species requires a collective memory of more abundant past populations. This talk will highlight links between perceptions of historical baselines and visions for the future, focusing on a case study in the Gulf of Maine. Here, conservation and recovery efforts are underway for both Atlantic cod, whose populations crashed in the 1990s, and endangered 18th-century right whales, whose populations failed to recover from 18th century whaling. It will emphasize the relevance of historical perspectives to species recovery, and highlight both the value and limitations of local knowledge in places that have experienced ecological change over centuries.

Saving seahorses means saving ocean spaces

Amanda Vincent[1],

[1] University of British Columbia

The charisma of seahorses is helping us save ocean spaces. Seahorses are wonderful flagship species in drawing attention to pressing issues in the marine environment and in mobilizing efforts to find and implement solutions. Many of the 46 species around the world are threatened by overfishing, damaging fishing practices, and habitat degradation. We have responded to these challenges on multiple layers, many of them related to spatial management. In the Philippines, efforts to recover seahorse populations have prompted the creation of 35 no-take marine protected areas, all of them community-based and community-managed. In driving the first global export regulations on marine fishes under CITES, we are encouraging countries to use marine protected areas to meet their obligations to sustainable use. In pushing to end the destruction of bottom trawling, we are promoting trawl exclusion zones and an end to bottom trawling in marine protected areas.

Shifting the conservation paradigm: goals and options for managing biodiversity and ecosystems under climate change (virtual presentation)

Suzanne Prober[1],

[1] CSIRO

Impacts of climate change on ecosystems and biodiversity are becoming increasingly apparent, requiring reconsideration of our approaches to ecological management and restoration. However, there is little consensus on how to establish nature conservation goals in a changing climate, or what types of management can effectively achieve such goals. In this talk I'll consider how we may need to change our thinking to optimise biodiversity outcomes under climate change. This includes a need for new principles, such as maintaining biogeographic structuring, to underpin decision-making when restoring 'what was' is no longer realistic. I will then introduce a typology of on-ground climate adaptation options for terrestrial biodiversity and ecosystems, including options ranging from 'low-regrets' to 'climate-targeted', and options that aim to ameliorate impacts and those that aim to enhance adaptive capacity. I will close with some thoughts on the challenges we face to gain evidence of effectiveness of potential adaptation options, and some potential ways forward.

CONCURRENT SESSIONS

Concurrent Session 01 (Climate Change Biogeography)
June 3rd 2:00 pm – 3:30 pm PT – Room 2/3

Body-size and food-web interactions mediate species range shifts under warming

Malin Pinsky[1,] Edward Tekwa[2,] James Watson,

[1] Rutgers University
[2] University of British Columbia

Species ranges are shifting in response to climate change, but most predictions disregard food-web interactions and, in particular, if and how such interactions change through time. Predator-prey interactions could speed up species range shifts through predator release or create lags through biotic resistance. Here, we developed a spatially explicit model of interacting species, each with a thermal niche and embedded in a size-structured food-web across a temperature gradient that was then exposed to warming. We also created counterfactual single species models to contrast and highlight the effect of trophic interactions on range shifts. We found that dynamic trophic interactions hampered species range shifts. All species experiencing dynamic trophic interactions shifted more slowly than single-species models would predict. In addition, the trailing edges of larger-bodied species ranges shifted especially slowly because of ecological subsidies from small shifting prey. Trophic interactions also reduced the numbers of locally novel species, novel interactions, and productive species, thus maintaining historical community compositions for longer. Current forecasts ignoring dynamic food-web interactions and allometry may greatly overestimate species' tendency to track climate change.

Rising minimum temperatures due to climate change contributed to 50-years of butterfly community shifts in high-latitude, western North America*

***(moved to on-demand presentation)**

Vaughn Shirey[1,] Leslie Ries[1,] Naresh Neupane,

[1] Georgetown University

Global climate change is contributing to the restructuring of biodiversity on the planet; however, many regions remain understudied and under-sampled which leads to gaps in our knowledge of potentially changing species distributions. High-latitude regions are experiencing notable climate change but are often under-sampled, even for popular groups such as butterflies. Using unstructured museum and citizen science data, we reconstructed patterns in occupancy for high-latitude butterflies in western North America to determine drivers of community change from 1970-2020. We found that rising minimum temperatures explain turnover in communities to reflect more warm-associated, southern species over time. Finally, we demonstrate via a separate simulation study that our results are robust despite the use of unstructured data. These findings parallel inference in other high-latitude regions where structured datasets are more accessible and provide a pathway for the use of museum and citizen science data in other studies involving long-term macroscale trends on a changing planet.

Tree productivity and thermophilization across a latitudinal forest gradient

Timothy Perez[1], Nicole Bison[2], Isaac Borrego, Lachlan Byrnes[3], Hugo G. Candido[4], Tim S. Fox, Josef Garen[2], Joel L. Scott, Milos Simovic[2], Vanessa Buzzard[5], Brian Enquist[5], Sean T. Michaletz[2],

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[2] UBC
[3] UCI
[4] UFV
[5] UA

Thermophilization refers to the increase in the abundance of species from warmer climates, and may act as a tool for predicting changes in the global carbon budget because of its effect on forest carbon sequestration in forest communities. Currently, it is unclear if thermophilization reduces, increases, or has no effect on forest productivity. For example, mortality-driven thermophilization could impair forest carbon sequestration, while growth recruitment, growth, or survival of species from warmer climates may promote carbon sequestration. Alternatively, zero-sum forest dynamics predicted by metabolic scaling theory suggests that thermophilization should have no effect forest on productivity. In our study, we used annual forest census data from nine 0.5ha forest communities that span a 40˚ latitudinal gradient to test if changes in community-level tree growth can be explained by thermophilization. We observed that forests from the hottest climates were more likely to experience thermophilization and a reduction in stem abundance. These results indicate mortality and no recruitment may be driving thermophilization. Tree growth exhibited weak deceleration in all plots and was not correlated with thermophilization, which suggests growth may compensate for mortality and poor recruitment at the plot level, consistent with the zero-sum forest dynamics.

Tree-ring records reveal that climate-envelope approaches underestimate population vulnerability to recent climate change

Daniel Perret[1], Margaret Evans[2], Dov Sax,

[1] Brown University
[2] University of Arizona

Forecasts of species' climate change responses often make the simplifying assumption that all populations have the same climatic tolerances, reflecting those of the species as a whole. This assumption underlies the use of climate envelope approaches for forecasting range dynamics. However, recent empirical work shows that population-level climate responses can vary widely, consistent with local adaptation, and even be opposite in sign to species-wide responses. Thus, the question is whether species' fates in future climates will be determined by population-level sensitivities or species-wide responses. Here we analyse tree-ring data to examine whether species-wide or population-level patterns better match observed responses to recent climate change. We focus on 24 populations of ponderosa pine across the western US that have experienced varying degrees of climate warming over the past century. We divided growth data from each population into pre-warming (1900-1982) and post-warming (1983-2015) periods, defined empirically with breakpoint regression of climate time series. We trained generalized linear mixed models on pre-warming tree growth as a function of climate normals, reflecting the species-wide response to spatial climatic variation, and annually-varying seasonal climatic variables, reflecting population-specific climate sensitivities. The species-wide model predicted significant growth increases in 60% of populations, reflecting a range-wide positive relationship between mean temperature and mean growth. However, observed post-warming growth never matched these predicted increases. Instead, observed growth closely matched population-level predictions, which also correctly predicted growth declines in the fastest-warming sites. Our results highlight the importance of population-level processes in determining species' responses to climate change, suggesting that climate envelope approaches can lead to incorrect conclusions about population vulnerability.

Biotic and Climate Velocities from the Last Glacial Maximum to present: Can the Trees Keep Up?

Andria Dawson[1,] Alissa Brown[2,] Antonio Castilla, Lauren Jenkins[3,] Sean Hoban[2,] John Robinson[4,] Adam Smith[3,] Allan Strand[5,] John Tipton[6,]

[1] Mount Royal University
[2] Morton Arboretum
[3] Missouri Botanical Garden
[4] Michigan State University
[5] College of Charleston
[6] University of Arkansas

A longstanding challenge in ecology is how to infer biotic velocities: the rate at which species' biogeographic ranges shift across landscapes. Understanding biotic velocity has practical importance for identifying which taxa can track modern climate change. Current understanding is primarily based on modern data limited in temporal extent, and with limited climate variability compared to the large and rapid predicted climate changes. Past periods of rapid climate change can serve as analogues, offering insight into the magnitude and direction of species' range shifts. Using a network of fossil pollen records, we infer biotic velocity for North American tree taxa from the Last Glacial Maximum to present. First we develop a Bayesian hierarchical spatio-temporal model to jointly estimate relative abundance of tree taxa. Then we quantify biotic velocity and its uncertainty from the Last Glacial Maximum to present. We do this using several measures of biotic velocity, allowing us to make inference about the nature of the taxon range shifts. More specifically, we quantify biotic velocity of the centroid and edges of the taxon range. We compare these biotic velocities to the rate of past climate change from Global Circulation Model output. This work extends previous efforts to quantify and compare biotic and climate velocities by inferring relative abundance of tree taxa from pollen without auxiliary information such as climate, and by characterizing uncertainty in velocity estimates. Results from this work will be used to make predictions about the potential of trees to keep up with expected rates of climate change.

Integrating physiology and biogeography: spatial variation of thermal tolerances of different insect taxa in central Europe and Pakistan.

Dr. Christian Hof[1,]
[1]Technical University of Munich (Germany), Chair for Terrestrial Ecology, BioChange Lab

To understand whether and how species will be able to cope with changing climatic conditions, the integration of thermal physiology and biogeography bears great potential. Specifically, knowledge about the variation of thermal tolerance ranges and limits across space will enhance our understanding of species' responses to climate change, and may improve biodiversity projections under future climate change scenarios. Here, we present results from our studies on the variation of thermal tolerances of three different insect taxa along elevational and climatic gradients. We collected physiological data on thermal tolerance limits of several thousand individuals of about 100 species of grasshoppers, damselflies, and ants in the German state of Bavaria as well as in the mountain ranges of central and Northern Pakistan. When exploring how and to which extent thermal tolerances vary within and among species, we found that while intraspecific variation was large, there were also clear patterns of interspecific differences that could only partly be explained by phylogenetic relatedness. Thermal limits such as critical temperature maxima decreased with elevation, as expected, but with subtle differences between different regions which were likely due to varying microclimatic. Overall, we argue that the multi-disciplinary integration of data and methods from biogeography, physiology and ecology as well as across taxonomic and spatial scales is a promising, albeit challenging, avenue towards more realistic projections of potential distributions and diversity patterns under global change.

Concurrent Session 02 (Species Distributions)
June 3rd 2:00 pm – 3:30 pm PT – Room 8

Birds on the Move: Forty Years of Breeding Range Shifts of Migratory Birds in Illinois

Wendy Dorman[1],

[1] University of Illinois - Urbana Champaign

Due to the warming climate many taxa have exhibited earlier and more rapid migration. While some species are migrating earlier, resulting in a mix of positive and negative impacts on population numbers by species, there is little information on how changing migratory behaviors impact the breeding distributions of migratory birds. Using data from the Illinois Spring Bird Count we were able to examine variations in relative abundance across the state of Illinois over a span of 40 years. By coupling these changes with eBird occurrence, Breeding Bird Survey, and Breeding Bird Atlas data we were able to estimate how migratory avian species' breeding ranges have shifted across the state. We will discuss the outcomes for avian species in the state of Illinois as well as implications for the future of migratory avian species.

Changes in small mammal species distributions following the terminal Pleistocene megafauna extinction

Kate Lyons[1], Catalina P. Tomé[2], Nick Freymueller, William Gearty[2], Jonathan Keller[3], Melissa Pardi[4], Emma Elliott Smith[5], Felisa Smith[6], Quentin Smith[1], Peter J. Wagner[1],

[1] University of Nebraska Lincoln
[2] University of Nebraska-Lincoln
[3] University of New Mexico
[4] Illinois State Museum
[5] Smithsonian Institution
[6] University Of New Mexico

Much attention has been paid to the decline of large-bodied mammals because of their importance as ecosystem engineers and their elevated extinction rates in the Pleistocene. Less is known about the coinciding shifts in ecological structure among small mammals. Here, we evaluate the response of small mammals at Halls Cave, TX to the terminal Pleistocene extinction using species abundance distributions (SADs). Differences in SADs can distinguish communities with little to no resource partitioning (saturated model) or where niche partitioning is a "zero sum" game (e.g., Geometric, Log-Series or Zero-Sum Multinomial models) from communities with complex guild structure (e.g., Lognormal, Zipf or Zipf-Mandelbrot models). We divided the small mammal record at Hall's Cave over the last 21,000 years into 16 intervals, 8 pre-, and 8 post- extinction. We fit each interval with the aforementioned models. Model likelihoods reflect the probability of observing X species with 1…n specimens given N total specimens. AICc weights were used to contrast the models. We find that although most intervals pre-extinction were best fit by a Lognormal, only one post-extinction interval was. Instead, post-extinction, SADs were best fit by saturated or Geometric models. Our results demonstrate that the Halls Cave small-mammal community was greatly altered after the terminal Pleistocene extinction, with underlying ecological structure severely disrupted or simplified. Moreover, our results suggest a loss of a more complex structure that never re-appeared. Future body size downgrading caused by the loss of currently at-risk large mammals is likely to result in similar simplification of surviving mammal communities.

Mapping known and undiscovered ant biodiversity across the globe and assessing agreement and mismatch with vertebrates

Jamie Kass[1], Benoit Guénard[2], Clinton Jenkins, Kenneth L. Dudley[1], Fumika Azuma[1], Brian L. Fisher[3], Catherine Parr[4], Heloise Gibb[5], John T. Longino[6], Philip S. Ward[7], Anne Chao[8], Steven Shattuck[9], David Lubertazzi[10], Michael D. Weiser[11], Walter Jetz[12], Robert P. Guralnick[13], Nathan J. Sanders[14], Robert R. Dunn[15], Evan Economo[16],

[1] Okinawa Institute of Science and Technology Graduate University
[2] University of Hong Kong
[3] California Academy of Sciences
[4] University of Liverpool
[5] La Trobe University
[6] University of Utah
[7] University of California, Davis
[8] National Tsing Hua University
[9] CSIRO
[10] Harvard University
[11] University of Oklahoma
[12] Yale University
[13] University of Florida
[14] University of Michigan
[15] North Carolina State University
[16] Okinawa Institute of Science and Technology

Global maps of biodiversity are essential for conservation yet are heavily biased towards terrestrial vertebrates, the groups that are best represented in available biodiversity data. However, a majority of described species, terrestrial animal biomass, and key contributors to ecosystem functions are invertebrate taxa, most of which suffer from data shortfalls and thus have large-scale biodiversity patterns that are poorly known. This makes locating centers of invertebrate biodiversity and comparing them to more well-known centers for vertebrates particularly difficult. Here, we present a high-resolution, global diversity map for ants, an important invertebrate group diverse in form and widespread geographically. We employed an occurrence database including all known ant species and developed custom pipelines for data georeferencing and spatial modeling. We estimated diversity using a species distribution modeling approach, but also tested other methods for comparison. We found both areas of agreement and mismatch between patterns of biodiversity for ants and terrestrial vertebrates, and we recovered the same general patterns regardless of modeling method. We additionally predicted undiscovered ant biodiversity across the globe using random forest models and estimated ant sampling intensity to guide future sampling efforts. Although the global species inventory is far from complete, our results demonstrate that we can develop informatics and modeling pipelines to resolve provisional diversity maps for under-studied groups and guide future discovery.

Multi-species distribution models and bias adjustments for large biodiversity datasets: an application to >10 000 species of the European Flora

Abbie Gail Jones[1], Brian Leung[2], Laura J. Pollock,

[1] McGill University
[2] McGill

Describing the spatial distribution of species is vital for successful species, habitat, or biodiversity conservation policies and recovery plans. In this context, species distribution models (SDMs) have become a commonly used numerical tool to estimate species ranges by joining occurrence data with geographic predictors. However, as the open-source geographic species data on which SDMs are fitted (e.g., GBIF) typically contain substantial systematic spatial and taxonomical biases, the validity of SDM projections remain questionable. The novel S2BaK model combines opportunistic species sightings-only data with systematic species surveys to generate

computationally efficient "bias-adjustment kernels", resulting in improved predictive power in comparison to traditional models. As S2BaK can adjust the output of any SDM, it retains the flexibility to use advances in the SDM literature and to be scalable to large systems. While this approach was previously successful in a small country with low data availability (Panama), this project tests and scales up the uses of S2BaK to a continental context by building integrative models for the data-rich and environmentally heterogeneous European Flora. We found high spatial biases, but interestingly, species level biases were small in sightings-only records. We show that the S2BaK model successfully removed these biases to allow accurate inferences, including for species not observed in any systematic survey. We provide an optimized continental plant α-diversity information layer, representing the most complete, speciose, and fine-scaled vegetation biodiversity baseline of Europe to date, which will be a key tool in answering ecological questions on plant distributions and their susceptibility to anthropogenic stressors.

Distributions are more than habitat amount: the metapopulation structure is a vital element to distribution change

Victor Cameron[1,] Dominique Gravel[2,]

[1] Sherbrooke University
[2] Université de Sherbrooke

Distribution modelling has traditionally used bioclimatic models, which are limited in their ability to model distribution dynamics and mostly assume single species with limited consideration of dispersal processes. We build upon recent mechanistic approaches, demonstrating that metapopulation theory can manage the complexity arising from processes such as biotic interactions, demography, and landscape structure. We developed a theoretical founding for predicting the responses of a habitat specialist to climate warming, and derived three predictions: i) changes in habitat availability affect top trophic levels, ii) linear changes in habitat availability generate nonlinear changes in distribution, and iii) the effects of environmental change on habitat can propagate upward and affect higher trophic levels. We used the Bicknell's thrush to illustrate changes in regional distribution. The Bicknell's thrush is a "threatened", patchily distributed bird species restricted to dense, high elevation balsam fir forests. We observed significant losses of suitable habitat patches under climate warming; moderate warming increased habitat amount in some regions, but intense warming had severe, negative effects. Our results imply important changes to the spatial structure of the species distribution. Changes in metapopulation persistence differed from those in habitat amount, suggesting that habitat amount alone is not enough to characterize regional distributional changes. Our results support the importance of integrating both habitat amount and landscape spatial structure in distribution modelling, for which metapopulation theory may be an ideal framework. We suggest that metapopulation models could increase the accuracy of distribution models and optimize conservation strategies.

Concurrent Session 03 (Biodiversity Patterns & Maintenance)
June 3rd 2:00 pm – 3:30 pm PT – Room 11

Unpacking patterns in mammal functional and phylogenetic diversity in the Anthropocene

Carson Hedberg[1], Kate Lyons[2], Felisa Smith,

[1] University of New Mexico
[2] University of Nebraska Lincoln

Patterns in functional and phylogenetic diversity reflect ecological and evolutionary relationships among taxa, and thus can offer key insights into the mechanisms behind species distribution and community structure. However, human activities have enormously impacted the global distribution of fauna, particularly mammals, over the past millennia. These profound anthropogenic impacts are often ignored when investigating large-scale patterns in species distribution, potentially skewing our understanding of the underlying mechanisms influencing biodiversity accumulation and community structure. Here, we investigated global patterns in mammalian functional and phylogenetic diversity using current ranges as well as estimated present natural ranges in the absence of anthropogenic influence. We used the PHYLACINE 1.2 dataset to generate species lists for 91x91 km grid cells under both scenarios. We then measured mean pairwise distances (MPD) and mean nearest neighbor distances (MNND) in phylogenetic and functional space for each regional community, as well as the ratio of functional to phylogenetic distance between species pairs. Results were compared to a null model to tease out significant drivers of community assembly across latitude. We find that harsher environments such as deserts and tundra exhibit lower mean functional distance, suggesting stronger environmental filtering. However, nearest functional neighbor distances are often greater than expected, which implies farther spacing between species within functional space, despite lower community-wide functional breadth. Patterns in functional and phylogenetic diversity are largely consistent when present natural ranges are used except in the new world, suggesting the impact of historic and pre-historic biodiversity decline was greatest in these regions.

Evolutionary history, paleo- and contemporary abiotic filters drive tropical mammal community structure

Chia Hsieh[1], Daniel Gorczynski[2], Patrick A. Jansen, Kelly Boekee[3], David Kenfack[3], Douglas Sheil[4], Robert Bitariho[5], Marcela Guimarães Moreira Lima[6], Fernanda Santos[6], Krisna Gajapersad[7], Patricia Alvarez-Loayza[8], Wilson R. Spironello[9], Ben Swanepoel[10], Vittoria Estienne[10], Ahimsa Campos-Arceiz[11], Christine Fletcher[11], Arafat Mtui[12], Francesco Rovero[13], Oscar Madrigal[14], Rodolfo Vasquez[15], Santiago Espinosa[16], Julia Salvador[17], Lydia Beaudrot[2],

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[3] Smithsonian Tropical Research Institute
[4] Forest Ecology and Forest Management Group, Wageningen University
[5] Institute of Tropical Forest Conservation
[6] Department of Mastozoology, Museu Paraense Emílio Goeldi
[7] Conservation International, Suriname
[8] Center for Tropical Conservation, Nicholas School of the Environment, University in Durham
[9] Instituto Nacional de Pesquisas da Amazônia
[10] Wildlife Conservation Society
[11] School of Environmental and Geographical Sciences, University of Nottingham Malaysia Campus
[12] Tropical Biodiversity Section, MUSE-Museo delle Scienze
[13] Tropical Biodiversity Section, MUSE-Museo delle Scienze;Department of Biology,University of Florence
[14] Organization for Tropical Studies, Puerto Viejo de Sarapiquí
[15] Missouri Botanical Garden
[16] Pontificia Universidad Catolica del Ecuador; Universidad Autónoma de San Luis Potosí, Mexico
[17] Pontificia Universidad Catolica del Ecuador

Multiple hypotheses have been proposed to explain the latitudinal diversity gradient, including evolutionary hypotheses related to time or energy stability for driving species diversification, and ecological processes on species co-existence. However, a single explanation from an evolutionary or ecological perspective may not be sufficient to explain the congruent high species richness among tropical realms. To better understand the underlying processes driving pantropical species richness, we used occurrence data from 15 sites collected by the standardized camera-trap monitoring protocol of the Tropical Ecological Assessment and Monitoring Network and evaluated the relative importance of evolutionary and ecological drivers of the phylogenetic and functional structure of ground-dwelling mammal communities. Specifically, we used linear regression models to test the relative importance of colonization time, climate change and anthropogenetic disturbance over deep time, and contemporary energy seasonality and environmental heterogeneity on community structure. We found that longer time since colonization resulted in higher extinction probabilities of some clades and speciation among closely related species, leading to the phylogenetically dispersed structure from the phylogenetic tree root, but clustered structure in closely related species and functional diversity. Increasing habitat heterogeneity may provide species more opportunities to adaptively diversify for each habitat type, contributing to phylogenetically and functionally overdispersed community structures. In contrast, higher anthropogenic disturbance over deep time and contemporary energy instability acted as abiotic filters to exclude intolerant clades, resulting in phylogenetically overdispersed but functionally clustered community structure. Our results provide insight into the generality of evolutionary and ecological processes driving pantropical mammal phylogenetic and functional community structures.

Extending trait-based inferences of ecological assembly processes to multitrophic communities

Jean-Philippe Lessard[1,] Emma-Liina Marjakangas[2,] Gabriel Munoz, Shaun Turney[1,] Jörg Albrecht[3,] Eike-Lena Neuschulz[3,] Matthias Schleuning[3,]

[1] Concordia University
[2] Centre for Biodiversity Dynamics, Norwegian University of Science and Technology
[3] Senckenberg Biodiversity and Climate Research Centre (SBiK-F)

The study of ecological networks has progressively evolved from a mostly descriptive science to one that attempts to elucidate the processes governing the emerging structure of multitrophic communities. To move forward, we developed a conceptual framework using trait-based inference of ecological processes to improve our understanding of network assembly and our ability to predict network reassembly amid global change. The framework formalizes the view that network assembly is governed by processes shaping the composition of resource and consumer communities within trophic levels and those dictating species' interactions between trophic levels. I will present a case study using traits to infer how the mode of assembly vary along an elevation gradient in Andean plant-frugivore networks. Results indicate that the mode of network assembly is mainly bottom-up controlled, suggesting that the filtering of plant traits has a larger effect on network structure relative to the filtering of frugivore traits.

Developing methods for invertebrate macroecology on the continental scale using the NEON pitfall network

Katie Marshall[1], Jarrett Blair[1], Michael D. Weiser, Cameron Siler[2], Michael Kaspari[2],

[1] University of British Columbia
[2] University of Oklahoma

Invertebrates are important drivers of biodiversity: the form the bulk of animal biodiversity and biomass. Yet macroecological studies of invertebrates are rare relative to their diversity. This is not just due to bias towards charismatic megafauna, but also because of the very real challenges of invertebrate macroecology: individuals are often small and hard to identify to species without dissection, species may only be visible for relatively brief periods of time, and taxonomic entanglements are common. The National Ecological Observatory Network (NEON) in the United States may provide one way forward: a network of pitfall traps, collected every two weeks, across the country. While this provides a standardized and long-term potential data source, the sheer number and taxonomic scale of the collection provides significant challenges. Here we describe the development of two complementary analytical methods for working with these samples. First, we developed DNA metabarcoding from the preservative ethanol to identify species in a sample on a presence/absence basis. Secondly, we used imaging and machine learning methods to identify and measure each individual specimen, allowing calculation of diversity measures, abundance, and body size. Finally, we are now developing algorithms for combining these two methods to ideally obtain “the best of both worlds”: the taxonomic specificity of metabarcoding combined with the abundance and body size measurements from machine learning to provide a holistic look at invertebrate biodiversity across the United States.

Deep learning in ecology and biogeography: making the most of temporal data

Ana Ceia-Hasse[1], Andrew M. Kramer[2], Christiaan Meijer, César Capinha[1],

[1] Centre of Geographical Studies, Institute of Geography and Spatial Planning, University of Lisbon
[2] Department of Integrative Biology, University of South Florida

Temporal data is pervasive in ecology and accurately differentiating these data into classes, such as biological entities or ecological states is a common challenge. The most frequently used conventional statistical and machine learning methods rely on transforming time series into user-defined features and then using these features as predictors. In contrast, recent deep learning techniques can achieve the classification directly from the time series, which removes subjective and resource-consuming data transformation steps, and can improve classification results. This is an asset in face of the growing availability of time series data, namely from species monitoring programs and environmental sensors, that can thus be directly fed into models. As such, we suggest using deep learning models as an alternative to the classical methods. We illustrate our approach in three case studies: a) species identification using spectrograms; b) species distribution modelling using climate time series and c) forecasting phenology with continuous meteorological data. Our deep learning approach provided accurate, ecologically sensible classifications, thereby showing its potential for a wider applicability across subfields of ecology and biogeography.

Borrowing predictive strength across species to map more of biodiversity

Kevin Winner[1], Shubhi Sharma[1], Walter Jetz,

[1] Yale University

Modern data collection efforts for biodiversity data, coupled with advances in modeling have significantly improved our ability to describe the distribution and/or niche of many more species than ever before. However, a significant proportion of at-risk species are "data-poor", lacking sufficient primary observational data to fit modern species distribution/ecological niche models. In this work, we explore potential existing and novel multi-species mechanisms to "borrow strength" from data-rich species to better serve data-poor ones. We focus on the potential and limitations of cooccurrence, biotic interaction, phylogenetic, and trait information with respect to this borrowing strength problem and make specific research and modeling recommendations for the community as we develop new multi-species distribution modeling approaches.

Concurrent Session 04 (Island Biogeography)
June 3rd 2:00 pm – 3:30 pm PT – Ballroom C

Dissecting dynamicity of fish communities in island-like marine lakes

Bailey Carlson[1,]

[1] University of California, Merced

Despite amassing information over ~5 decades, island biogeography studies highlighting young islands and the early stages of community assembly are sparse. Here, we explore the early stages of fish community assembly in stratified and mixed marine lakes—a timeline of young island-like habitats formed between 12 to 6 thousand years ago—and lagoons in Palau. We sought to determine how fish communities are structured in these varying environments. Alpha diversity measures were calculated using presence-absence surveys of 16 stratified and mixed marine lakes—representing a subset of older to younger lakes, respectively—and 3 lagoon sites; traits from FishBase; and phylogenetic distances from the Fish Tree of Life. Cluster and standardized analyses were used in calculating beta diversities. Taxonomic diversity showed high replacement (78-87%). Sites partitioned taxonomically into 3 groups based on stratification. Communities exhibited stochastic, overdispersed, or clustered trait assemblies. Functional traits tested were not significantly related to environmental factors. Phylogenetic distances were primarily stochastic in communities. Sites were inhabited by different species, but the traits and phylogenetic distances found in each environment were not significantly different. Traits tested here may be neutral to fish survival in these environments. Our results of different aged environments show how communities may have shifted taxonomically over brief time periods coupled with rapid environmental changes. The marine lakes may serve as a proxy for community assemblies of young islands that begin as a homogeneous singular habitat that experiences transformation, exposing species to increased habitat diversity, altering community assemblies due to shrinking habitat space.

How Invaded are Hawaiian Forests? Top-down and Bottom-up Views Provide Contrasting Assessments of Degradation by Non-native Plants.

Dr. Kevin Potter[1,]

[1]Department of Forestry and Environmental Resources, North Carolina State University

Tropical island systems are particularly vulnerable to invasive species, and the Hawaiian Islands are a leading global hotspot of non-native plant invasion. We conducted the first comprehensive and field-based assessment of native and non-native forest plants from forest floor to canopy across Hawaiʻi, using data from the USDA Forest Service’s Forest Inventory and Analysis (FIA) network of 238 standardized plots. Non-native species accounted for about a third of large tree stems and carbon, but two-thirds of sapling stems and carbon and seedling stems. Non-native species were present in 56% of Hawaiʻi’s forests and dominated 39%. In all forest types, non-native trees constituted a larger proportion of the understory than the overstory tree component. This lack of sufficient native regeneration may result in replacement of native canopy trees by non-native trees following tree mortality events. Overall, results indicated that Hawaiian forests exist across an invasion continuum: Low elevations on the oldest islands exhibited the highest degree of non-native species dominance, and high elevations on the youngest islands exhibited the highest degree of native species dominance. Forests on public lands, in conservation reserves, or in fenced areas managed as ungulate-free were less invaded by non-native trees and shrubs than those in other ownership or management types. For example, fenced plots were 75% less invaded than unfenced plots on average. These differences may reflect effective management and/or differences in initial conditions of those forests when fenced or designated. The study results are a concerning evaluation of the ecological integrity of Hawaiian native-dominated forests.

Source Areas and Dispersal Patterns within the Macaronesian Flora

Jonathan Price[1], Juli Caujapé-Castells[2], Carlos García-Verdugo, Christoph Kueffer[3], Rüdiger Otto[4], Maria Romeiras[5], Miguel Menezes de Sequeira[6], José María Fernández-Palacios[7],

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This study of the spermatophyte flora of Macaronesia examines several non-exclusive hypotheses about colonization to and dispersal within this insular oceanic region: 1) older archipelagos were colonized first and younger archipelagos later via stepping-stone dispersal, 2) archipelagos closer to source areas were colonized first (and more often), and 3) source areas reflect the habitats available within a given archipelago. Abundant phylogenetic studies allow us to identify the source regions for Macaronesian taxa. For native non-endemic (NNE) species, we use the non-Macaronesian distribution to estimate where the taxon likely originated. For larger clades, there is sufficient topological evidence to determine the number and direction of dispersal events among the four major archipelagos. Different source areas are overrepresented in the four archipelagos: North Temperate Europe in the Azores, the Mediterranean region in Madeira and the Canaries, and Tropical Africa in Cape Verde. Nonetheless, the Canaries exhibit the greatest diversity of source areas, reflecting their greater habitat diversity. Most large endemic lineages (radiations) extend across multiple archipelagos, having formed in one and dispersed to others; the most common patterns of dispersal are from the Canaries to Madeira (sometimes then to the Azores) and from the Canaries to Cape Verde. Overall, dispersal patterns are a function of archipelago age progression, habitat filters, and in situ diversification. The habitat diversity and age of the Canary Islands in particular appear to have promoted diversification (with associated habitat shifts) of several key clades, facilitating colonization of archipelagos with habitats substantially dissimilar to source areas.

Threatened and extinct island endemic birds: distribution, threats and ecological function

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While intensive research has focused on island bird conservation or extinction, few global syntheses have considered these factors together in the context of impacts on ecosystem function. We compile functional trait data to provide a global summary of the status and ecology of island birds and the implications for functioning of island ecosystems. We find that almost half of all island endemic birds extant in 1500 CE are currently either extinct or threatened with extinction. While there is overlap between the hotspots of threatened and extinct island endemics birds, there are some notable differences, including that the Philippines and Indonesia support a substantial number of threatened species but have recorded no post-1500 CE extinctions. In contrast, certain island groups are hotspots of extinctions but support much fewer threatened species, indicating that the most vulnerable species have already been lost. Threatened island endemic birds are unevenly distributed across orders, with both similarities and differences to the same patterns for all bird species. Traits associated with threatened island endemic birds are large body mass, flightlessness, aquatic predator, omnivorous and vertivorous trophic niches, and marine habitat affinity, and, paradoxically, higher dispersal ability. Critically, we find that threatened island endemics represent substantial unique areas of the overall functional space of island endemics, and caution that their loss will have severe effects on avian functional diversity. Overall, our assessment provides the most up-to-date overview of the global conservation status of island endemic birds, the threats they face, and the traits that drive their extinction risk.

Schizomids: little arachnids, big implications for the generality of island diversity patterns in Palau (Micronesia)

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The Palau archipelago is an arc-trench island system in Western Micronesia which is at least 30 million years old and includes hundreds of limestone karst islands that feature primary lowland tropical rainforest. This unique geology and geography provides necessary context for understanding the biogeography of Oceania and the generality of island biodiversity patterns. In this study we use the phylogeography of Schizomida, a small arachnid order of fewer than 400 described species, in Palau and surrounding regions to test the generality of patterns such as the Island Progression pattern and the Taxon Cycle. We generated sequence data for 93 specimens collected throughout the archipelago and assembled a phylogeny using these sequences combined with 162 additional sequences from a previous study. We show that a variety of patterns emerge, from microendemism to genetically similar taxa with broad distributions. Widespread taxa were more likely to occur in low islands and beaches, consistent with the Taxon Cycle. Some of the deepest phylogenetic divergences occurred among taxa on older islands, consistent with the predictions of the Island Progression pattern. However, the overall phylogeny is complex and not necessarily in neat concordance with existing island biogeography paradigms. More broadly, we discuss the extent to which Palau may have been a stepping-stone between islands of Micronesia and source biotal areas in Southeast Asia and Papua New Guinea.

Fossil pollen sequences reveal changing biodiversity dynamics after human arrival on islands

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Intensified human activities are dominating ecological systems and are often considered the main drivers of ecosystems transformation. In contrast to continents, many island systems have been colonized by people within the last hundreds to thousand years. This relative recent start of human impact provides the unique opportunities to quantify the critical ecological transition from pre-human to human-dominated ecosystems and allows anthropogenic impacts on ecosystems to be placed within the context of long-term pre-human ecological dynamics.

Integrating fossil pollen sequences from multiple islands globally enables tracing vegetation community change over the past thousands of years. Results quantify a global trend of accelerated change in rates of compositional turnover following human arrival and reveal how fundamental island ecosystems have been transformed since human arrival. The later humans arrived in uninhabited island systems, the stronger was their immediate impact on island vegetation.

The strong global anthropogenic transformation in ecosystems revealed by tracing the transition from pre-human to human-dominated ecosystems on islands makes it evident that research in biogeography needs to acknowledge the large degree to which ecological changes today differ from pre-human dynamics. Fossil pollen sequences may be one tool to assess how processes we investigate in a human dominated world have shaped biodiversity dynamics before human impact.

Concurrent Session 05 (Climate Change & Conservation Biogeography)
June 3rd 4:00 pm – 5:45 pm PT – Room 2/3

Climate change winners and losers among North American bumble bees

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Mounting evidence suggests that climate change, agricultural intensification, and disease are impacting bumble bee health and contributing to species' declines. Identifying how these factors impact insect communities at large spatial and temporal scales is difficult, partly because species may respond in different ways. Further, the necessary data must span large spatial and temporal scales, which usually means they comprise aggregated, presence-only records collected using numerous methods (e.g., diversity surveys, educational collections, standardized ecological surveys, haphazard collections). Here, we use occupancy models, which explicitly correct for biases in the species observation process, to quantify the effect of changes in temperature, precipitation, and floral resources on bumble bee site occupancy over the past 12 decades in North America. We find no evidence of genus-wide declines, but do find that occupancy is negatively correlated with temperature, but only weakly related to precipitation or floral resources. We also find that more species are likely to be climate change "losers" than "winners" and that this effect appears primarily associated with changing temperature. Importantly, all trends were highly species-specific, highlighting that genus or community-wide measures may not reflect diverse species-specific patterns that are critical in guiding allocation of conservation resources.

Planted to thrive? Climatic viability of tree species in forest restoration plots under climate change

Gabriela Barragan[1,] Tongli Wang[1,] Jeanine M. Rhemtulla,

[1] University of British Columbia

Ambitious large-scale forest restoration initiatives rely on tree planting as a strategy to meet multiple goals, including climate change mitigation. Paradoxically, climate change could pose a challenge for species planted in restoration plots if the trees planted are not resilient to changing climatic conditions. To understand how climate change might affect planted trees in large-scale restoration initiatives, we examined the future climate viability of tree species planted from 2014-2017 in Ecuador's National Reforestation Initiative. Using 1237 restoration plots in Northwest Ecuador, we assessed future climatic viability of 10 commonly planted species in 2030, 2050, and 2070. We modeled the probability of suitable climate for the species in restoration plots under two emission scenarios (i.e., RCP 4.5 and RCP 8.5) and 14 General Circulation Models. We assessed species climatic viability using continuous data, instead of the more commonly used binary approach. We found that 70% of the species which showed medium and high climatic viability are species with high climatic tolerance range, native to the location of the restoration plots. The other 30% were species native to the country but from a

different bioregion. Our results suggest that planting species native to the area of intervention is a good option if restoration planners are not able to consider climate change projections in their planning. Given that climate change effects are projected to vary among species and sites, and that many large-scale national restoration initiatives include non-native species, incorporating climate change assessment scenarios to improve species and site selection will help to ensure that planted trees with thrive into the future.

Geographic Range Dynamics of Māori and Moa

Mark Lomolino[1], Sean Tomlinson[2], Damien Fordham,

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The central challenge of conservation biogeography is to develop a better understanding of the geography and dynamics of nature and to then apply these lessons to conserve the ecological context of focal species and the communities that they are embedded in. Geographic dynamics includes the spatio-temporal patterns of range collapse along with the patterns of spread of the putative extinction forces. Here we describe how our research program in macroecology and biogeography is providing some intriguing insights on the historical drivers (climatic and anthropogenic) of geographic range collapse in an extinct guild of flightless birds – New Zealand's moa. Lessons learned from the past in this way will provide tools essential for conservation of extant species threatened with extinction.

A Mammoth buffet: resolving extinct herbivore community structure through multiproxy coprolite analysis

Alessandro Mereghetti[1], Mikayla Mason[1], Valeriy Plotnikov, Albert Protopopov[2], Ethan Mackenzie[1], Noa Buzby[1], Jacquelyn Gill[1],

[1] University of Maine
[2] Academy of Science of the Republic of Sakha

During the Pleistocene, the Arctic was inhabited by a diverse community of cold-adapted large herbivores that disappeared during the last 20,000 years. The mechanisms that allowed the coexistence of a high biomass of different herbivore species (including Mammuthus primigenius, Coelodonta antiquitatis, Bison priscus, Equus sp., Rangifer tarandus) in a high-latitude environment, supposedly low in plant diversity and productivity, is still debated. According to niche theory, coexistence between herbivore species is promoted by dietary specialization, with species-specific forage preferences. Most of the studies on Pleistocene Arctic herbivore diets are based on isotopic analysis of bones, that due to low taxonomic resolution give us conflicting results on the degree of dietary overlap. To better understand how extinct herbivores partitioned their diet, we analyzed a unique set of 59 coprolites (sub-fossil feces) from Yakutia, Siberia, deposited between ~20,000 and ~50,000 years before present. Our approach combines both traditional (macrofossils, pollen, phytoliths) and cutting-edge (ancient DNA) paleoecological tools to achieve a high taxonomical resolution for dietary reconstruction. The large number of samples from the same region coupled with the use of complementary dietary proxies allows us to reconstruct the diet of extinct Arctic herbivores with unprecedented accuracy. Our work contributes to shed light on the mechanisms that allowed the coexistence of Arctic megafaunal herbivores, potentially informing the reasons behind their final demise and giving us tools to investigate the impact of their extinction on surviving plant communities and high-latitude ecosystem processes.

The effects of climate change on Australia′s only endemic Pokémon: Measuring bias in species distribution models

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Species distribution models (SDMs) are frequently used to predict the effects of climate change on species of conservation concern. Biases inherent in the process of constructing SDMs and transferring them to new climate scenarios may result in undesirable conservation outcomes. We explore these issues and demonstrate new methods to estimate biases induced by the design of SDM studies. We present these methods in the context of estimating the effects of climate change on Australia's only endemic Pokémon. Our models suggest that climate change will impact the suitability of habitat for G. kangaskhani. However, we also find that using SDMs to estimate the effects of climate change can be accompanied by biases so strong that the data themselves have minimal impact on modelling outcomes. We show that the direction and magnitude of bias in estimates of climate change impacts are affected by every aspect of the modelling process, and suggest that bias estimates should be included in future studies of this type.

Genetic patterns and distribution of the worldwide invasive red-eared slider turtle and its native congeners.

Dr. Ella Vázquez-Domínguez[1,]
[1] UNAM

Non-native (invasive) species offer a unique opportunity to study the geographic distribution and range limits of species, wherein the evolutionary change driven by interspecific interactions between native and non-native closely related species is a key component. The red-eared slider turtle, Trachemys scripta elegans (TSE), has been introduced and successfully established worldwide. It coexists with its native congeners T. cataspila, T. venusta and T. taylori in Mexico. We performed comprehensive fieldwork, executed a battery of genetic analyses and applied a novel species distribution modeling approach to evaluate their historical lineage relationships and contemporary population genetic patterns. Our findings support the historical common ancestry between native TSE and non-native (TSEalien), while also highlighting the genetic differentiation of the exotic lineage. Genetic patterns are associated with their range size/endemism gradient, the microendemic T. taylori showed significant reduced genetic diversity and high differentiation, whereas TSEalien showed the highest diversity and signals of population size expansion. Counter to our expectations, lower naturally occurring distribution overlap and little admixture patterns were found between TSE and its congeners, exhibiting reduced gene flow and clear genetic separation across neighboring species despite having zones of contact. We demonstrate that these native Trachemys species have distinct climatic niche suitability, likely preventing establishment of and displacement by the TSEalien. Moreover, we found major niche overlap between TSEalien and native species worldwide, supporting our prediction that sites with closer ecological optima to the invasive species have higher establishment risk than those that are closer to the niche-center of the native species.

Landscape fragmentation of the Natura 2000 network and its surrounding areas

Alexandra Lawrence[1], Fabian Friedrich[1], Carl Beierkuhnlein,

[1] University of Bayreuth

Habitat loss from anthropogenic development has led to an unprecedented decline in global biodiversity. Protected areas (PAs), such as the Natura 2000 (N2k) network the world's largest coordinated network of protected areas, exist to counteract this degradation of ecosystems. However anthropogenic development can affect even the interiors of PAs. In this study we attempt to quantify the degree to which all N2k PAs in the EU are insulated from development pressures. We use a comprehensive dataset of effective mesh density (seff) to measure aggregate fragmentation inside and within a 5 km buffer surrounding N2k PAs. Our results show a strong correlation ($R^2 = 0.78$) between fragmentation (seff) within and around N2k PAs. This result applies to all biogeographical regions in Europe. Only a narrow majority (58.5%) of N2k PAs are less fragmented than their surroundings. Remote and mountainous regions show the lowest levels of fragmentation. These regions also tend to hold the largest N2k PAs as measured by area. 24.5% of all N2k PAs are classified as highly to very-highly fragmented. N2k PA age since initial protection does not correlate with the difference in exterior and interior fragmentation of N2k PAs. These results indicate that PAs in Europe are not sheltered from anthropogenic pressures leading to fragmentation. Hence, we argue that there is a high potential for improving PA efficacy by taking pre-emptive action against encroaching anthropogenic fragmentation and by targeting scarce financial resources where fragmentation pressures can be mitigated through enforced construction bans inside PAs.

Concurrent Session 06 (Gradients & Range Limits)
June 3rd 4:00 pm – 5:45 pm PT – Room 8

Living up to thermal potentials: Global patterns of thermal niche filling in ectotherms

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Temperature is one of many factors that shapes the large-scale distribution of life. As a result, the global redistribution of species is already occurring in response to climate warming. Yet range shifts are variable among taxa, suggesting different relationships between temperature and species' ranges. While some range limits are set by temperature, others may be set by dispersal, biotic interactions, or other environmental tolerances. To assess the role of temperature in limiting species' ranges, we explore patterns in how species fill their potential thermal niche in both niche (environmental) space and geographic (spatial) space. We find marine and terrestrial species fill their thermal niches differently; while both terrestrial and marine species underfill warm temperatures in their potential thermal niche, patterns across latitude differ and marine species have greater spatial underfilling. We also find that, measured in both ways, thermal niche filling is explained by realized range size but not by species' traits related to other range-limiting factors, like dispersal ability, body size and trophic position. While these results are robust to assumptions about thermal trait plasticity, sensitivity of results to modelling behaviour on land highlights the importance of considering how behavioural thermoregulation alters the temperatures organisms experience. We discuss the implications of our findings for species' vulnerabilities to climate change.

How to get high: Positive and relaxed selection on mitochondrial genes at high elevation

Erik Iverson[1,] Justin Havird[1,]

[1] The University of Texas at Austin

Species turnover within a genus is often observed across climatic gradients, and the search for 'speciation genes' has suggested that climatic differences in allopatry may select for alleles that cause incompatibilities in hybrid offspring upon secondary contact. One such incompatibility may be that between the mitochondrial (mt) and nuclear (N) genes that function together in oxidative phosphorylation (OXPHOS) to generate cellular energy. Mt divergence between sister species is often thought to be a neutral process, but mt haplotypes within and among species often segregate with temperature, food availability, or elevation, all of which are known to impact the efficiency of OXPHOS. For this reason, climatically-driven co-evolution between the mt and N genomes may set the stage for post-zygotic reproductive isolation between species. To investigate how climate shapes mtDNA divergence, we analyzed the signature of natural selection on the protein-coding regions of the mt genome. We obtained mitogenomes of terrestrial vertebrates in 130 three-species clades containing two closely-related species inhabiting relatively high and low elevations and a low-elevation outgroup. Values of the dN/dS ratio, a measure of the strength of selection, were elevated in high-elevation taxa relative to their low-elevation sister species. The effect was strongest in birds and mammals, and weaker in amphibians, non-avian reptiles, freshwater fishes, and arthropods. Because dN/dS ratios can be elevated by relaxed selection as well as positive selection, we employed a test for relaxed selection; results indicated that many cases of high dN/dS at elevation are best explained by relaxed selection, perhaps due to smaller population sizes. We discuss additional tests for biological traits and range characteristics that might help to explain these patterns, and end by discussing the implications of these findings for montane biodiversity under climate change.

Mathematically and biologically consistent framework for presence-absence pairwise indices of diversity

Petr Keil[1], Arnošt Šizling[2], Even Tjørve, Kathleen Tjørve[3], Jakub Žárský[2], David Storch[2]

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Large number of indices comparing two species assemblages have been proposed. Their interpretation varies across literature, despite efforts for clarification and unification. Most effort has focused on the mathematics behind the indices, their relationships to diversity, and to each other. However, following issues have been neglected: (i) inter-dependence of indices based on their informational value, (ii) overlap of biodiversity phenomena that the indices aim to capture, (iii) effect of spatial autocorrelation on the information provided by the indices, (v) requirement that a small re-arrangement of assemblages should only cause a small change in an index, and (vi) inferences from the indices about diversity patterns. Underappreciation of these issues has led to invention of indices without increasing their information value.

We offer a unified framework for pairwise diversity indices that accounts for these issues. We introduce a general definition of an index that covers all existing presence-absence indices. We show independence of these indices in terms of their information content. Further, we: (1) classify existing indices into six independent families, (2) show what can be inferred about spatial diversity phenomena from different indices, (3) demonstrate problems with most indices of nestedness, (4) provide formula linking mathematically (informationally) dependent indices, (5) show which combinations of indices can be used for meaningful ecological inference, and (6) show how to calculate any index from two presence-absence indices, which can be used to compare indices across literature.

We conclude that it is impossible to purify an index of one phenomenon (e.g. turnover) from effects of other phenomena (e.g. nestendess), since phenomena inevitably bound each other. Instead, a proper approach is to use a combination of classical indices from information-independent families.

The global drivers of tree range-edge hotspots

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Understanding the reasons for species distribution arrest has been a fundamental question in macroecology, biogeography, and evolution. Multiple theories have been hypothesized as to how species range expansions come to a rest at the edge between contrasting environments. In trees, these questions are further enforced considering their long lifespan, on the one hand, and their sessile nature, on the other. To better decipher the drivers of range-edge formation among tree populations, we analysed the spatial distribution of tree species at a global scale using GBIF database of >6000 species. By accurately defining the distribution of species and characterizing their range edges, we were able to identify geographical areas of range-edge hotspots and find drivers for species arrest. We found a strong association of range edge hotspots to low precipitation levels and steep climatic gradients. More specifically, we found that most range-edge hotpots occur at the edge of desert and tundra biomes. We discuss the implications of our results in understanding and characterizing the evolutionary constraints that account for a lack of adaptation to novel environments, and the significance of these results to better understanding the limits to the extent that species will endure the ongoing climate change.

Physical constraints drive morphological evolution and geographical size gradients in bats

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Ecologists have long used the physical linkage between morphology and energy balance to explain why endotherms display smaller body sizes in warm than in cold climates (i.e., Bergmann's rule). In bats, body size evolution and ecogeographical size gradients deviate from the patterns observed in other endotherms, probably because physical constraints on flight limit morphological adaptations. So far, few modeling exercises have aimed at investigating these constraints from first principles. Here, we developed a biophysical model based on heat transfer and aerodynamic principles to investigate how energy costs of thermoregulation and flight affect morphological evolution in bats. Our biophysical model predicts that the energy costs of thermoregulation and flight respectively impose upper and lower limits on the relationship of wing surface area to body mass (S-MR), giving rise to an optimal S-MR at which both energy costs are minimized. A comparative analysis of 278 species of bats strongly supports our model's predictions that (1) S-MR evolves towards an optimal shape, and (2) the strength of selection is higher among species experiencing greater energy demands for thermoregulation in cold climates. We propose that physical constraints on thermoregulation and flight drive morphological evolution in bats, hence shedding light on a longstanding debate over bats' conformity to ecogeographical patterns observed in other mammals.

Drivers of plant-pollinator interaction rewiring across a spatial gradient

Kaysee Arrowsmith[1,] Berry Brosi[1,]

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Plant-pollinator communities frequently experience interaction rewiring, in which plant-pollinator interactions shift despite the maintenance of the plants and pollinators involved in those interactions. Recent studies have identified spatial patterns in this rewiring; however, the forces driving these patterns have not yet been identified. Theory suggests that rewiring is influenced by the biotic and abiotic contexts in which interactions occur – for instance, temperature or community composition. In this study, I empirically test the effects of these proposed drivers of rewiring in a subalpine plant-pollinator system over two years (2020 & 2021). Using a geographic and elevational gradient, I evaluate plant-pollinator rewiring across 17 sites that comprise a consistent pool of plant and pollinator species but different abiotic conditions. I compare rewiring patterns across these sites to differences in variables like temperature, soil moisture, and species abundance. With this site setup, I am able to distinguish between geographically driven rewiring and rewiring attributable to environmental or biological differences between sites. My preliminary analyses confirm my hypothesis that environmental and biological dissimilarity are stronger drivers of rewiring than geographic or elevational distance alone and highlight the importance of the ecological context in which interactions occur. This framework for understanding interaction change is especially important when considering how climate change may affect plant-pollinator communities: environmental pressures may alter not only the ranges of plants and pollinators, but also the ranges of interactions between these organisms.

New tree-level temperature response curves document sensitivity, acclimatization, and adaptation to high temperatures

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Temperature is a key climate indicator, whose distribution is expected to shift right in a warming world. However, the high temperature tolerance of trees is less widely understood than their drought tolerance, especially when it comes to sub-lethal impacts on tree growth. In this paper, we use a large data set of annual tree ring widths, combined with a flexible degree-day model, to estimate the relationship between temperature and tree radial growth across different ecoregions of the US. We find that tree radial growth responds non-linearly to temperature: temperature increases are beneficial or mostly neutral for tree growth up to around 20-25°C in humid regions and 10-15°C in dry regions, beyond which temperature increases are harmful to tree growth. Six additional degree-days above the local optimal temperature lead to an average decrease in tree ring width of around 1%, with variation across ecoregions and seasons. In dry regions particularly, the low temperature threshold partially reflects the influence of temperature-mediated drought, winter temperature response, and lagged weather impacts. We find limited evidence that trees acclimatize to high temperatures within their lifetime: local variation in exposure to high temperatures, which stems from local variation in the timing of tree birth, does not significantly impact tree growth response to high temperatures. Conversely, we find that trees adapt to high temperatures in the long-run: across humid ecoregions of the US, high temperatures are 43% less harmful to tree growth, in locations where their average incidence is one standard deviation above the average.

Concurrent Session 07 (Phylogeography/Biodiversity)
June 3rd 4:00 pm – 5:45 pm PT – Room 11

Modeling genetic divergence and mapping phylogeographic breaks using machine learning

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[1] City College of New York

Understanding the distribution of genetic lineages within species can inform conservation decisions and protect genetic diversity. However, doing this for multiple species requires extensive field work, time and resources. Here, we aim to create a model to identify locations that separate different genetic lineages within a species. Such a model has the potential to inform conservation planning informed by genetic information without the need for extensive sampling. We present preliminary results using Random Forest (RF), a Machine Learning technique, which we used to train a model to predict the levels of genetic differentiation across populations. We tested this approach with genetic data from 28 birds of the Atlantic Forest biome of South America, a diverse and threatened Neotropical region. Using published mtDNA data, we calculated pairwise DXY and FST estimates among all pairs of localities, using it as the response variable. As predictor variables, we utilized geographic distance and present and past environmental dissimilarity among pairs of localities Our preliminary results include a total of 1375 mtDNA sequences and 7689 pairwise comparisons across localities. The locations of high genetic differentiation agree with previous studies in the area, suggesting our data is representative of known genetic breaks in this biome. Geographic distance was the most important predictor of genetic differentiation, followed by environmental dissimilarity during the Younger Dryas Stadial period (12 kya). Mean squared error was lower for models predicting FST than models predicting DXY. Our results suggest this approach is promising to predicting metrics of genetic differentiation. Our next steps will include incorporating ecological traits of species as possible predictors and extending our model to include ectothermic groups (e.g., amphibians).

Climatic instability through time shaped the global distribution of polyploid diversity in flowering plants

Eric Hagen[1], Thais Vasconcelos[1], Jeremy Beaulieu,

[1] University of Arkansas

The proportion of plants that are polyploid in a given area increases with latitude, and different hypotheses have been proposed about what climatic and biogeographic factors are the main drivers of global patterns in plant cytotype distribution. A question that remains is, are polyploids better able to move into and colonize polar regions? Or are there particular conditions in these areas, such as environmental instability through time, that promote in situ radiation of polyploids in the rare occasions when ancestors do successfully colonize polar regions? Answering this question requires examining the global distribution patterns of polyploids in the context of phylogenetic relationships between species. Here we examine the general geographical patterns of polyploid diversity in light of their phylogenetic diversity by modeling the distribution of 3182 polyploid and 7494 diploid flowering plant species to identify areas where phylogenetic diversity is above or below than expected for local polyploid species richness. Higher than expected phylogenetic diversity indicates that local polyploid species tend to be more distantly related, pointing towards constant movement of possibly pre-adapted lineages, whereas lower than expected phylogenetic diversity means that local polyploid species tend to be closely related, indicating in-situ radiations. Our results show that global phylogenetic diversity of polyploids is generally higher in subtropical and temperate areas of the Northern Hemisphere. Areas where interglacial refugia during the Quaternary were abundant, such as Eastern North America, Eastern Asia and Scandinavia, all present lower than expected phylogenetic diversity in contrast to their total polyploid diversity. Overall, these results show that the formation of the global gradient of polyploid diversity has a complex evolutionary history, but it appears to be mainly a result of in situ radiation due to the climatic oscillations of the Pleistocene.

Biogeographic inferences across spatial and evolutionary scales

Van Wishingrad[1,] Robert Thomson[2,]

[1] University of Hawai'i
[2] University of Hawaiʻi

The field of biogeography unites landscape genetics and phylogeography under a common conceptual framework. Landscape genetics traditionally focuses on recent-time, population-based, small geographic scale spatial genetics processes, while biogeography typically investigates deep past, lineage- and species-based processes at large geographic scales. Here we investigate spatial patterns of population genetic structure in western fence lizards (Sceloporus occidentalis) across spatial and evolutionary scales. We found significant concordance in landscape genetics inferences at 1225, 2500, and 4225 km-sq spatial scales, where river canyons appear to be important features maintaining genetic connectivity. However, at the largest spatial scale (6400 km-sq) there is a loss of resolution in the fine details of the landscape features that inhibit gene flow. Phylogeographic results identify five major clades over our sampling range, three of which are limited to distinct river drainages, while the other two are restricted to distinct hydrologic regions. At a more recent evolutionary scale, we find minor clades are restricted to a single river canyon in the majority of cases, while the remainder of river canyons include samples from at most two clades. Overall, the broad scale pattern of river canyons as key features linking populations in the landscape genetics results, and isolation by river canyon in the phylogeographic results, is consistent across the spatial and evolutionary timescales examined here. As landscape genetics and phylogeography share many of the same objectives, synthesizing theory, models, and methods between these fields will help bring about a better understanding of ecological and evolutionary processes structuring genetic variation.

Is the Tongue of the Ocean a phylogeographic barrier for Bahamian reef fishes?

Katriina Ilves[1,] Edward Myers[2,] Andrea Quattrini, Ron Eytan[3,] Mark Westneat[4,] Gordon Chaplin[5,] Carole Baldwin[6,]

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As a marine diversity hotspot with over 1,500 species of fishes, including more than 500 reef-fish species, the Caribbean Sea is a compelling arena in which to explore questions about biogeographic history. Historically, four biogeographic provinces in this region were defined based on patterns of endemism (Caribbean, West Indies, Panamanian, Brazilian), but these have been questioned due to a purported lack of endemicity and the identification of alternative breaks within these larger regions. We aim to add to the growing body of work on Caribbean phylogeography by using a broad dataset of taxa, loci, and samples from across the region to test longstanding questions and generate new insights about Caribbean biogeography in a statistical framework. The current study is a first step in this larger plan and aims to test the hypothesis of whether the Tongue of the Ocean (TOTO), a deep (1,100 – 2,000 m) trench separating Andros Island from other islands of The Bahamas, is a phylogeographic barrier for shallow-water reef fishes. This pilot project focused on four phylogenetically and ecologically disparate species (Apogon maculatus, Chromis cyanea, Gramma loreto, and Rypticus carpenteri)

where samples spanning TOTO were sequenced with both next-generation (genotype-by-sequencing) and Sanger (COI, cytb) approaches. Analyses of both datasets showed a lack of differentiation across this region, suggesting that TOTO is not a dispersal barrier for shallow-water reef fishes. Future comparisons with these, and additional species, will be made across the Florida Strait and other regions of the Caribbean to further test for phylogeographic breaks.

Integrating fossils and phylogenies reveals a boreotropical origin of the tea family (Theaceae)

Yujing Yan[1],

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The tea family (Theaceae) has a highly unusual amphi-Pacific disjunct distribution: most extant species in the family are restricted to subtropical evergreen broadleaf forests in East Asia, while a handful of species occur exclusively in the subtropical and tropical Americas. Here, we used an approach that integrates the rich fossil evidence of this group with phylogenies in biogeographic analysis to study the processes behind this distribution pattern. We first combined genome-skimming sequencing with existing molecular data to build a robust species-level phylogeny for c.130 Theaceae species, resolving most important unclarified relationships. We then developed an empirical Bayesian method to incorporate distribution evidence from fossil specimens into historical biogeographic analyses and used this method to account for the spatiotemporal history of Theaceae fossils. We compared our method with an alternative Bayesian approach and show that it provides consistent results while significantly reduces computational demands which allows analyses of much larger data sets. Our analyses revealed a circumboreal distribution of the family from the early Cenozoic to the Miocene and inferred repeated expansions and retractions of the modeled distribution in the Northern Hemisphere, suggesting that the current Theaceae distribution could be the remnant of a larger continuous distribution associated with the boreotropical forest that has been hypothesized to occupy most of the northern latitudes in the early Cenozoic. These results showcase the necessity of integrating fossil and molecular data in phylogeny-based parametric biogeographic models to improve the reliability of inferred biogeographical events.

Detecting the phylogenetic signal of glacial refugia in a bryodiversity hotspot outside the tropics

Ernest Wu[1], Jonathan Davies[2], Yang Liu,

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Glacial refugia have likely been important in shaping diversity gradients outside the tropics. Many taxa that have high extra-tropical diversity in the present day, such as mosses, may have persisted in glacial refugia. However, the biogeographical histories of most species within refugia remains unclear. In this study, we reconstructed the regional phylogeny of the mosses of Haida Gwaii archipelago, a putative glacial refugium and ‘hotspot’ of moss diversity on the northwest coast of British Columbia, Canada, and used phylogenetic comparative methods to examine the macroecological imprint of glacial refugia on the geographic range structure and phylogenetic attributes of present-day moss assemblages. We found that many mosses have widespread, but disjunct distributions, with few close relatives on the islands. We suggest that these features reflect the imprint of glacial history, whereby species within refugia represent isolated populations of previously more widespread species that may have diversified elsewhere. We also observed evidence for phylogenetic over-dispersion of species within high elevation habitats, which best match the climatic regime of the historical glacial refugium. Our results are consistent with the filtering of evolutionarily distinct glacial relicts within these habitats, which contrasts markedly with the patterns of phylogenetic clustering observed across other non-refugial habitat types. Our study illustrates how the present-day phylogenetic structure of mosses on Haida Gwaii may have been shaped by glacial history, and highlights the importance of glacial refugia in maintaining extra-tropical moss diversity.

Diversification cradles in the Sahara-Sahel: contrasting evolutionary histories in functional groups urges a reassessment of priority conservation zones

André Liz[1], Dennis Rödder[2], Duarte Vasconcelos Gonçalves, Guillermo Velo-Antón[3], Pierre-André Crochet[4], Silvia B. Carvalho[1], José Carlos Brito[1],

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The Sahara-Sahel Desert presents distinct bioclimatic and phytogeographical regions, where desert communities aggregate in localized biodiversity hotspots that arose from historical eco-evolutionary processes. These hotspots may differ across functional groups, due to the variable biogeographical affinities of desert taxa. The current characterization of hotspots is based on assessments at the species level (e.g., endemism richness) and lacks information on intra-specific genetic variability, despite its crucial importance for species persistence. Herein, we infer diversification cradles across the Sahara-Sahel taking into account differences in species habitat requirements. Phylogenetic diversity was mapped for well-sampled representatives of mesic and xeric desert taxa across the study area. Main diversification cradles were located in mountain areas and low sand-dune fields for mesic and xeric taxa, respectively. Mountain cradles match with the main potential mesic refugia for the ongoing climate crisis. Further studies on the barely-known Central Sahara highlands are needed to understand the magnitude of their regional diversity, even if they are already included in conservation strategies. On the contrary, xeric cradles remain ignored in conservation planning, due to the presumed low ecological diversity of sand-dune ecosystems. Xeric cradles may be particularly threatened by global warming, as species occur close to their physiological limits, and human pressures, including the expansion of extractive activities, green energy and agro-forestry. Thereby, we call for an urgent need to consider xeric diversification cradles in conservation planning. The location of diversification cradles in the Sahara-Sahel largely overlaps with inaccessible areas subjected to long-lasting conflicts, which greatly constrains research and conservation efforts.

Concurrent Session 08 (Models & Methods in Biogeography)
June 3rd 4:00 pm – 5:45 pm PT – Ballroom C

A joint SDM to study different observational data sets and account for their sampling designs

Jussi Makinen[1], Jeremy Cohen[1], Walter Jetz,

[1] Yale University

Joint analysis of multiple survey data sets improves predictions of species geographical distributions, but the improvements are conditional on properly accounting for different sampling processes of each data set. This has been a general obstacle for scaling up joint data analysis for wider taxonomical and geographical scopes in species distribution modeling. Here we develop an approach for integrating data sets from non-structured survey designs while addressing their sampling processes and examine the benefit of the approach for continental to global scale biodiversity research. We tailor the method for Ebird and Gbif, which are the data richest platforms for geographical biodiversity data of birds. Ebird provides information about species presence-absence status along with information about sampling intensity, and species observations have gone through a quality check. We support the analysis by integrating non-validated observations from GBIF in the model and examine the benefits of the joint data approach for biodiversity research given careful specification of sampling processes related to all data sources. We demonstrate the approach with South American hummingbirds.
Our results show that accounting for preferential sampling is important for modeling multiple non-structured species data sets jointly. Joint analysis is beneficial especially for species which have low prevalence in Ebird data, originating from low population density or spatial mismatch between sampling intensity and species range. These two findings expand the use of non-structured data sets, such as Ebird, and the general model developed here can be well applied to other data sets and species.

Niche Divergence Plane: New conceptual framework to classifying and quantifying ecological niche divergence between taxa

Alfredo Ascanio[1], Jason Bracken[1], Hank Stevens, Tereza Jezkova[1],

[1] Miami University

Comparisons between the ecological niches of two taxa are often performed by contrasting hypervolumes generated using ecologically relevant environmental variables. Currently, most of these hypervolume comparisons test the null hypothesis of niche conservatism or equivalency, with niche divergence representing the departure from the former. However, niches can diverge in different ways and directions because each species niche can shift, expand, shrink, or tilt. Additionally, individual environmental axes might diverge in different ways and magnitudes. Thus, our objective is to introduce a new methodological and conceptual framework that allows quantification and classification of niche divergence between two taxa along a niche axis. This new method, the Niche Divergence Plane, relies on positioning a niche axis in a two-dimensional plane defined by two indices. These indices are derived from comparing response curves of two taxa: niche exclusivity represents the range of values along the axis that is exclusive to each taxon, and niche dissimilarity relates to the area under response curves not shared between the two taxa. The latter also considers the differences in niche preference, even when there is significant niche overlap (i.e., low niche exclusivity). Based on the position of the two indices on the divergence plane, we distinguish four general types of niche divergence: hard, soft, weighted, and nested. Quantifying and classifying niche divergence in this way can give us greater insights about the processes driving the evolution of the ecological niche. We present a case study using species pairs of Ambystoma salamanders.

From tropics to treeline: Drivers of global variation in plant mortality rates

Isaac Borrego[1,] Tim Perez[1,] Nicole Bison, Lachlan Byrnes[2,] Hugo G. Candido[3,] Tim S. Fox, Josef Garen[4,] Joel L. Scott[5,] Milos Simovic[1,] Vanessa Buzzard[6,] Brian Enquist[7,] Sean T. Michaletz[4,]

[1] University of British Columbia
[2] UCI
[3] UFV
[4] UBC
[5] U.S. Forest Service
[6] University of Arizona
[7] UA

Understanding the drivers of variation in plant mortality rates is a central challenge for global change biology. Metabolic scaling theory (MST) predicts mortality rates will scale as the -2/3 power of stem diameter, but does not account for additional potential drivers of variation in mortality rates such as climate and functional traits. For example, it's hypothesized that the temperature dependence of mortality rates should reflect the activation energy of photosynthesis ($E = 0.58$ eV), and that shifts in functional traits across climate gradients will maximize plant performance and yield a relative invariance of mortality rates. Empirical evaluation of these predictions is needed. Here we 1) build on insights from MST and ecological stoichiometry to extend theory for plant mortality rates, and 2) test the theory using long-term data from nine Forest MacroSystems (FMS) network sites arrayed across global climate gradients. Mortality rates varied inversely with stem diameter, but the diameter scaling exponent was lower than the value of -2/3 predicted by MST. The temperature-dependence of mortality rates followed an activation energy of $E = 0.51$ eV, which was statistically indistinguishable from the value of 0.58 eV for photosynthesis. Plant functional traits varied significantly with climate, but a composite trait derived from theory did not predict variation in mortality rates, suggesting that covariation of traits with climate yields an invariant mortality rate across climate. Thus, global variation in plant mortality rates appear to be driven primarily by size and temperature.

Null models suggest that mammalian endemism is constrained by geography, not species niche breadth

Benjamin Shipley[1,] Jenny McGuire[1,]

[1] Georgia Institute of Technology

Endemic species, or species with restricted range sizes, represent an important aspect of biodiversity. These species are ecologically and evolutionarily distinct from their non-endemic relatives, often filling unique ecological roles. Because of the ecological and conservation importance of endemic species, understanding which landscape factors influence the distribution of such species and rates of endemism is a defining question in biogeography. Generally, regions of stable climate and rough topography lead to higher rates of endemism. However, the extent to which endemism is influenced by the niche evolution of species compared to geography (i.e., landscape heterogeneity, elevational gradients, landmass shape) is still debated. We created null models that account for historical ecological processes by randomizing the climatic niche breadths of species living in each region. Using these null models, we explored the drivers of continental mammalian endemism and examined the effects of geography in the absence of niche evolution on the distribution of endemic mammals. Comparing the null models to the true endemism values, we determined that regions of high endemism do not have disproportionately many species with small climatic niches. In addition, we found that species richness trends accounted for much of the influence of climate stability on endemism. This research illuminates the geographical influences on trends in species distributions and endemism, suggesting that endemism is primarily a geographical, rather than an evolutionary, phenomenon.

New survey data might be key to understanding limitations of species distribution and abundance models for arctic shrubs

Nathalie Chardon[1], Jacob Nabe-Nielsen[2], Jakob Johan Assmann, Ida Bomholt Dyrholm Jacobsen[3], Maya Guéguen[4], Signe Normand[2], Sonja Wipf[5],

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[5] Swiss National Park, Switzerland

Improving Species Distribution Models (SDMs) and Species Abundance Models (SAMs) of woody shrubs is critical for predicting biodiversity changes in the Arctic, which is experiencing especially high warming rates. Yet, it remains relatively unexplored if SDMs and SAMs can explain local-scale patterns. We aim to identify differences in predictor importance for the distribution versus abundance of two wide-spread Arctic shrub species with high resolution models, and to compare validation approaches to assess the models' predictive ability. We conducted separate field surveys in two adjacent fjords in Southwest Greenland to construct ~90 m SDMs and SAMs for Betula nana (Betulaceae) and Salix glauca (Salicaceae). We analyzed the predictive influence of local-scale climate, topography, and soil moisture indicators on each species' distribution and abundance. We then alternatively trained and validated models in either fjord, and compared these results with the common split-sample validation approach. Finally, we assessed if including local scale biotic predictors improves SAM performance. For both species, temperature extremes and precipitation best predicted the distributions of both species, whereas insolation and soil moisture indicators best predicted abundance. Compared to split-sample validation, both SDM and SAM performances were substantially reduced with separate survey validation. Including local-scale biotic parameters improved SAM performance. Substantial differences in model performance between validation approaches highlight the usefulness of using a separate survey for validating model predictive performance, and provide insight into the models' limitations. We emphasize the need to include predictors relevant at the spatial scale of study, such as local scale biotic interactions, for improved predictions at high spatial resolution.

Using herbarium specimens to quantify changes in insect herbivory in northeast North America over the past century

Heather Kharouba[1], Stephanie Rivest[1], Sarah Dolson, Devin Empey[1], Sharla Foster[1], Hannah Keefe[1], Katherine Peel[1], Megan Reich[1], Maisy Roach-Krajewski[1],

[1] University of Ottawa

Given that insect herbivory is a key ecological process, it is among the most consequential biotic interactions expected to be impacted by climate change, and could have major implications for ecosystem structure and function (e.g., changing plant biomass and nutrient cycling). Short-term empirical studies have reported varying effects of warming on rates of herbivory. However, long-term data needed to determine how herbivory has changed over recent decades remains rare. Using herbarium specimens, we investigate how insect herbivory has changed over the past 160 years for two well-collected herbaceous plants— Trefoil (Desmodium canadense), Red Oak (Quercus rubra)—in northeast North America. We found that herbivory has weakly increased over the past century. However, it has not changed over the past four decades, the period defined by anthropogenic climate change. Despite temporal variation in herbivory rates, the temporal change in herbivory was consistent across latitudes. Our results suggest that climatic warming may not lead to changes in herbivory but examining the temperature sensitivity of herbivory rates at this scale is needed. Given the variation in herbivory rates we observed, predicting how climate warming will affect herbivory remains challenging. Our work demonstrates the key role natural history collections can play in understanding species' responses to climate change.

Continuous land cover change detection in Subtropical Thicket ecosystems

Craig Mahlasi[1],

[1] University of Cape Town

The Subtropical Thicket Biome is a unique and highly biodiverse ecosystem in Southern Africa. Estimates indicate that as much as 63% of the biome is already severely degraded, with agricultural expansion the main driver of transformation. While several studies have sought to document and map the long term transformations, there is a lack of information on disturbance events that allow for timely intervention by authorities. Furthermore tools that seek to perform continuous land cover change detection are often developed for forests and thus tend to perform poorly in thicket ecosystems. This study investigates the utility of earth observation data for continuous land cover change detection in subtropical thicket ecosystems.A dataset of dated clearing events was used to train Temporal Neural Networks on time series of Sentinel-2 observations. The model obtained 0.93 accuracy, a recall score of 0.93 and a precision score of 0.91 in detecting Thicket disturbances. This is an improvement in performance compared to previous studies that rely on traditional supervised post-classification change detection. The study demonstrates the potential of continuous land cover change detection in Subtropical Thicket ecosystems.

Concurrent Session 09 (Climate Change Biogeography)
June 4th 2:00 pm – 3:30 pm PT – Room 2/3

Using standardized genomic offsets to add an evolutionary perspective to climate change biogeography

Susanne Lachmuth[1,] Thibaut Capblancq[2,] Anoob Prakash, Stephen Keller[3,] Matt Fitzpatrick[1,]

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[3] The University of Vermont, Department of Plant Biology, USA

Genomic offsets quantify the disruption of existing genotype-environment associations across the landscape under environmental change and can provide an evolutionary perspective often absent from climate change biogeography. We combine genomic offsets derived from gradient forest modeling of genomic turnover along climatic gradients and niche modeling (ENM) to assess the vulnerability of red spruce (Picea rubens), a cold-adapted tree species endemic to eastern North America, to climate change. We evaluate the predictive power of the offsets using growth data from three common-gardens before predicting disruption of genotype-climate associations across the current range under end of 21st century climate. We show how genomic offsets can be standardized relative to contemporary genomic turn-over across the landscape. We then consider all cells of the current range as potential donors for natural or assisted migration to potential recipient habitats. By summing, for each recipient cell, the inverse offsets of all donor cells from which immigrants could transfer without disrupting local adaptation (empirical offset threshold obtained from common-gardens), we calculate 'recipient importance'. This novel metric can be interpreted as habitat suitability accounting for intra-specific variation in climate adaptation and is compared to ENM-based projections of climate suitability. Our approach extends previous applications of the genomic offset concept as it constrains donor - recipient matches relative to the contemporary genomic turnover across a species range in a standardized manner and can facilitate management applications such as seed source and planting site selection for assisted migration that maximizes the representation of adaptive genomic variation present in a species.

Trends in shifting phenologies and asynchrony in response to recent changes in climate

Deirdre Loughnan[1,] Elizabeth Wolkovich[2,] Heather Kharouba, Geoffrey Legault[1,] Simon Joly[3,]

[1] University of British Columbia
[2] The University of British Columbia
[3] University of Montreal

Global climate change is impacting ecosystems in a myriad of ways, such as the effects of rising temperatures on the timing of species life history events or phenologies. For many species we have observed phenological advances, while others have experienced delays or no changes in their timing. Being able to predict these changes in species timing and the synchrony of interactions is critical given their importance in shaping community structures and ecosystem services. Previous studies have explored whether this variation in phenology relates to differences across trophic levels, habitat types, or species physiology, but have found incongruous trends. In our meta-analysis, we used long-term phenological data of diverse phenological events to test for differences in the rate of phenological trends across trophic levels and functional groups, while also testing for changes in the phenological synchrony of interacting species. We further tested for species responses across latitudinal gradients and in relation to changes in temperature, as well as phylogenetic relatedness. On average, species advanced in the timing of their phenological events, however, we did not observe strong differences across trophic levels or functional groups. We also did not observe gradients in species responses across latitudes or in relation to the extent of rising temperatures or strong phylogenetic effects. These results

reflect the extent of variation in species phenological responses to climate change, and highlight the limitations of available data and need to incorporate the inherent variation in phenologies for us to better understand the mechanisms driving trends globally.

Natural and dammed rivers: which is better for salmons′ summer?

Matteo Redana[1,] Fingal Summers[1,] Lesley Lancaster,

[1] University of Aberdeen

Juveniles of *Salmo salar*, can experience temperature outside their thermal optimum (i.e., > 20°C) or causing them thermal stress (i.e., >23°C) due to a consistent increase in water temperature in recent years; however, thermal refugia, can represent an important buffer against these thermal peaks. Dams alter river water temperature due to the release of thermally stratified water, making dammed rivers cooler in summer and warmer in winter. However, dammed rivers are usually not considered for their potential benefits as thermal refugia. We studied a confluence site between a natural and a dammed river in Scotland. We collected water temperature (Tk) values using loggers and an Unmanned Aerial Vehicle (UAV)-mounted thermal camera to produce high resolution Tk maps of the site (with average Mean Absolute Error =-0.28°C ± 0.5 °C). The first aim was to evaluate water Tk spatial distributions and temporal trends during summer to verify if the dammed river can consistently offer a cooler thermal habitat for juvenile salmon. We found that the natural river can frequently pass the 23°C threshold, while the dammed river rarely passed 20°C, with these results spatially consistent. Following, we investigated Tk spatial distribution during the spawning season (late autumn 2021). The timing for adult salmon females' eggs deposition depends on water temperature in nests site area. We found that in early winter, the time frame for egg laying, the dammed river is consistently warmer than the natural river of 2°C in average. Considering these findings along with the well-known territorial behavior of juveniles Atlantic Salmon, we discuss if the potential summer thermal suitability of dammed river is canceled out by the winter Tk alteration, making them unsuitable river patches for eggs deposition.

Climate change drives mountain butterflies towards the summits

Dennis Rödder[1,] Thomas Schmitt[2,] Patrick Gros, Werner Ulrich[3,] Jan Christian Habel[4,]

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Climate change impacts biodiversity and is driving range shifts of species and populations across the globe. To understand the effects of climate warming on biota, long-term observations of the occurrence of species and detailed knowledge on their ecology and life-history is crucial. Mountain species particularly suffer under climate warming and often respond to environmental changes by altitudinal range shifts. We assessed long-term distribution trends of mountain butterflies across the eastern Alps and calculated species' specific annual range shifts based on field observations and species distribution models, counterbalancing the potential drawbacks of both approaches. We also compiled details on the ecology, behavior and life-history, and the climate niche of each species assessed. We found that the highest altitudinal maxima were observed recently in the majority of cases, while the lowest altitudes of observations were recorded before 1980. Mobile and generalist species with a broad ecological amplitude tended to move uphill more than specialist and sedentary species. As main drivers, we identified climatic conditions and topographic variables, such as insolation and solar irradiation. This study provides important evidence for responses of high mountain taxa to rapid climate change. Our study underlines the advantage of combining historical surveys and museum collection data with cutting-edge analyses.

Limited protection and ongoing loss of tropical cloud forest biodiversity and ecosystems worldwide

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Tropical cloud forests (TCFs) are one of the world's most species- and endemism-rich terrestrial ecosystems. While still under-documented due to their complex terrain and isolation, TCFs are believed to harbour the world's greatest diversity of epiphytes, mosses, ferns, lichens, bromeliads and orchids and, in turn, an array of animals adapted to them for food and habitat that provide critical ecosystem functions. Many of these species are highly range restricted and therefore vulnerable to primary habitat loss. TCFs are threatened by direct human pressures and climate change, yet the fate of these extraordinary ecosystems remains insufficiently quantified. With discussions of the post-2020 biodiversity framework underway, TCFs are a defining test case of the success and promise of recent policy targets and their associated mechanisms to avert the global biodiversity crisis. We present a global assessment of the recent status and trends of TCFs and their biodiversity and evaluate the efficacy of current protection measures. We show that cloud forests occupied 0.4% of the global land surface in 2001 and harboured ~3,700 species of birds, mammal, amphibians and tree ferns (~15% of the global diversity of those groups), with half of those species entirely restricted to cloud forests. Worldwide, ~2.4% of cloud forests (in some regions, more than 8%) were lost between 2001 and 2018, especially in readily accessible places. A large proportion of loss in TCF cover is still occurring despite formal protection. Increased conservation efforts are needed to avert the impending regional or global demise of TCFs and their unique biodiversity.

Conservation prioritization in the European Alps: the Mediterranean and Alpine Flora at risk

Yohann Chauvier[1], Wilfried Thuiller[2], Laura J. Pollock, Peter Verburg[3], Drik Karger[4], Loïc Pellissier[5], Sébastien Lavergne[6], Niklaus Zimmermann[4],

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Adopting a multifaceted diversity approach in conservation planning is essential, and systematic conservation prioritization (SCP) has been increasingly employed to maximize the protection of current alpha/beta species (TD), phylogenetic (PD) and functional diversity (FD). Nevertheless, most SCPs still ignore the potential impacts of global changes on future shifts of multifaceted diversity. Protecting the full spectrum of biodiversity also implies to maintain an efficient long-term conservation of the multifaceted biodiversity uniqueness (i.e. endemism, distinctiveness and rarity) which is often forgotten within conservation studies. Conservation in the European Alps is a central topic, as this region is one of the largest natural diversity hotspot in Europe. However, a thorough conservation assessment and prioritization, based on multifaceted diversity/uniqueness, for present and future global change conditions is critically needed. Here, we investigate the efficiency of the European Alps' reserve network, and of its potential expansion, in protecting the plant multifaceted diversity/uniqueness of half of the Alps Flora at present, and for the year 2050/2080 under two SSP and three dispersal scenarios. Each distribution of TD, PD, FD and related uniqueness were modelled, and SCPs were run accounting for the irreplaceability and complementarity of each species, phylogenetic branches and functional roles. Overall we found the unlimited dispersal scenarios to be highly over-optimistic, multifaceted diversity/uniqueness to generally decrease in the future, the Mediterranean and Alpine flora to be greatly at risk for all scenarios, and the SCP recommendations to follow these geographical threats. Furthermore, although the design of the European Alps’ reserve network showed a good adaptability towards current and future SCP recommendations, a reserve expansion of at least 20% would be necessary to protect half the diversity and uniqueness of the European Alps.

Concurrent Session 10 (Paleoecology & Paleobiogeography)
June 4th 2:00 pm – 3:30 pm PT – Room 8

Spatio-temporal distribution of pollen traits to interpret long-term changes in plant communities

Sandra Nogué[1,] Lea de Nascimento[2,] Laura Graham, Luke Brown[3,] Alvaro Castilla-Beltrán[2,] Josep Penuelas[4,] Robert Whittaker[5,] José María Fernández-Palacios[2,] Kathy Willis[5,]

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[2] University of La Laguna
[3] University of Southampton
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[5] University of Oxford

The identification and distribution of plant traits that permit species to cope with environmental change has been highlighted as an important research goal. However, the contribution of pollen traits has been largely overlooked to date. Our paper focuses on the laurel forest of La Gomera and Tenerife (Canary Islands) and aims to determine the spatio-temporal distribution of pollen traits related to dispersal (ornamentation, and dispersal unit) and desiccation tolerance (wall thickness, presence of furrows and pores, and pollen size). We used fossil pollen and modern pollen rain from 19 forest plots expanding an elevational gradient of 1050 m and all laurel forest types (cold, dry, humid, and crest heath). We quantified pollen trait composition across space using community weighted mean and also a measure of functional dispersion to analyse how the combination of pollen traits changed over 9600 years. Results, showed certain degree of adaptation to the local environmental conditions with more prevalence of pollen traits related to desiccation tolerance on the drier areas of the laurel forest distribution than on the humid laurel forest sties. In addition, we found more prevalence of ornamented pollen grain in the core of the laurel forest, where pollinators might be more present. Finally, when focusing on long-term changes, we found an increase in functional dispersion towards the present, suggesting a laurel forest response to a past regional climate change towards drier conditions. Our approach demonstrates the potential of incorporating pollen traits into the plant functional traits framework.

Expanding ecometric analyses to explore geographic patterns of faunal responses to change

Rachel Short[1,] Jenny McGuire[2,] Michelle Lawing,

[1] Texas A&M University
[2] Georgia Institute of Technology

Functional traits describe how organisms interact with their local environments, and community-level trait-environment alignment is essential for ecosystem function. Certain functional traits, such as locomotor morphology and dental characters, are frequently preserved in the fossil record and strongly relate to environmental conditions. Thus, they provide a ‘common currency’ to work across temporal, spatial, and taxonomic scales. A powerful research strategy is to use ecometric analyses to evaluate relationships through time to establish how these relationships shift as conditions change. We discuss the utility of ecometric analyses for evaluating how expanding human footprints affect trait-environment relationships, but first we need to refine our understanding of how to best assess these trait-environment relationships. We have investigated different estimation methods used in ecometric studies and found that maximum likelihood consistently produced the most accurate estimates of environment from community-level functional traits. We also extended the taxonomic scope over which an ecometric trait can be applied. Calcaneal gear ratio is known to be related to ecoregion and vegetation cover in carnivoran communities, and we showed that this relationship holds for artiodactyl communities, making it useful for integrating ecometric studies. Using this expanded toolset for evaluating ecometrics, we have begun applying these methods to fossil sites to investigate the timing and synchronicity of trait shifts as environments change and anthropogenic impacts arise. Overall, ecometrics is an emerging and highly informative field that can use trait-environment relationships to develop long-term understanding of faunal responses and support conservation of mammalian communities.

How long does it take for related species to coexist? Biodiversity gradients in species coexistence, the space and time of diversity accumulation.

Francisco Henao-Diaz[1], Matthew W. Pennell[1], Benjamin Freeman,

[1] University of British Columbia

A limiting step in the diversification process is the time required for incipient species pairs to coexist in sympatry. Variation in how long it takes for related species to coexist may also explain differences in diversity among groups and areas. Several hypotheses propose that the waiting time to coexistence is predicted by variables including latitude, elevation, productivity, and species traits (e.g., dispersal capability, territoriality). Using detailed range data and time-calibrated molecular phylogenies including 1,483 bird species, we estimated the time to secondary sympatry for passerine assemblages living in 16 montane regions in the New World. We used this data to test multiple factors hypothesized to explain variation in waiting time to coexistence at different spatial scales. We investigated whether the observed differences in time to secondary sympatry can help explain regional, local, and continental diversity. Regional coexistence refers to related species living on the same mountain range, while local coexistence is where related species live at the same elevation band within the same region.

We found that the median time to regional coexistence varied from 6 to 10 Myr. Time to regional coexistence did not correlate with latitude or elevation. Thus, while recent research has shown that speciation is often faster at high latitudes and elevations, the tempo of diversity build-up within regions appears to be similar across space. When analyzed by mountain regions, species pairs with ~50% of elevation range overlap had higher times to local than regional coexistence. While the time to regional coexistence is not associated with the mid-elevation range, the proportion to elevation overlap is higher in lowlands than in highlands, albeit widely idiosyncratic.

Variation in the productivity-diversity relationship in during last 21,000 years indicate both equilibrium and disequilibrium dynamics

Irena Šímová[1], Alejandro Ordonez[2], David Storch[1]

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Environmental productivity is considered a universal correlate of species richness. Nevertheless, as most species-productivity studies are only contemporary, the question of whether and at what temporal scale richness tracks changes in productivity remains unresolved despite its importance for predicting future diversity dynamics.

We explored temporal fluctuation in pollen type richness of woody species (‘richness’) in the USA and Canada and climate since the Last Glacial Maximum. We used reconstructed paleoclimate to estimate productivity. We tested for 1) the site-specific relationships between richness and productivity time series and 2) the spatial richness-productivity relationships in 1000-year time bins.

Richness increased with increasing productivity during the period of rapid climate change in the early Holocene/Late Pleistocene but not in the climatically stable Holocene. Conversely, when focusing on spatial

relationships in particular time bins, richness increased with increasing productivity in the period of climate stability only. Nevertheless, differences occurred between the western and eastern parts of the continent. In the climatically stable west, the temporal richness-productivity relationship was weak, but the spatial relationship was strong. Conversely, in the climatically unstable east, we found evidence for temporal richness-productivity relationship throughout the entire period, but the spatial relationship was weak.
There is a mismatch between the temporal and spatial richness-productivity relationship. Richness tracks productivity in time only if the magnitude of climate change is high, but spatially it remains in disequilibrium with productivity. The strong spatial relationship between richness and productivity formed under climatically stable mid/late Holocene when richness reached an equilibrium with productivity.

Survivors of the Ice Age: Rancho La Brea mesocarnivores from late Pleistocene to modern-day

Mairin Balisi[1,] Jessica Blois[2,] Aisling Farrell, Gary Takeuchi[1,] John Southon[3,] Emily Lindsey[1,]

[1] La Brea Tar Pits and Museum
[2] UC-Merced
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While much of North American mammal fossil history was characterized by large carnivores and prey, most carnivores today are small (“mesocarnivores”): a transition that took place after the last Ice Age following a combination of climatic change, megafaunal extinctions, and human disturbance. Here, we evaluate response to these major impacts in the late Pleistocene to Holocene mesocarnivore guild at the Rancho La Brea (RLB) asphalt seeps in Los Angeles, California, USA. Excluding coyotes, RLB preserves five mesocarnivore species each represented by >=10 individuals: American badger (Taxidea taxus), bobcat (Lynx rufus), grey fox (Urocyon cinereoargenteus), striped skunk (Mephitis mephitis), and long-tailed weasel (Mustela frenata). In multiple linear functional traits, RLB specimens differ significantly from historic (<100 years old) representatives of the same species from the same geographic area. Fossil mesocarnivores were generally larger—decreasing in body size through time by as much as 27%—and exhibited greater tendencies for carnivory, perhaps in response to competition presented by megafaunal predators. Species-specific differences in postcranial morphology highlight shifts in locomotor ability, potentially reflecting environmental changes. Contrary to common assumptions about these asphalt deposits, a preliminary radiocarbon chronology suggests that not all species inhabited RLB at the same time. Rather, almost all specimens of bobcats and grey foxes date from before the Last Glacial Maximum while badgers appear to have been a latest Pleistocene addition. Stable isotope analyses currently in progress will complement these ecomorphological analyses, providing another proxy for diet and illuminating the roots of today’s mesocarnivore guild in the last Ice Age.

Concurrent Session 11 (Historical Biogeography)
June 4th 2:00 pm – 3:30 pm PT – Room 11

Blooming on the roof of the world -- The origin and assembly of the alpine biodiversity in the Tibeto-Himalaya-Hengduan region

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The mountain-building process in the Tibeto-Himalaya-Hengduan (THH) region during the Cenozoic has shaped the world highest mountains range and largest plateau which harbors the potentially richest alpine plant diversity around the world. Yet the origin and the assembly of this unique alpine biota is poorly understood. Here, we examine the tempo (when, how fast) and mode (through what processes) by which the alpine biome was assembled through time and across the THH using comparative phylogenetic analyses from 18 of diverse clades of flowering plants. We demonstrate that the alpine biome assembled asynchronously over time and space, triggered or promoted by independent orogenic events mainly after the Oligocene-Miocene Transition and intensification of Asian monsoon systems since the middle Miocene. Each evolutionary process contributes disproportionately across regions. Our work synthesize complementary analysis by incorporating molecular dating, biogeographic, and diversification rates analysis of multi-clades to link the evolutionary process with the past geological and climatic changes and the new biogeographical model we applied integrating the evolution of range and biome and makes it possible to estimate the biome-dependent diversification through time.

Stability of knowledge about mammal-pathogen interactions through time and space

Ángel Luis Robles Fernández[1,] Nathan Upham[1,]

[1] Arizona State University

The transmission or ‘spillover’ of wildlife pathogens to humans is a critical threat to global health, with major outbreaks of viral, bacterial, and protozoan pathogens originating in wild mammals. As researchers have sought outbreak origins, pathogen discovery efforts have markedly increased over the last 50 years. However, it is unclear whether knowledge of pathogen sharing networks are yet stable enough to yield reliable predictions of spillover risk, or whether additional sampling is needed. Here we investigate the relative stability of mammal-pathogen networks via metrics of matrix symmetry (W) and edge number (E) through time and space, querying the Global Mammal Parasite Database (GMPD) using sliding windows of collection date and latitude. Comparing systems of viral, helminth and bacteria interactions as corrected for per-species discovery effort and pathogen prevalence, we find evidence in support of the null hypothesis that W is drawn from a Normal distribution during every 5-year time window from 1985-2010, and that E has increased through time as a function of discovery effort. In contrast, W changes predictably from the tropics to the poles with increasing in asymmetry for each successive 10-degree latitudinal band. Thus, we find no evidence supporting the instability of mammal-pathogen knowledge. Instead, W appears to have been unbiased through time, effectively having been drawn randomly from the same global distribution. The predictable latitudinal bias in W is consistent with fewer mammal host species being present on average at temperate than tropical latitudes, which manifests as part of the well-known latitudinal biodiversity gradient. Spillover risk models should account for biases in latitudinal network symmetry and discovery effort, but otherwise are expected to yield stable inferences through time.

Do the small-ranged species of mammals diversify slower?

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The relationship between range size and diversification potential of species is a cornerstone of many macro-evolutionary theories, such as neutral theory of ecology or equilibrium theory of biodiversity dynamics. These theories typically assume that the small-ranged species have lower rates of net diversification, due to slower speciation and faster extinction. This assumption is, at least seemingly, at odds with practical observations that small-ranged species are often less evolutionary distinct than large-ranged species, forming spatially localized hotspots of neoendemism and putative cradles of diversification. The research of range-size evolution is a notoriously complex task, because the range sizes evolve not only anagenetically (range expansion or contraction), but also cladogenenetically (range size change between mother and daughter species during speciation). Here we use a cladogenetic state-dependent model of range size evolution covering both these processes to explore relationship between range sizes and the rates of diversification in placental mammals. We show that in general, small-ranged species indeed diversify slower, as theoretically expected. In closer look, this pattern is however reversed in some mammalian taxa, such as ungulates (Cetartiodactyla), bats (Chiroptera) or insectivores (Eulipotyphla). Moreover, the ancestral state reconstructions suggest that both range-size evolution and diversification are strongly influenced by spatially localized events, such as entrance to an archipelago, mountain system or particular biome, overdriving thus the theoretically described processes of range-size evolution. We conclude that, while the range size is an important factor influencing species diversification, its effect in real-world systems is often locally modified or even inverted by idiosyncratic geographic setups.

The interaction of climate history and evolution impacts alpine biodiversity assembly differently in freshwater and on land

Luiz Jardim de Queiroz[1], Carmela J. Doenz[2], Niklaus Zimmermann, Ole Seehausen[1],

[1] Eawag/University of Bern
[2] University of Bern

Quaternary climate fluctuations can affect biodiversity assembly through speciation in two non-mutually-exclusive ways: a glacial species pump, where isolation in glacial refugia accelerates allopatric speciation, and adaptive radiation during ice-free periods. Here we detect biogeographic and genetic signatures associated with both mechanisms in the generation of diversity in the European Alps. The age distributions of endemic and widespread species within aquatic and terrestrial taxa (amphipods, fish, amphibians, butterflies and flowering plants) revealed that endemic fish evolved only in lakes, are highly sympatric and mainly of Holocene age, consistent with adaptive radiation. Endemic amphipods, however, are ancient, suggesting preglacial radiation with limited range expansion and local Pleistocene survival, perhaps facilitated by a groundwater-dwelling lifestyle. Terrestrial endemics are mostly of Pleistocene origin and are thus more consistent with the glacial species pump. The lack of evidence for Holocene adaptive radiation in the terrestrial biome may be attributable to a faster dispersal rate of these taxa after glacial retreats, though larger environmental fluctuations may also have contributed to differences between terrestrial areas and lakes. The high proportion of young, endemic species make the Alps especially vulnerable to climate change, but the mechanisms and consequences of species loss will likely differ between biomes because of their distinct histories.

Life-history traits mediate avian demographic responses under past climate change

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Human-induced changes to global climate are affecting biodiversity at an unprecedented rate. Determining how contemporary populations will respond to climate change in the near future requires understanding the demographic history of species over paleo-ecological time scales of intense global climate fluctuations. Modern genomic tools allow for unprecedented insight into the demographic history of species via patterns of historical recombination events. Such molecular ‘log books’ reveal changes in effective population size (Ne) over thousands-to-millions of years that can be cross-referenced with paleo-records to infer demographic change during periods of abrupt climate warming or cooling. We use full-genome sequence data from 233 bird species representing all major families to identify common demographic responses to climate fluctuations over the past one million years. We further test a suite of species-specific traits to identify those associated with demographic sensitivity to past climate change, with the aim of determining the role of life-history variation in adapting to changing environments. Our results identify direct and indirect effects of key traits representing survival, reproduction, and dispersal processes on long-term demographic responses to climate change and highlight traits most likely to influence population responses to current climate warming.

Concurrent Session 12 (Biodiversity Patterns, Species Distributions & Maintenance)
June 4th 2:00 pm – 3:30 pm PT – Ballroom C

Analysing the Drivers of Speciation in the Hengduan Mountains, China

Zili Yuan[1,]

[1] ETH Zurich

Understanding the patterns and drivers behind speciation has always been one of the ultimate goals of evolutionary ecology. Sister species, because of their shared short lineage history, allow for direct analysis of the patterns and drivers of speciation. On a global scale, the Hengduan mountains represent one of the hotspots of both plant diversity and endemism, harbouring more than 30,000 vascular plant species, with local endemism reaching up to 50% in some areas. This is thought to be caused by an interplay of drivers behind the complex regional topography as a result of its unique geological and environmental history. In this study, based on newly published phylogenies, we focus on local lineage with a board coverage and identified around 600 pairs of sister plant species from 20 different genera. At least one of the sisters was selected to be endemic and important to the Hengduan Mountains. Their ecological/geological attributes are compiled from different sources including floras to herbarium specimens. These attributes are then analysed for geographic vs. environmental niche segregation in the null model tests, allowing us to identify the proportion of sympatric vs. allopatric speciation might in the region and across genera. We further identify the exact attributes that are strongly affecting the speciation, including the shift in growth forms, flowering time, etc. of the analysed sisters. Finally, we assess the interplay between different attributes and how they affect speciation patterns will be explored using generalized linear and structural equation models.

Species distribution models affected by positional uncertainty in species occurrences can still be ecologically interpretable

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Species distribution models (SDMs) have become a common tool in studies of species-environment relationships, and previous findings suggest that their performance is negatively affected by positional error uncertainty in species occurrences. However, previous studies have focused on the association between positional uncertainty and model predictive performance, whereas the effect of positional uncertainty on the ecological interpretability of species-environment relationships remain unknown. To address this gap, we used simulated data and two case studies to investigate the downstream effect of positional uncertainty on the interpretability of SDMs. We examined the effects of varying levels of positional uncertainty by simulating positional error in species occurrences and used Maximum Entropy methods to model species distributions. We evaluated the direct effect of positional uncertainty on model performance and explored how positional uncertainty affects the models' ability to detect underlying species´ responses to environmental variables as well as the relative importance. Results showed that, as expected, positional uncertainty decreased model predictive performance regardless of the species' ecology. However, species-environment relationships and the relative importance of predictors of models built with different degrees of positional uncertainty in the data were generally similar. Only at extreme levels of positional uncertainty and high heterogeneity in variables, positional errors obscured the main patterns. Thus, the drivers of species' distributions and the overall biodiversity trends can be reliably predicted based on spatially uncertain data. Our finding highlights the potential of niche modelling for a large proportion of occurrence data sets and for providing information for many taxa over large regions.

The links between larval and adult fish diversity

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[1] Tel Aviv University
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The processes determining biodiversity patterns has been a major focus for ecologists. However, diversity estimates mostly represent ‘snapshots’ of adult communities, notwithstanding the changing requirements and interactions throughout ontogeny. Incorporating the ecology of early life stages is particularly important for species with a complex life cycle, such as marine fish. As the dispersal of marine fish species generally occurs during the larval phase, adult diversity is the combined outcome of larval supply and the following processes of settlement and recruitment. However, in marine systems, the difficulties in obtaining species-level abundance estimates of larvae have thus far precluded comparisons of different life stages assemblages, hindering a better understanding of the processes shaping adult communities. Here, we assessed larval diversity of coral reef fishes in the Gulf of Aqaba using species-specific quantitative estimates of larval abundances, obtained using a novel Meta-genomic larval Identification and Abundance method (MIA). In total, 219 reef associated fish species from 343 samples were used to construct estimates of larval diversity. We paired these to adult fish diversity estimates and found that the larval community is more even than the adult community, with higher proportions of rare species (17% and 7%, respectively). Thus, post-settlement processes (e.g., environmental filtering, biotic interactions) act together to decrease adult diversity. We show the effects of community-wide post-settlement processes for the first time and demonstrate that they act to decrease the diversity of adult coral reef fish, elucidating the ecological bottlenecks linking larvae and adults.

Drivers of past ecological change in Tonga and Vanuatu.

Nichola Strandberg[1,] Sandra Nogué[1,] David Sear, Peter Langdon[1,]

[1] University of Southampton

Many Pacific islands are considered biodiversity hotspots but are subjected to a range of disturbances such as volcanic eruptions, sea-level change, climate change, and human impacts. To investigate drivers of past ecological change in Tonga and Vanuatu we synthesised palaeoecological data (pollen and chironomids) to determine how terrestrial (mangroves and tropical forest) and aquatic ecosystems (chironomids) responded to drivers of change over 7000 years across the Pacific region. We focused on both low elevation coastal fens (Avai'o'vuna Swamp, Finemui Swamp, Lotofoa Swamp and Ngofe Marsh) and a higher elevation lake (Emaotul). Our aim was to assess patterns of local and regional biodiversity changes under different environmental conditions. Our results indicated that at coastal sites in Tonga the decline in mangroves at Ngofe Marsh and Avai'o'vuna Swamp was driven by a fall in sea-level between 2500–5000 cal years BP. At Ngofe Marsh and Avai'o'vuna Swamp, burning, which can likely be attributed to human presence, played a role in the transformation of the primary rainforests to secondary rainforest. At Lake Emaotul, located at 114 masl, pollen turnover increased during a period of climate change 1100 cal years BP, which was likely caused by the shifting position of the South Pacific Convergence Zone. The Lake Emaotul record also indicated increased vegetation turnover related to the cataclysmic Kuwae eruption of CE 1450s. Vegetation responses to disturbance within these islands indicates that disturbance events lead vegetation to become more homogenous between islands.

Diversity dynamics in birds of New World

Antonin Machac[1,]

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Three prominent explanations have been proposed to explain the dramatic differences in species richness across regions and elevations, (1) time for speciation, (2) diversification rates, and (3) ecological limits. But the relative importance of these explanations and, especially, their interplay and possible synthesis remain largely elusive. Integrating diversification analyses, null models, and GIS, I study avian richness across regions and elevations of the New World. My results reveal that even though the three explanations are differentially important (with ecological limits playing the dominant role), each contributes uniquely to the formation of richness gradients. Further, my results reveal the likely interplay between the explanations. They indicate that ecological limits hinder the diversification process, such that the accumulation of species within a region gradually slows down over time. Yet, it does not seem to converge toward a hard ceiling on regional richness. Instead, species-rich regions show suppressed, but continued, diversification, coupled with signatures of possible competition (esp. Neotropical lowlands). Conversely, species-poor, newly-colonized regions show fast diversification and weak to no signs of competition (esp. Nearctic highlands). These results held across five families of birds, across grid cells, biomes, and elevations. Together, my findings begin to illuminate the rich, yet highly consistent, interplay of the mechanisms that together shape richness gradients in the New World, including the most species-rich biodiversity hotspots on the planet, the Andes and the Amazon.

Chemical properties of key metabolites determine the global distribution of lichens.

Andreas Schweiger[1],

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In lichen symbioses, fungal secondary metabolites provide UV protection on which lichen algae such as trebouxiophycean green algae – the most prominent group of photobionts in lichen symbioses – sensitively depend. These metabolites differ in their UV absorbance capability and solvability, and thus vary in their propensity of being leached from the lichen body in humid and warm environments, with still unknown implications for the global distribution of lichens. In this study covering more than 10,000 lichenized fungal species, we show that the occurrence of fungal-derived metabolites in combination with their UV absorbance capability and their probability of being leached in warm and humid environments are the main eco-evolutionary drivers of global lichen distribution. Fungal-derived UV protection seems to represent an indirect environmental adaptation in which the lichen fungus invests to protect the trebouxiophycean photobiont from high UV radiation in warm and humid climates and, by doing this, secures its carbon source. Based on our observations, we argue that the likelihood of the evolution of such indirect environmental adaptations might depend on a trade-off between the costs of these adaptations for the benefactor (i.e., production of lichen substances by the mycobiont) and the gain the benefactor receives from the susceptible, beneficiary partner (i.e., carbon gain from the photobiont). The results and conclusions of our study emphasize the importance of macrophysiological study approaches to unravel prominent eco-evolutionary drivers of the global distribution of organsims and highlight the potential of such approaches to be broadly important to the study of biodiversity gradients.

Concurrent Session 13 (Conservation Biogeography)
June 4th 4:00 pm – 5:30 pm PT – Room 2/3

Modeling the biodiversity enhancement value of seagrass beds

Jennifer McHenry[1,] Andrew Rassweiler[2,] Gema Hernan, Christopher K. Uejio[3,] Stephanie Pau[3,] Alexandra K. Dubel[2,] Sarah E Lester[3,]

[1] Florida State University
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[3] Florida State University, Department of Geography

Seagrass beds provide essential habitat for fish and invertebrates, leading to enhanced biodiversity in coastal marine ecosystems. However, biogeographic patterns of the biodiversity enhancement effect of seagrass beds are poorly resolved, limiting our ability to implement proactive management strategies when facing climate changes, such as sea-level rise (SLR). Here we estimated the biodiversity enhancement value of seagrass beds using spatial models and detailed long-term monitoring datasets from seagrass ecosystems in the Florida Gulf Coast. We used these models to describe the distribution, total cover, and species composition of seagrass beds and to estimate their effects on spatial patterns of faunal species richness under three scenarios. Specifically, we: 1) quantified the biodiversity enhancement value of current seagrass beds, 2) inferred the biodiversity enhancement value of potential restoration areas, and 3) projected potential changes in the distribution and biodiversity enhancement value of seagrass beds assuming low (+0.50m) and high (+1.0m) SLR forecasts for 2100. We found that current seagrass beds support 43-64% more species than bare substrate and that seagrass restoration of potential habitats could yield comparable increases in biodiversity in the near-term. However, model projections indicate that SLR could cause a significant reduction in biodiversity enhancement value of these areas, as seagrass distributions contract and decline in total cover. Still, we predict many suitable locations for seagrasses by 2100, with some having either comparable or potentially increased enhancement value. Our findings highlight the importance of considering biogeographic patterns of biodiversity benefits when planning for habitat conservation and restoration under climate change.

Classification and biogeography of Antarctic ice-free ecosystems

Aniko Toth[1,] Aleks Terauds[2,] Steven Chown, Justine Shaw[3,] Jonny Stark[2,] David Keith[1,]

[1] University of New South Wales
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[3] University of Queensland

The Antarctic represents one of the most untouched wildernesses left in the world, but it is simultaneously threatened by human disturbance and a broad suite of climate related changes. Antarctica's unique system of governance, the Antarctic Treaty System and its parties are committed to base conservation and management decisions on scientific knowledge. We present the first comprehensive ecosystem classification of ice-free Antarctic lands, which host the vast majority of the continent's documented biodiversity. Our factor analysis and expert elicitation-based hierarchical approach yielded 28 continent-wide ecosystem types within five environmental groups. The scale of these ecosystems highlights regional differences that are not captured in the broad delineations of the Antarctic Conservation Biogeographic regions, originally developed in 2012. The cryogenic conditions and processes associated with adjacent ice, together with the distinctive gradient created by juxtapositions of ice, land and ocean generate powerful evolutionary pressures and assembly filters that have created and sustain distinctive ecosystems found nowhere else. This typology generates testable predictions that can be used to frame future research and situates Antarctic ecosystems in the global ecosystem typology. Importantly, it provides a framework for standardized risk assessments to inform policy responses to imminent anthropogenic and climatic threats.

Predicting the present and uncertain future for Canada's terrestrial vertebrates and plants

Laura Pollock[1], Isaac Eckert[2], Dominique Caron, Abbie Gail Jones[2], Andrea Brown[2],

[1] McGill
[2] McGill University

Climate is changing rapidly in northern latitudes such as Canada. Predicting how species will respond to climate change is inherently uncertain, but this uncertain is compounded in Canada because biased sampling means we know less about the biodiversity in the areas that are set to change the most. Using a variety of predictive models and data for all vertebrates (breeding birds, mammals, amphibians, and reptiles) and all native plant species, we show: where the known biodiversity is (species and functional diversity); where we are likely under-estimating biodiversity; where climate change is likely to be a threat to biodiversity; and where climate change is a threat and biodiversity is under-estimated. From these results, we then identify areas of conservation importance by delineating 'win-win' areas (high biodiversity that is predicted to be stable into the future), 'northern paradox' areas (high potential species influxes which could increase total diversity), and 'need-to-know' areas that are essential locations for future biodiversity data collection.

Iterative ecological niche modeling and field surveys of the rare *Ivesia webberi*

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In this study, we combined iterative modeling approach and model-guided field surveys to improve the ecological niche model framework and identify the ecological drivers of *Ivesia webberi* niche. Four modeling iterations and five field surveys were conducted between 2015 and 2020, starting with 23 occurrence points and 72 assembled ecological predictors. Habitat suitability map projections were produced using weighted average ensembles of six algorithms for each of the modeling iterations. Novel locations and absence points generated during visits to the predicted suitable sites were integrated into the modeling framework, which produced updated habitat suitability maps that were used for further field surveys. Tests of niche overlap, equivalency, similarity, expansion, and stability based on a principal component analysis (PCA) between the original and new occurrence points were conducted. Also, differences between the projections of the initial (year one) and final (year five) niche models were also compared. Field surveys, using adaptive sampling, resulted in the discovery of nine new locations of I. webberi and expanded the northern reach of the distribution range by 65 km. These newly discovered occurrence locations resulted in a 7% expansion of I. webberi niche, while a 44% niche overlap between the original and new points was observed. Furthermore, the perennial herbaceous vegetative cover and topo-climatic variables contributed the most to I. webberi niche. The results show that iterative niche modeling and field surveys can be used to increase or validate existing understanding of species-environment relationships, and reliably assess a species rarity for conservation prioritization.

Setting priorities for long term conservation: A flexible selection approach.

Alke Voskamp[1]
[1] Senckenberg Biodiversity and Climate Research Centre

Identifying priority areas for nature conservation is challenging and depends on the specific conservation objective. Whilst halting biodiversity loss is a major challenge that humanity is facing for the 21st century, the expectations towards protected areas are manifold and have increased over time. Ranging from protecting biodiversity and providing ecosystem services to contributing to climate change mitigation. Since both, available land and conservation funding are limited, optimizing the selection of protected areas for long-term funding is vital. Here we use the newly founded Legacy Landscapes Fund (LLF) as a case study. We identify six conservation objectives that are in line with the basic selection criteria of the LLF: Biodiversity, Wilderness, Climatic stability, Land-use stability, Climate protection and Size. We then explore synergies and trade-offs between the different conservation objectives and look into their impact on the prioritization of suitable candidate sites. Our results show that trade-offs between different conservation objectives are frequent. Hence a flexible site selection approach can aid the development of conservation strategies and dynamic site prioritization. For this purpose, we developed a decision support tool that facilitates discussions between different stakeholders and supports conservationists and decision makers to select priority areas for conservation.

Biogeography and conservation of marine crabs

Aurore Maureaud[1,] Walter Jetz[1,] Gabriel Reygondeau, Kate Ingenloff[1,] Kevin Winner[1,] Les Watling[2,] Jessica Vigneron[1,]

[1] Yale University
[2] University of Hawaii

The regionalization of habitats into biogeographic units is the basis for understanding species distribution and informing biodiversity conservation. In the oceans, biogeography has mostly characterized coastal and pelagic environments. To this day, there is no global biogeography for benthic marine species, limiting our understanding of seafloor habitats and species distributions. From shallow to deep waters, the ocean seafloor includes a high diversity of habitats and organisms of high conservation priority and commercial importance, including marine crabs. My work synthesizes what we know about where crabs are in the oceans. To associate crab species with their preferred habitat, I created the first global benthic biogeographic layer, using previously existing expert regionalization for continental shelves and the deep sea. By intersecting a data synthesis of crab species taxonomy, distribution data, and the benthic biogeography, I estimate the first global regional diversity of the group. At the regional scale, crab diversity and coverage by marine protected areas already show successes and opportunities for the conservation of marine crabs. While continental shelves do not extend similarly along coastlines, we also show that the seafloor regions are shared between marine jurisdictions, requiring global cooperation for the conservation and management of the crab species assemblages they host. This new seafloor biogeography is the first step towards understanding the global distribution of marine crabs and benthic species to inform distribution maps and conservation.

Concurrent Session 14 (Functional Biogeography)
June 4th 4:00 pm – 5:30 pm PT – Room 8

The Ecorichness - Area Relationship (ECAR) as a tool to explore community assembly

Spyros Sfenthourakis[1], François Rigal[2],

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[2] Université de Pau et des Pays de l'Adour, France

Most common applications of species-area relationship approaches use presence-absence of species, either for total, endemic, or guild-based richness. An alternative approach has been recently proposed by the authors and colleagues, which is based on substituting presences with a measurement of habitat range exploitation, adding up per island and standardized by total richness. This metric has been called 'ecorichness' and expresses the community-level ecological divergence of species per island. 'Ecorichness' has been found to show a humped-shaped, unimodal response to Area, and in the present work we explore this relationship further on additional datasets from different taxa. The unimodal response is expected when species with narrow habitat ranges (more specialist) are added at higher rates in larger island communities. In systems controlled mostly by habitat heterogeneity, this effect should be stronger, whereas in systems where 'area per se' or passive sampling are the main drivers of species diversity, such an effect would not be seen or at least should be weaker. This is because narrow habitat range exploitation (specialization) is not necessarily expected to show a strong linear relationship with species abundance, which plays the main role in the passive sampling and 'area per se' hypotheses. 'Ecorichness' can be seen as a general approach that might encompass a variety of ecological specialization metrics, such as niche breadth or functional diversity, and is expected to shed new light onto community assembly of insular systems, but also in others. For example, it might be expected that nested systems too should show a unimodal response of 'ecorichness' to area, since specialist species richness should again be expected to increase at higher rates as area increases. We suggest that ECARs should be evaluated in combination with SARs in order to improve understanding of processes shaping diversity patterns.

Global variation in avian functional traits: introducing AVONET, a new standard of morphological, ecological and geographical data for all birds.

Suzanne Fritz[1], Joseph Tobias[2], Catherine Sheard[3], Alex Pigot[4], Adam Devenish[5], Yingyi Yang[5], Ferran Sayol[4], Carsten Rahbek[6], Gavin Thomas[7], Matthias Schleuning[8]

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Functional traits offer a rich quantitative framework for developing and testing theories in evolutionary biology, ecology and ecosystem science. However, the potential of functional traits to drive theoretical advances and refine models of global change can only be fully realised when species-level information is complete. Here we present the AVONET dataset containing comprehensive functional trait data for all birds, including six ecological variables, 11 continuous morphological traits, and information on range size and location. Raw morphological measurements are presented from 90,020 individuals of 11,009 extant bird species sampled from 181 countries. These data are also summarised as species averages in three taxonomic formats, allowing integration with a global phylogeny, geographical range maps, IUCN Red List data and the eBird citizen science database. The AVONET dataset provides the most detailed picture of continuous trait variation for any major radiation of organisms, offering a global template for testing hypotheses and exploring the evolutionary origins, structure and functioning of biodiversity.

Predictive mapping of intraspecific trait variation among California's grasses

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Plant species can show considerable morphological and functional variation along environmental gradients. This intraspecific trait variation can have important consequences for community assembly, biotic interactions, ecosystem functions and responses to global change. However, directly measuring trait variation across many species and wide geographic areas is often infeasible. Thus, a method to predict spatial variation in a species' functional traits could be valuable. We measured functional traits of grasses across California, covering 59 species at 230 sampling locations. We trained random forests to predict local trait values for any species at any location based on phylogenetic position, local climate and species characteristics. We then examined how much these local predictions alter patterns of assemblage-level trait variation across the state. Most species exhibited higher SLA and grew taller at higher temperatures and produced larger leaves in drier conditions. The random forests predicted spatial variation in functional traits very accurately, with correlations up to 0.97. Because trait records were spatially biased towards warmer areas, and these areas tend to have higher SLA individuals within each species, species means of SLA were upwardly biased. As a result, using species means over-estimates SLA in the cooler regions of the state. Using only species mean traits to characterize the functional composition of communities risks introducing substantial error into trait-based estimates of ecosystem properties including decomposition rates or NPP. The high performance of random forests in predicting local trait values provides a way forward for estimating high-resolution patterns of ITV without a massive data collection effort.

Winegrape cold tolerance at the range edge: the influence of genetic variation and climate change

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Species ranges are strongly influenced by the interaction between physiological tolerances and climatic conditions. Climate change is shifting species potential ranges, but by how much will depend on multiple factors. One important factor is how much genetic variation there is in a species' physiological tolerances; species with greater variation will be able to adapt better to shifts in climate within their current range and have more potential to exploit marginal climate at the range edges. To study genetic variation in physiological tolerances, we focus on cold tolerances in domesticated winegrapes (Vitis vinifera) growing in the Okanagan Valley, BC, Canada. Winters regularly get cold enough to damage and even kill winegrapes in this region, so cold tolerance is an important factor constraining winegrape range. We use a Bayesian dose response model to estimate maximum cold tolerance of winegrapes using mean winter temperatures. Our model has a hierarchical structure, allowing us to partition the variance between the 18 different genotypes included in our model. Combining our estimates of genotype maximum cold told tolerances with gridded Okanagan Valley climate data from the 1950s-2010s allows us to assess recent changes in cold damage risk. We estimated maximum cold tolerance as winegrapes at around -22°C, with the most cold-tolerant genotypes approximately 4°C more cold tolerant than the lest cold tolerant. Frost risk has decreased across the Okanagan Valley for all species, but there is still more suitable climate for more cold tolerant genotypes. Increased habitat suitability with warming was also patchy, with many areas of the region still cold enough to pose substantial risk. Despite warming in the Okanagan Valley, therefore, more cold tolerant genotypes are still better able to exploit new potential habitat in the northern range edge location than their less cold tolerant counterparts.

What may shape local persistence of plant species on edaphic islands? Insights from a functional island biogeographic approach

Gianluigi Ottaviani[1], Luisa Conti[2], Francisco Emmanuel Mendez-Castro,

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Strategies that may promote plant on-spot persistence, hence possibly offsetting local extinction risk, remain underexplored in insular systems. Studying relationships between insularity and persistence-related traits may therefore provide key insights into which strategies may boost or hinder local persistence of individual plants and populations. To test this idea, we focused on edaphic islands as model system. We examined how traits of plants specialized to these "special environments" – defined by patchy distribution of discrete bedrocks or topographic discontinuities in a landscape, such as fens, rocky outcrops, mountaintops studied here – relate to insularity metrics. We expected that, at the interspecific level, insularity promotes individual persistence abilities (such as enhanced clonality, large and protected bud bank, heavy seeds) while reducing trait variability towards fine-tuned values (i.e. more similar traits), and we found widespread support. At the intraspecific level, we collected field-data for persistence-related traits, microclimate and soil parameters within one edaphic island system, namely outcrops. We hypothesized that species belonging to different life histories (clonal and non-clonal perennial herbs) would respond differently to insularity, while controlling for effects associated with soil and climate. We indeed found that clonal species showed consistent responses, with enhanced individual persistence abilities in more insular sites. Conversely, non-clonal plants exhibited highly species-specific responses, combining different strategies. Overall, our findings suggest that edaphic island plant specialists may offset, or delay, local extinction risk associated with strong insularity by boosting their local persistence chances through a variety of strategies, which can largely vary between different life histories.

Drivers of Phylogenetic and Functional diversity of terrestrial mammals across biogeographic zones of India

Nilanjan Chatterjee[1], Ankita Sinha[1],

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Phylogenetic diversity (PD) and Functional diversity (FD) account for the evolutionary histories of species present and can facilitate a comprehensive understanding of biodiversity. We collected presence data of terrestrial mammals from 67 camera trap studies across India to test how patterns varied across different biogeographic zones. We tested whether different biogeographic zones differed in their biodiversity. Since species richness has a strong positive correlation with phylogenetic diversity, we standardized values for PD and FD across sites. We modelled the standardized mean PD and FD of each site with large-scale habitat variables in each biogeographic zone. We tested the hypothesis that there is significant difference between the standardized richness measures across biogeographic zones. A total of 97 mammals were recorded with a found strong positive correlation between species richness and phylogenetic (r = 0.89, 95% Cl 0.82-0.93) and functional diversity (r = 0.82, 95% Cl 0.72-0.88). The standardized functional and phylogenetic mean distance and mean nearest neighbor distance was significantly different across biogeographic zones. Human modification was the best predictor for taxonomic diversity while functional and phylogenetic diversity was explained majorly by actual evapotranspiration and climatic variables. Although, some studies have documented the limitations of phylogenetic diversity, it can potentially complement species richness in order to provide a holistic understanding of processes shaping biodiversity patterns. Moreover, integrating functional and phylogenetic approaches can reflect various historical and evolutionary processes operating at different scales thus helping to understand potential drivers behind current species distribution and how natural and anthropogenic alterations will affect them.

Concurrent Session 15 (Invasion Biogeography/Species Distributions/Diversity)
June 4th 4:00 pm – 5:30 pm PT – Room 11

Ecological sampling cover estimation for dung beetles (Coleoptera: Scarabaeidae) in Turkey

Seda Akkurt Gumus[1], Yakup Senyuz[2], Jorge Ari Noriega,

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Detection of gaps in ecological sampling is essential to identify areas with missing taxon data. In this way, the “holes” in the species distribution can be eliminated by focusing on the regions lacking information, and the biodiversity protection procedure can be applied to the priority regions. This study aims to determine where the family Scarabaeidae (Aphodiinae and Scarabaeinae) is sampled in Turkey. For this purpose, an exhaustive search of all the existing literature of the group for the country was carried out. In addition, we used a grid of 1 x 1 degree to estimate the sample coverage. Sixty-six scientific articles were registered for Turkey, but only 12 (18.1%) correspond to ecological studies with complete sampling methods descriptions that were included in the analysis. A total of 76 sampling localities were obtained. The country sample coverage was 30.8% showing a 69.2% coverage not sampled rigorously or without published data. There is a clear effect associated with collection in places close to large urban centers. The biogeographic area where the highest number of studies is the Mediterranean region. The results revealed an uneven sampling coverage in the main bioregions, evidencing a lack of studies in the Black Sea region. Most publications were on open meadow and forest ecosystems in Western Anatolia’s mountainous territories, and fewer studies were carried out in coastal dunes, meadows, pastures with agricultural plantations, and some agricultural areas in Thrace and Aegean regions. For this reason, it is crucial to complete the sample coverage to the national level, focusing on regions of high importance for conservation and determining their exact distribution areas. In the next stage of this study, species distribution modeling will be performed to predict the potential distribution in areas showing a lack of sampling.

Introduced herbivores restore Late Pleistocene ecological functions

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Large-bodied mammalian herbivores dominated Earth’s terrestrial ecosystems for several million years before human-associated extinctions and declines during the Late Pleistocene (LP). These declines led to widespread ecological changes due to the loss of their ecological functions, as driven by their unique trait combinations. However, recently, humans have increased herbivore species richness through introductions in many parts of the world, potentially counteracting LP losses. Here, we will present on research evaluating the extent to which introduced herbivore species restore lost—or contribute novel—functions relative to pre-extinction LP assemblages. We constructed multidimensional trait spaces using a trait database for all extant and extinct mammalian herbivores ≥10 kg known from the earliest LP (~130,000 ybp) to the present day. We found that extinction driven contractions of LP trait space have been offset through introductions by ~39% globally.

Analysis of trait space overlap reveals that assemblages with introduced species are overall more similar to those of the LP than native-only assemblages. This is because 64% of introduced species are more similar to extinct rather than extant species within their respective continents. Many introduced herbivores restore trait combinations that have the capacity to influence ecosystem processes, such as wildfire and shrub expansion in drylands. We will then present on how studying introduced species in the context of Earth's history can reveal hidden ecological processes and relationships, such as ecosystem engineering of desert water availability by feral equids and novel trophic cascades between cougars and feral donkeys.

Landscape connectivity from the perspective of ectomycorrhizal fungi

Liam Johnson[1], Jason Pither[1],

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Ectomycorrhizal fungi (EMF) are root symbionts important to the success of many tree species, as they provide their hosts with soil nutrients and protection from pathogens and facilitate seedling establishment and survival. Correspondingly, considerable attention has been paid to the role EMF play in governing the range dynamics of their hosts, including how they might influence tree migration under climate change and the invasion of exotic trees into new regions. In contrast, less attention has been paid to understanding what governs shifting distributions of EMF themselves, in part because key parameters that govern the distribution of EMF remain poorly resolved. Host breadth, or the diversity of plant taxa with which a given EMF can associate, directly limits the extent of available habitat and yet is ill-defined for many EMF. Dispersal capacity is subject to similar uncertainty. Among the minority of well-studied EMF for which these parameters are well characterised, considerable variety exists; it is therefore difficult to predict the potential distributions of under-studied EMF, as their host compatibilities and dispersal abilities resist broad generalisation. In light of this uncertainty, we constructed a spatially-explicit simulation designed to explore how (i) host breadth, (ii) dispersal capacity, and (iii) spatial distribution and abundance of hosts individually and interactively affect landscape connectivity from the perspective of EMF. We demonstrate how contrasting assumptions about host breadth and dispersal capacity interact in dramatic ways with realistic landscape structure to affect potential range expansion, and generate testable predictions for orienting future experiments.

Birdlife range maps differ from statistically derived ones but not enough to alter conclusions on drivers of diversity

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The result of any analysis is never better than the quality of the input data. Macroecological analyses for many groups have been made possible by the substantial publicly available data such as the range maps provided by Birdlife or the International Union of Conservation (IUCN). However, the use of these range estimates in macroecological studies has been criticised because the maps are expert derived and therefore difficult to reproduce. Here we tested whether the range maps from Birdlife and macro-ecological conclusions drawn from them are reproducible with geo-statistic methods based on observed occurrences. We estimated the geographic ranges of over 7.000 bird species, using publicly available point occurrences from eBIRD and environmental restrictions. We quantified the spatial overlap between these maps and the Birdlife range estimates and compared global species richness patterns emerging from both data types. We find that the geo-statistically derived range estimates only overlap on average by 59% with expert generated range maps. The global species

richness patterns from both data types yield similar patterns although with some differences. Despite these differences the estimated effect size of potential drivers of diversity were similar between the two data types. Our results suggest that expert derived estimates of species distributions remain unreproducible by data-driven approaches, even for well-sampled taxa such as birds. However, these uncertainties are unlikely to have substantially changed our understanding of the drivers of spatial patterns in diversity.

A global analysis of habitat change research in reptiles and amphibians: What have we done so far?

Nicholas Wei Cheng Tan[1], Anthony Herrel[2], Dennis Rödder[1]

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Habitat change and fragmentation is the primary cause of biodiversity loss worldwide. Recent decades have seen a surge of funding, published papers and citations in the field as current threats to biodiversity continue to rise. However, how research directions and agenda are evolving in this field is still poorly understood. In this study, we examined the current state of research on the most threatened groups of vertebrates, reptiles and amphibians. We did so by conducting a global scale review of geographical and taxonomical trends regarding habitat change (agriculture, logging, fragmentation, urbanisation and roads) and the associated sampling methods and response variables. We reveal a number of biases, in particular that existing research efforts are characterised by distinct continents (e.g. North America, Europe and Australia) and study groups (e.g. amphibians) and a surplus of studies measuring species richness and abundance with seemingly contradictory results. However, we found a recent shift in research agenda towards studies utilising technological advancements including genetic and spatial data analyses. Our results suggest important associations between sampling methods and the response variables measured which are commonly used in explaining effects of different types of habitat change. Increased research investment with appropriate sampling techniques is crucial in biodiversity hotpots such as the tropics where unprecedented threats to herpetofauna exist.

Mechanistic SDMs and connectivity models: The highly invasive African Clawed Frog (Xenopus laevis) in Europe.

Philip Ginal[1], Dennis Rödder[1]

[1]Zoological Research Museum Koenig

One main threat promoting the worldwide amphibian decline is the introduction of non-indigenousamphibians, like the African Clawed Frog Xenopus laevis, which is now one of the widest distributedamphibians occurring on five continents with ongoing expansion including large parts of Europe. Different types of statistical models can be useful tools in invasion biology. Species Distribution Models (SDMs) and the concept of ecological niche are essential to predict the invasive risk of those species, while connectivity models can be used to reconstruct past dispersal routes or to highlight areas of risk for future invasion. On a macroecological scale, we used mechanistic SDMs to predict the potential distribution for X. laevis across Europe. Based on physiological performance trials we calculated size and temperature dependingresponse surfaces, which were scaled to the species' range matching the critical thermal limits. Theseecophysiological performance layers were used in a standard correlative SDM framework to predict the potentialdistribution in South Africa and Europe. We found thermal performance differed significantly among native andinvasive populations indicating some degree of fundamental niche change, which lead to different potentialdistribution patterns for the native and invasive populations in the respective ranges. Furthermore on a local scale, we used connectivity models based on remote-sensing derived resistance kernels to reconstruct the X. laevis invasion for Portugal and identified several areas, which might be corridors for future invasion risk.

Concurrent Session 16 (Biodiversity Patterns & Maintenance)
June 4th 4:00 pm – 5:30 pm PT – Ballroom C

The clustering of spatially associated species to unravel patterns in species distributions

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The identification of species groups with uniquely similar geographical distributions underpins many basic and applied questions in ecology, biogeography, evolution, and conservation. The lack of transparent and quantitative support, however, limits the utility and reproducibility of such groups. We propose the Clustering of Spatially Associated Species (CSAS) approach to overcome these limitations, which aims to statistically classify species based on quantifiable interspecific spatial associations (ISA). Here, we develop and illustrate the CSAS approach and apply it to distributions of tree species in Borneo. To facilitate robust decision making when applying the CSAS approach, we also investigate how the choice of ISA index and clustering algorithm affects the clustering and performance of resultant dendrograms. We then classify species based on the best performing methods and evaluate the impact of land-use change on each group. We found the ISA index and clustering algorithm both to engender substantial variations in clustering outcomes and are thus important considerations of the CSAS approach. Clusters using WARD (clustering algorithm) based on Hellinger's distance (ISA index) performed best, which identified 10 distinct patterns of tree distribution. Land-use change affected each pattern differently, where those with distributions traditionally associated with coastal and peat swamp forests suffering the greatest decline. The impacts also differed temporally, indicating potential land-use regime shifts in 1996 and 2004. We argue that such quantitative assessments of associations and species groupings will offer opportunities for more nuanced inference in biodiversity assessments, spatial and community ecology, applied biogeography, and conservation decision making.

Equilibrium Theory of Biodiversity Dynamics: Interplay between patterns of diversity, abundance and energy

David Storch[1], Jordan Okie

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There is increasing evidence that large-scale diversity patterns are affected by environmental limits or a carrying capacity for species richness, so that different stable diversity equilibria exist for different regions. We propose a formal, species-based Equilibrium Theory of Biodiversity Dynamics (ETBD) which shows that equilibrium diversity is determined by the balance of population size-dependent species origination and extinction, modulated by energy or resource availability. In contrast to other theories of diversity dynamics, ETBD deals with non-trivial links between total community abundance and species richness, assuming not only that community abundance limits the number of species with viable populations, but also that higher diversity allows better resource utilization and so higher community abundance, thus reconciling conflicting views on species richness saturation. The theory makes realistic predictions on mutual scaling of energy availability, species richness and community abundance, and thus explains the enigmatic pattern of species-energy relationship being more pronounced than the relationship between energy availability and community abundance. ETBD is in accord with patterns observed on paleoecological time series, as well as with spatial diversity patterns, and can be used as a framework for elucidating the role of varying extinction and origination rates in driving diversity variation along large-scale environmental gradients. We argue that although species richness is often out of equilibrium, regional diversity equilibria represent attractors of biodiversity dynamics and ultimately drive major macroecological diversity patterns including the latitudinal diversity gradient.

Impact of geological and climate factors on plant biodiversity patterns in the Hengduan Mts, China

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Mountain regions usually harbor disproportionally high biodiversity levels on Earth, which can hardly be explained solely by climate. The complex interactions between the geological and climate dynamics in the mountain system could provide a unique substrate for species to diversify, leading both to higher diversity and endemism in mountains. The Hengduan Mountains region is a unique biodiversity hotspot outside of the tropics, and is characterized by complex geological and climate histories due to the Indian-Eurasia plate collision and monsoon intensification shaping surface processes. These unique and complex histories are expected to have shaped landscapes across millions of years shaping the dispersal, speciation and extinction of lineages but little is known about the relative influence of those interacting processes . By mapping the seed plant biodiversity pattern at 1 km resolution combined with mapped abiotic variables, we quantified the relative contribution of climate, tectonic and geomorphology in shaping hotspots. In this presentation, we will show that the Hengduan mountains region displays a hotspot within the region, where biodiversity peaks in the Three-River region. Using structural equation models, we will show how this pattern is mainly driven by both unique geological features (e.g. in-situ relief, river captures) and climate oscillations in the past few million years. Finally, we will demonstrate how different clades inhabited in different elevational bands respond to these geological and climate processes. Taken together, we will show how the Hengduan Mts region plays both museum and cradle roles in driving species diversity patterns.

By land, air or sea: foraging in distinct media shapes the evolution of functional trait specialisation in birds

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It is widely assumed that species with extreme functional traits provide specialised functional roles within ecosystems. However, the assumption that extreme functional traits correspond to specialisation in functional roles has rarely been tested. Using quantitative measurements of key eco-morphological dimensions of body shape across all birds, we show that specialisation in foraging niches is largely unrelated to a species' position in functional trait space. Species with specialised foraging niches occur both at the periphery and centre of functional trait space. Instead, we find that species with extreme functional traits are associated with specialisation in different locomotory tasks-moving through air, water or across solid surfaces. This specialisation in locomotion is decoupled from specialisation in foraging niches as some specialist niches (e.g. arboreal gleaning) require species to perform multiple locomotory tasks whereas others (e.g. aerial screening) do not. The presence of the same extreme functional traits is also replicated across bioregions, suggesting widespread ecological convergence. While our results support the notion that extreme functional traits are associated with specialisation to perform distinct functional tasks, they also show how specialist functional roles within an ecosystem can be provided by phenotypic generalists adapted to perform multiple functional tasks. More generally our results warn against the use of simple functional trait metrics as indicators of specialisation in conservation and biodiversity studies.

Ecological and evolutionary processes shape below-ground springtail communities along an elevational gradient

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Compared to above-ground taxa, elevational patterns and processes of below-ground animals are little studied. We investigated how environmental gradients across elevation may affect species divergence in the past and act as filters of contemporary assembly of soil detritivores via traits. We asked: (1) Are environmental filtering processes due to elevation, vegetation or microhabitat-related factors driving isotomid springtail community assembly across elevation; (2) did species divergences occur after mountain uplift; and (3) are there environmental factors related to species divergences in the past. We collected isotomid springtails from 800 to 2150 m above sea level from Changbai Mountain, north-east China, and reconstructed the phylogeny using mitochondrial genome sequencing. We inspected the body length, number of ommatidia and pigmentation, and determined their evolutionary patterns. The results indicate that isotomid springtails differed more in traits when co-occurring in environments with lower soil nitrogen, typically at higher elevations. Most communities exhibited phylogenetic clustering, but this pattern was not related to elevation or any environmental variables. These isotomid species mainly diverged in the Mesozoic with some divergence events associated with soil N and pH, as well as other factors covarying with the contemporary elevational gradient studied. The current communities comprised old phylogenetic lineages possessing traits that have undergone evolutionary drift. Our study suggests that while environmental gradients act as filters for below-ground detritivores, evolution of traits preconditions their assembly. Species divergence likely resulted from filtering processes of past environments resembling the present day. Below-ground diversity in Changbai Mountain is mainly based on the persistence of old phylogenetic lineages, while recent speciation is of little importance.

Concurrent Session 17 (Anthropocene Biogeography)
June 5th 2:00 pm – 4:00 pm PT – Room 2/3

Assessing biodiversity changes across a continuum of spatio-temporal scales

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Magnitude assessment of biodiversity changes is challenging, even in well surveyed groups such as birds. Especially, trends of biodiversity can be driven by the spatial and temporal scales considered, specifically by spatial grains (i.e. area of a sampling unit), geographic extent (i.e. size of the area of interest), temporal grain (i.e. duration of a sampling event) and temporal extent (i.e. length of the time series). However, the influence of spatio-temporal scales on biodiversity trends is seldom documented. Here, we empirically address this issue by using high-quality spatially and temporally heterogenous time-series on bird biodiversity of Czech Republic. A first dataset comes from atlases of Czech Republic and represent the highest spatial and temporal scales. The second one is composed of local time series with high resolution spatial and temporal scales. We show that trends of species richness are stronger with increasing spatial grains, showing that the intensity of macroecological processes varies with spatial scaling. The same analysis is conducted on colonization and extinction processes. We also found that biodiversity reaches a plateau with increasing temporal grains allowing inference of an optimal census time. In addition, we use tree-based ensemble models to predict biodiversity metrics at locations, spatial grains and temporal grains for which data are lacking. Together with the unprecedented biodiversity data, these machine learning methods 1) highlight the link between biodiversity metrics and spatio-temporal scales and 2) hold promises for estimation of biodiversity trends in data-poor regions.

Humans are disrupting a longstanding trophic-size structure in vertebrates

William Gearty[1], Robert S. C. Cooke[2], Abbie S. A. Chapman, Jillian Dunic[3], Graham Edgar[4], Jonathan S. Lefcheck[5], Gil Rilov[6], Craig R. McClain[7], Rick Stuart-Smith[4], Kate Lyons[8], Amanda Bates[9],

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Diet and body mass are inextricably linked in vertebrates: while herbivores and carnivores have converged on much larger sizes, invertivores and omnivores are, on average, much smaller, leading to a roughly “U-shaped” relationship between body size and trophic guild. Although this U-shaped trophic-size structure is well-documented in extant terrestrial mammals, whether this pattern manifests across diverse vertebrate clades and biomes is unknown. Moreover, the emergence of the U-shape over geological time and future persistence are unknown. Here we compile a comprehensive dataset of diet and body size spanning several vertebrate classes and show that the U-shaped pattern is taxonomically and biogeographically universal in modern vertebrate groups, except for marine mammals and birds. We further find that, for terrestrial mammals, this U-shape emerged by the Paleocene and has thus persisted for at least 66 million years. Yet disruption of this fundamental trophic-size structure in mammals appears likely in the next century, based on projected extinctions. Actions to prevent declines in the largest animals will sustain the functioning of Earth's wild ecosystems and biomass-energy distributions that have persisted through deep time.

Do vertebrate species traits influence species' responses to land-use and climate change?

Adrienne Etard[1,]

[1] University College London

Land-use and climate change are two of the most important drivers of biodiversity loss. Nevertheless, not all species respond similarly to these pressures. Species ability to cope with anthropogenic disturbances depends on their functional traits. By preferentially removing certain functional types, land-use and climate change are reshaping the functional composition of ecological communities. Understanding such impacts is key to assess the consequences for ecosystem functioning. Moreover, assessing whether and which traits influence species' responses can help put into place conservation measures. In my work, I used global records across terrestrial vertebrate species to investigate (1) how traits influence species responses to land-use change and (2) which traits are most important in underpinning sensitivity to climate change. I found that sensitivity to land-use and climate change is distributed unevenly across the tree of life and differs according to species traits. While traits that relate to the use of geographical space (e.g., habitat breadth) predict sensitivity to both land-use and climate change consistently across classes, the effects of life-history and dietary traits on species responses are class-dependant. My results highlight that the influence of such traits on vertebrate responses should not be generalised. Further, land-use and climate change are likely to globally impact local ecosystem processes, and, consequently, services rendered by terrestrial vertebrates.

Towards a predictive biogeography of crop-pests and pest control: integrating experiments, large temporal datasets, and models.

Ignacio Morales-Castilla[1,]

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As species undergo spatial and temporal shifts tracking climate change, the networks of species interactions are expected to change in terms of both the identity of interacting species and the strength of the interactions. Being able to forecast these changes would be particularly useful in the context of agricultural pests where inferring shifts in pest incidence or in the potential for pest biological control may allow for more efficient pest management planning. Here, we leverage recent research to (1) explore the role of crop diversity in modulating temporal shifts that could alter the degree of phenological synchrony between crop and pest, (2) test the potential of published physiological models for pest development to be extrapolated across space and time and, (3) assess biogeographical patterns in the potential for pest control by reconstructing tri-trophic networks (i.e., crops, pests and pest predators) based on proxies. Our review of study cases highlights that reliable forecasts of pest incidence and biocontrol potential may still be restricted to a handful species with data and methods at hand. While our results focus on species relevant to Mediterranean agriculture, the approaches and conclusions would apply to agricultural landscapes at different latitudes. Even if limited, current attempts at inferring crop-pest interactions may become a valuable tool to guide field validations and to identify species and regions in need for additional data and experiments.

Three thousand years of island insect decline inferred with community genomics

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Recent reports of insect declines have caused worldwide alarm, but the nature and scope of such declines are hotly debated. Most empirical studies of declines, however, have focused on field counts conducted over the past few decades. Yet, humans have been impacting the planet for thousands of years, and whether declines are products of the modern era, or the continuation of longer-term trends remains unknown. Genomic techniques offer a deeper-time window into population and community trends in human-dominated ecosystems over longer timescales. Here, using the ant community (>100 species) of the Fijian archipelago as a model case, we take a community genomics approach to using contemporary biodiversity collections to estimate community assembly and population demography trends. We find that the highly endemic Fijian ant fauna was assembled through a series of colonizations and radiations over millions of years, followed by more recent arrivals of regionally widespread and alien species from outside the region. Using demographic modeling, we show that the vast majority of endemic species are in decline, with reductions beginning around the arrival of humans 3000 years ago and continuing until the present. The few endemic species that are not declining are preadapted to more disturbed habitats now dominated by widespread and alien species, which are all increasing in population. Our results show that indeed different species are winners and losers in the Anthropocene, but on islands the losers are geographically restricted endemic species.

Human-driven speciation could counter global species losses but not losses in phylogenetic diversity

Søren Faurby[1], Rasmus Østergaard Pedersen[2], Jens-Christian Svenning, Alexandre Antonelli[3],

[1] University of Gothenburg, Department of Biological and Environmental Sciences
[2] Aarhus University, Department of Biology - Ecoinformatics and Biodiversity
[3] Royal Botanic Gardens Kew

Human activities are causing massive increases in extinction rates, but may also lead to drastic increases in speciation– for example following the human-mediated spread of species to otherwise unreachable islands. The long-term net anthropogenic effects on biodiversity, therefore, remain uncertain. Here we assess these effects by estimating extinctions and speciations of terrestrial mammals globally. We show that if all species introduced into new landmasses developed into new species, the number of anthropogenic speciation and extinctions would be similar, with different simulated scenarios differing in whether the number of anthropogenic extinctions or speciations would be marginally higher. However, this is only true when analyzing species numbers, which is just one component of biodiversity. For phylogenetic diversity, our estimates suggest instead that for all simulated scenarios, it will still take millions of years to recover from historical and predicted near-term human-driven extinctions, even after accounting for an anthropogenic increase in speciation. Our results highlight that human-induced biodiversity declines are not adequately captured by species richness alone.

Fast or slow? Rates of climate changes of multiple variables over the last decadesFast or slow? Rates of climate changes of multiple variables over the last decades

Alejandro Ordonez[1,]

[1] Aarhus University

Mapping and ranking the speed at which climate is changing is fundamental to formulate successful mitigation and adaptation strategies. However, the rates at which climate conditions are changing are not homogenous. Here, I measure and rank how fast multiple climate variables have moved over the last half-century ranking these in a fast-to-slow spectrum. Using the velocity of climate change, I establish how fast have three types of temperature or precipitation climatic variables (average, phenological, and extreme conditions) changed between 1959 and 2013, placing these rates in a fast-to-slow continuum at a global, continental, and biome scale. Subsequently, I establish the implication of a fast-to-slow continuum of change by estimating the time needed for each evaluated climatic isocline to move across a given protected area (residence time).
Results: Changes across temperature or precipitation climatic variables show a distinctive fast-to-slow gradient. Still, the gradient of responses was stepper for temperature than precipitation related variables. At a global scale, periods of excessive warmth and dryness (warm/climate spells) showed the fastest changes, and cumulative extreme temperatures (heatwaves and frost frequency) and periods of excessive wetness (wet spells) showed the slowest changes. These same variables are the fastest or slowest variables in most areas across the globe, continents and biomes. Based on the current velocities of change, a complete change in average and extreme conditions for most protected areas is expected within the next few decades. Mapping the gradient in climatic changes across multiple variables highlight the heterogeneity in exposure to climatic changes and the low climatic safeguard potential of the global network of protected areas. Mitigation and adaptation strategies aimed at avoiding, reducing, or compensating for the impact of accelerating climatic changes will need to consider such heterogeneity.

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80 years of anthropogenic change and its impact on Canadian butterfly taxonomic and phylogenetic diversity

Jayme Lewthwaite[1,] Arne Mooers[1]

[1] Simon Fraser University

Several recent studies have documented net zero change in average plot-level species richness but with much variation around this mean. It is unclear how anthropogenic drivers (such as climate change or land use change) contribute to this variation in species richness, and we also do not know how these drivers might impact other plot-level measures biodiversity, e.g. if traits dictate species responses and if relatedness is correlated with trait similarity, then the impacts of anthropogenic change may be clustered on the phylogeny. I examine change in assemblage phylogenetic structure in response to two main documented drivers of change -- climate change and land use change -- across approximately 300 Canadian butterfly species, 75 years and 96 well-sampled areas distributed across Canada. I find a small increase in assemblage level species richness, however no evidence for net change in phylogenetic structure. I find that climate change as well as agricultural development is associated with reduced assemblage-level species richness, and assemblages associated with the highest increases in cropland have become phylogenetically overdispersed relative to expectation. Interestingly, agricultural abandonment is having the opposite effect: I find increasing species richness and decreasing distance between species in assemblages in areas with the highest rates of abandonment. Consistent with previous research, small changes in local species richness may conceal change in other facets of biodiversity.

Concurrent Session 18 (Paleoecology & Paleobiogeography)
June 5th 2:00 pm – 4:00 pm PT – Room 8

Past spatio-temporal variability of boreal forest carbon storage: an Alberta case study

Jo-Mary Crowchild-Fletcher[1], Kaitlyn Russell[1], Nimrat Sandhu, Andria Dawson[1],

[1] Mount Royal University

Terrestrial ecosystems play an important role in regulating Earth's climate. As atmospheric carbon dioxide concentrations increase, understanding forest response to these changes is critical. Previous studies show that forests act as a global terrestrial carbon sink; however, the role of forests in biosphere carbon fluxes is not well understood.

Boreal forests account for about a third of Earth's forested area and carbon stocks. Ecosystem models forecast decreases in boreal forest biomass due to changes in temperature and precipitation. These changes are not uniform across space; southern boreal forest biomass is predicted to decrease more than northern boreal forest biomass. In practice, it is difficult to measure forest carbon flux, so estimates of spatio-temporal variability in these fluxes are lacking. Flux towers, satellites, and remote sensing are used to quantify current forest productivity, whereas tree rings provide evidence of past productivity.

Here, we use tree ring data from sites across a climate gradient in the Alberta boreal forest to estimate past carbon storage. Using tree ring data from sites dominated by white spruce and aspen, we use allometric equations to reconstruct aboveground biomass increment (ABI). These ABI reconstructions are then used to assess the spatial variability in biomass increment trajectories with respect to the climate gradients and stand characteristics. Finally, we use the North American Carbon Program (NACP) stand age maps to derive carbon storage estimates for Alberta from ABI. These results inform understanding of spatio-temporal variability in forest ABI and provide empirical constraints that can improve ecosystem forecasts.

Using global climate data and the fossil record to determine the driving factors in the late-Quaternary megafauna extinctions

Rhys Lemoine[1], Jens-Christian Svenning[2],

[1] Biochange, Aarhus University
[2] Department of Biology, Aarhus University

The disappearance of a large proportion of the world's megafauna during the late Quaternary is the source of one of the most contentious and long lasting debates in the scientific world. Though several explanatory hypotheses exist, the two most prevalent are climate change and pressure from modern humans (Homo sapiens). Many studies have attempted to address this issue, but there is a tendency to treat it as a local occurrence. The late-Quaternary extinction was a global event lasting tens of millennia, and consequently a global biogeographic analysis is needed in order to adequately address this phenomenon. In this study, we use updated global data on late-Quaternary climate change, megafauna ranges (for all Late Quaternary mammal species weighing ≥9 kg (~20 lbs), including 487 species, 158 of which are extinct), and hominin biogeography to determine, statistically, the strongest predictors of extinction severity. Based on a GLM approach, our results strongly support a primarily human-driven model, with an R2 of 0.73842. Some climatic predictors did improve the combined models to a small degree ($0.05>p>0.01$, highest R2 of 0.74643), but purely climatic models had low explanatory power (highest R2 of 0.21999). These results are strongly consistent with a global extinction event driven primarily by human expansion and activity, with climate change exerting only minimal influence.

Changes in small mammal community composition over the last 25,000 years across multiple western North American cave localities

Julia Schap[1], Jenny McGuire[1], Julie Meachen,

[1] Georgia Institute of Technology

Natural Trap Cave (NTC) is an 80-foot deep karst sinkhole located at the base of the Bighorn Mountain range in Wyoming, USA. An exceptional fossil record of microfaunal remains are found from well-stratified layers in the cave stretching back 30,000 years ago, before the end-Pleistocene megafauna extinction, up until a few hundred years ago. While many studies have examined how communities respond to environmental changes in a single location through time, few have observed how community responses vary across different habitats. We compared standardized richness, evenness, and relative abundances, using NISP, of the small mammal communities from NTC, Samwell Cave, Two Ledges Chamber, and Homestead Cave to observe how small mammal communities shifted through time across diverse landscapes. Results from a PCoA found that NTC and Samwell Cave were more similar to each other than to Homestead Cave and Two Ledges Chamber. Despite differences in local environments, open and arid at NTC and closed and forested at Samwell Cave, small mammal accumulation at both these caves are the result of packrat midden collection. Richness and evenness were then compared between NTC and Samwell Cave. We found that evenness decreased at both caves from the Late Pleistocene to the Late Holocene. Richness also decreased through time at Samwell Cave but increased through time at NTC, though this may be influenced by small sample sizes in the Late Pleistocene. High evenness and richness are good indicators of a stable community, meaning small mammal communities may be threatened in the modern.

Holocene history of mangrove distribution and migration along the Gulf of Mexico coast, U.S.A.

Kam-biu Liu[1], Qiang Yao[1], Marcelo Cohen, Érika Rodrigues[2], Junghyung Ryu[1], Alejandro Aragon-Moreno[1], Nina S.N. Lam[1],

[1] Louisiana State University
[2] Federal University of Pará, Brazil

Little is known about the Holocene biogeographic history of the three species of mangroves (Rhizophora, Avicennia, Laguncularia) to shed light on the causes of its disjunct distribution along the northern Gulf of Mexico coast today. We reconstructed the Late Holocene migration history of mangroves by means of palynological and stratigraphic analyses of sediment cores collected from five coastal wetlands from Florida to Louisiana to document the chronology of mangrove colonization and population dynamics at each site. Rhizophora (red mangrove) arrived in the Everglades, Florida, at least 3800 years ago as sea level rose, followed closely by Avicennia (black mangrove) and Laguncularia (white mangroves). Avicennia, and subsequently Laguncularia and Rhizophora, spread to Cedar Keys, Florida, at ~1300 yr BP. Avicennia and Rhizophora migrated to Dog Island, Apalachicola, Florida, less than 200 years ago, and to adjacent St. George Island only two decades ago. In Port Fourchon, Louisiana, where both Rhizophora and Laguncularia are absent, Avicennia pollen started to appear no more than 100 years ago and black mangrove has since proliferated in coastal wetlands. Mangroves never colonized the coastal areas of southwestern Louisiana during the Holocene. Our paleoecological data do not support the range contraction hypothesis. Instead, they are consistent with the scenario that mangroves migrated from the Everglades to Cedar Keys by diffusion along the coast but were dispersed to southern Louisiana and Apalachicola by jump dispersal. Mangrove populations are expected to continue to spread along the northern Gulf Coast in response to anthropogenic global warming.

Quantifying Holocene albedo change from paleoecological land cover for northern North America

Ruby Morillo[1,] Andria Dawson[1,]

[1] Mount Royal University

Mitigating the impacts of climate change relies on understanding how climate-vegetation feedbacks affect climate variations. These feedbacks depend on biophysical land cover characteristics including albedo, which impacts radiative forcing. However, the narrow temporal extent of direct observations of albedo makes it difficult to quantify centennial to millennial scale shifts in forest structure and composition. Previous work used both historical and modern land-cover datasets to quantify albedo changes resulting from land use shifts, finding that the deforestation cooling effect is reduced by secondary forest growth. This highlights the importance of forest successional changes on climatic feedbacks. Networks of fossil pollen data offer an observational constraint on biophysical land cover change that extends throughout the Holocene. Here we reconstruct Holocene albedo for northern North America from a spatio-temporal network of fossil pollen records from the Neotoma Paleoecology Database, and Moderate Resolution Imaging Spectroradiometer (MODIS) satellite albedo data-products. We do this in two steps: calibration and prediction. In the calibration step, we develop a statistical model that characterizes the relationship between modern pollen samples and seasonal albedo. In the prediction step, we use the calibration model to reconstruct albedo from historical pollen records. Results indicate that mid-latitude albedo has decreased, while albedo in northern latitudes has increased. This indicates shifts in land cover, and in the position of the boreal-tundra ecotone, coincident with shifts in climate. This work provides new insight about the nature of climate-vegetation feedbacks and ecotone shifts, and an empirical constraint on ecosystem forecasts.

A novel tool to detect non-random time trends in assemblages

Arnošt Šizling[1,] Petr Pokorný[1,] Valentin Rineau, David Storch[1,]

[1] Charles University

Revealing temporal shifts in composition of paleo-assemblages is a complex task. At the same time, it is a desirable skill, because accurate identification of non-random trends in paleo-assemblages would improve our understanding of the human and climate impacts on biodiversity change. The main problems with trend identification are a temporal variation in the quality of (sub)fossil record, and that there are usually fewer consecutive samples within the trend period than statistically necessary. Using real data on palaeoassemblages, we introduce a method for identifying non-random trends that deals with the above problems and that requires only three samples within a trend period. We demonstrate ability of the method to indicate Holocene pollen successional sequences (i) that followed fire management and (ii) that occurred in abandoned settletments, as well as Cretaceous rudist fossil sequences following known adaptive radiations and mass extinctions. The method is suitable to paleo-studies where the shortest period between samples is decades or longer. However, the method can also be applied to recent successional sequences and spatial transects if time is replaced with space. In addition, the method can be adopted by archaeologists to identify trends in artefactual/cultural traits over both time and space.

The time-integrated host diversity hypothesis for geographic variation in the species pool richness of mycorrhizal fungi

Jason Pither[1], Brian Pickles[2],

[1] University of British Columbia
[2] University of Reading

Efforts to explain variation in the species pool richness of mycorrhizal fungi (MF) have focused primarily on contemporary abiotic and biotic factors, but historical-biogeographical influences are increasingly being considered. Here we propose and rationalize the “time-integrated host diversity hypothesis”, which posits that the size (richness) of the MF species pool available to a given host in a given location is determined in part by the diversity of host plant species that the location, and its surrounding landscape, has harboured from deep time (hundreds to thousands of years) to the present. This hypothesis emerges from four sets of observations that, until now, have largely been considered in isolation: (i) the diversity MF often correlates with host diversity in both space and time; (ii) soil can harbour a diverse, persistent propagule assemblage, both local and regional in origin, (iii) through host switching, MF can persist in landscapes where their preferred hosts have long since disappeared, and (iv) especially where edaphic conditions permit, host roots can penetrate deep belowground, and could therefore integrate decades of accumulated diversity in the soil. As a first step towards testing this hypothesis, we use paleoecological data to estimate and generate a map of time-integrated (since the last glacial maximum) richness of tree genera across North America. Aside from its primary goal of improving our understanding of the causes of geographical variation in the richness of MF species pools, our hypothesis reveals a number of exciting avenues for future research in belowground ecology.

Global phanerozoic biodiversity – can variation be explained by spatial sampling intensity?

Daniel Phillipi[1], Jesse Czekanski-Moir[2], Linda Ivany,

[1] Syracuse University
[2] SUNY-ESF

Variation in observed global generic richness over the Phanerozoic must be influenced by sampling heterogeneity, including differences in the number of samples taken through time and their spatial distribution. To better understand how spatial sampling heterogeneity might be influencing fossil richness estimates, we create a steady-state model of diversity by resampling a modern biodiversity dataset with the same spatial fidelity of sampling in fossil time bins spanning the Phanerozoic. Fossil occurrences from the Paleobiology Database (PBDB) are parsed into ~11 myr time bins and spatially gridded into equal-area grid cells. For each time slice, the number of taxa and occurrences are recorded for each cell, along with the cell’s latitudinal and longitudinal coordinates. Then, modern grid cells are selected to match the geographic distribution of fossil cells such that the spatial distribution of cells is as equal as possible for both the modern and fossil data. Occurrences are randomly drawn from the selected modern cells such that the total number of occurrences and their distribution among cells is identical to the fossil record sampling, and the total number of unique genera found is recorded. Using linear regression analysis, we then compare richness estimates over time derived from the PBDB to predictions of the steady state model. While our intent was to reject the null hypothesis that richness has not changed through time, preliminary results suggest that the steady state model cannot be rejected. Possible implications arising include 1) fossil richness estimates are flawed when spatial sampling is limited, or 2) marine invertebrate diversity has not significantly changed through time. While we focus on the importance of these results regarding the study of Phanerozoic biodiversity, our findings also have implications for the use of spatially unevenly sampled global specimen databases in the study of contemporary biodiversity.

Concurrent Session 19 (Biodiversity/Richness/Species Distributions)
June 5th 2:00 pm – 4:00 pm PT – Room 11

Spatial range traits drive plant exposure to climate and land use change in the California Floristic Province

Brooke Rose[1],

[1] University of California, Riverside

Understanding how vulnerability to global change varies across species is a key component of conservation management and predictive frameworks for identifying vulnerable species are needed in the face of rapid climate and land use change. Characteristics of species' spatial distributions -- spatial range traits -- influence their vulnerability to global change. Rare species are often more vulnerable to changing environments than common species, due to small range sizes, narrow habitat requirements, and/or small populations. Similarly, "location-based" aspects of species' distributions, such as topographic complexity and distance to the coastline, affect their vulnerability to changing environmental conditions. To better understand how species' spatial range traits mediate their vulnerability to future climate and land use change for a set of plant species in the California Floristic Province (CFP), I used species distribution models (SDMs) to predict geographic range loss (exposure) for 111 plant species under two climate and land use change emissions scenarios (RCP 4.5 and 8.5). A combination of flexible regression methods and decision trees reveal that species with small, topographically homogenous ranges will be especially exposed to both climate and land use change. However, the relationships between spatial range traits and exposure were not always unidirectional for climate and land use change, i.e. high elevation species were most exposed to climate change while low elevation species were most exposed to land use change. This research supports that spatial range traits interact and are important determinants of climate and land use change exposure in the CFP.

Dynamics of the Northern Humboldt Current System pelagic fish community structure under El Niño Southern Oscillation scenarios

Paola Lisset Galloso Sanchez[1], , Pierre Legendre[1], Giancarlo Helar Moron Correa[2]

[1]Université de Montréal
[2] Oregon State University

The Northern Humboldt Current System (NHCS) is a highly productive upwelling system that covers the northern-central area of Peru. NHCS is the area where the El Niño Southern Oscillation (ENSO) is most noticeable, with resultant climate variability. The variations of El Niño, the ENSO warmer phase, and La Niña, the cold phase, trigger changes in the biological productivity of the ocean as well as in species behavior across different trophic levels. This study aims to describe the changes in the spatial structure and composition of the NHCS pelagic fish community under three scenarios: El Niño, La Niña, and Neutral. A spatially constrained clustering and temporal beta-diversity index (TBI) were performed, to identify the same community ecological regions for each scenario and measured its dissimilarity, respectively. El Niño scenario brings out the highest values of alpha diversity and species richness, and La Niña yields the lowest values. The spatial structure of the community shows predominantly three areal groups which vary in terms of areal extension and species richness across scenarios. The spatial effect of the observed temporal changes of the fish pelagic diversity is important since the interaction between species depends on their spatial distancing. The main factor controlling spatial dynamics of the NHCS pelagic community seems to be is the temperature and environmental stability, due to the different areal groups formed during the El Niño scenario, and in addition, to the variation in the beta diversity and presence-absence of species during a normal period and a warmer one.

GreenMaps: a Tool for Addressing the Wallacean Shortfall in the Global Distribution of Plants

Barnabus Daru[1,]

[1] Texas A&M University-Corpus Christi

The exponential growth of species occurrence data can facilitate dynamic biodiversity analyses. However, raw biodiversity data alone should not be used indiscriminately due to inherent sampling biases, impediments that contribute to the Wallacean shortfall (i.e. the paucity of species' geographic information). It has been suggested that the Wallacean shortfall is a common phenomenon across taxa, however, there is no global assessment geared toward overcoming this impediment for plants, despite the fundamental role of plants in ecosystem stability, food security and biodiversity conservation. Here, I present GreenMaps, a new tool that will permit a rapid initial assessment of the Wallacean shortfall for plants by building base maps of species' predicted distributions upon which citizen science participation could contribute to spatial validation of the actual range occupied by species. The initial stages of GreenMaps have now been accomplished, providing a massive dataset of modeled range maps for over 230,000 vascular plant species. This will make it the largest and only global assessment of geographic distributions for plant species at scales relevant to research and conservation. Ultimately, GreenMaps will interface with a mobile application to enable volunteers from any region of the world to validate predicted species distributions to be used for the generation of new and improved global maps of plant distributions.

How plant dispersal syndromes shape the relationship of species richness with area and isolation

Anna Walentowitz[1,] Claudia Troiano[2,] Julie B. Christiansen, Manuel Steinbauer[1,] Anders S. Barfod[3,]

[1] University of Bayreuth
[2] University of Naples Federico II
[3] Aarhus University

What determines insular species richness? This question has been under debate since the origin of island biogeography. So far, the contribution of plant dispersal syndromes has been very little explored to explain species richness patterns on islands. We investigate how plant dispersal syndromes relate to area and isolation and if they help to explain richness patterns on islands. Our study reports from European islands at the mesoscale that are highly underrepresented in biogeographical research. Plant species lists were compiled for all target islands and single species categorized by their dispersal syndrome (zoochory, anemochory, hydrochory and autochory). Generalized linear models were used to detect relationships of richness and dispersal syndromes with area and isolation. We found that the richness of plants with animal- and wind-dispersed seeds increased with area while plants with water-dispersed seeds became fewer. Plant dispersal syndromes help to understand the relationship of basic biogeographic factors such as area and isolation with species richness. Despite the strong human alterations of European islands, fundamental biogeographic drivers have not been levered out.

Pacific eDNA Coastal Observatory: how to capture biogeography with a simultaneous and systematic snapshot of biodiversity

Kate Sheridan[1], Ben Millard-Martin[2], Matt Lemay, Evan Morien[3], Thomas O'Calleghan-Brown[1], Emmett Duffy[4], Jay Stachowicz[5], Margot Hessing-Lewis[3], Jennifer Sunday[1],

[1] McGill University
[2] McGill
[3] Hakai Institute
[4] Smithsonian
[5] UC Davis

Monitoring biodiversity change at large spatial scales is effort-intensive but necessary to track and understand responses to climate change and conservation efforts. In recent years, marine environmental DNA (eDNA) has been used to survey regions on increasingly large scales, with incredible potential to uncover biodiversity changes across space and time. However, guidance is needed to optimally distribute samples across a marine landscape for biogeographic-scale questions. Here we present an analysis of nearshore regional biodiversity 'coverage' as a function of eDNA sampling effort, which can guide optimal design of regional biodiversity surveys in the Pacific temperate region. We next demonstrate the implementation of one sampling design across multiple regions from a coast-wide network, the Pacific eDNA Coastal Observatory, currently representing 16 regions between Alaska and southern California and covering about 25 degrees of latitude. Together with our partners, we sampled eDNA targeting fish species from seagrass beds in summer of 2021, alongside visual fish surveys in select regions. We discuss emerging patterns of seagrass-associated fish biogeography, as well as lessons learned from initiation of the observatory.

Can we propose more laws for biogeography?

Mark John Costello[1], Robert Whittaker[2], Shane Wright,

[1] Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway.
[2] University of Oxford

The understanding and science of biogeography has advanced through testing of rules, effects, principles and theories, including Island Biogeography, Mid-Domain, Bass-Becking's (Bjerenick's), Rapoport's, Bergman's, Cope's, Damuth's, Thorson's, Gloger's, Allen's, and the Generation Time law. We suggest that a set of "biogeography laws" to help understanding of the geographic patterns of biodiversity. They are: Taxa with wide dispersal will have high gene flow and fewer species than taxa with restricted dispersal; Species in geographically isolated habitats (as distinct from areas and endemism) must have good dispersal mechanisms; Taxa that have very large population sizes (abundant) will have high genetic diversity but low species richness; Microscopic taxa are passively and more easily dispersed than macroscopic taxa in air, water and attached to substrata such as large animals and flotsam; Macroscopic taxa dispersal is limited by predation risk; Dispersal of large taxa is limited by energetic costs; Aerial dispersal is many times faster than aquatic which is faster than terrestrial; Temperature is the most important drivers of genetic diversity and potential for speciation; Habitat complexity provides more opportunities for niche specialisation and sympatric speciation; Higher primary production provides more food for higher trophic levels, and thus higher abundance of herbivores and predators; Most species are rare and a few dominant in any habitat. We outline some support for these laws, all of which can be regarded as hypotheses to be tested.

What controls plant richness on mountainous oceanic island: area, productivity, or water and energy?

Ole Vetaas[1,] Kuber Bhatta[1,]

[1] University of Bergen

Geographic variation in species richness along elevational and latitudinal gradients may be controlled by energy, water, and productivity, but spatial factors such as area and geometric constrain may also play a role. This is the first study that us large mountainous oceanic islands to test established plant diversity models such as area, mid domain effect (MDE), actual evapotranspiration (AET, energy), water energy dynamics (WED), and net primary production (NPP). The outcome will have clear implications for global diversity theory.

We compiled entire floras with elevation specific occurrence information for eight mountainous oceanic islands around the world. For each of the eight islands, the plant richness was estimated by interpolation for each 100m elevation bands. We compared Area, MDE, AET, NPP (MODIS), and WED employing Generalized Linear Models, and use Akaike Information Criteria and deviance explained to find which model has the best explanatory power of the variation in plant richness along the elevation gradients on mountainous islands.

We found a remarkably consistent pattern where the most superior model in all cases was WED, although the precipitation term was significant. WED was far better than the energy productivity model based on AET or NPP. The spatial models' Area was significant but inferior, whereas and MDE failed to offer a good explanation to species richness. Although precipitation on ocean islands is not a good indicator of available liquid water the WED model is superior to explaining richness on the mountainous island compared to NPP and energy alone.

Geography and timeline of the initial domestication and spread of Persian walnuts: Early Bronze Age or Silk Road?

Susanne Renner[1,]

[1] Washington University

Persian walnut (Juglans regia) occurs naturally from Turkey to western China and was deliberately introduced in western Europe during Roman times. Its closest relative, the iron walnut, J. sigillata, is endemic in Southwest China and is also used for its nuts and wood. Competing scenarios exist for the initial domestication of walnuts, namely that they were domesticated in Western Asia and spread via the Silk Road, which connected Rome to China from about ~100 AD onwards, or that it was instead domesticated and spread already during Neolithic or Bronze times. We have used genome-wide SNPs from almost 100 individuals of J. regia from throughout Europe, Iran, Kazakhstan, Pakistan, and China as well as 26 J. sigillata to infer these species' divergence times, demographic histories, and possible gene introgression. We found that the two species diverged from each other by 0.86 Ma, with later unidirectional gene flow from J. regia into J. sigillata, including of the shell-thickness gene, with a thinner shell perhaps facilitating domestication of J. sigillata at ~20 generations ago. Our results support that J. regia cultivation originated in the Irano-Anatolian region and that population sizes of its western and eastern clades began decreasing dramatically by 80 generations ago, consistent with a serious bottleneck caused by human selection. Our genomic data match archeological finds from tombs and markets in Armenia and Kashmir that point to people gathering and trading walnuts by the Early Bronze Age.

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Concurrent Session 20 (Biodiversity Patterns & Maintenance)
June 5th 2:00 pm – 4:00 pm PT – Ballroom C

An integrated high-resolution mapping shows congruent biodiversity hotspots of Fagales and Pinales

Lisha Lyu[1],

[1] ETH Zurich

The documentation of biodiversity gradients through species range identification is crucial for macroecology and biogeography studies. However, especially for plants, species range maps remain scarce and often inaccurate. Here, we present a novel approach to map species ranges at a global scale, integrating polygon mapping and species distribution modelling (SDM). We develop a new polygon mapping algorithm by considering distances and nestedness of occurrences. In addition, we apply an SDM approach considering multiple modelling algorithms, complexity levels, and pseudoabsence selections to map the species at a high spatial resolution and intersect it with the generated polygons. We use this approach to construct range maps for all available (1,958 of 1,961) species of Fagales and Pinales. Using these maps, we construct high-resolution global species richness maps of these important plant clades, and document diversity hotspots for both clades in southern and southwestern China, eastern and western North America, and Borneo. We compare two representative genera, Quercus and Pinus, from the two orders with previously published coarser range maps, and find a good match. By efficiently producing high-resolution range maps, our mapping approach offers a new tool in the field of macroecology for studying global species distribution patterns and supporting ongoing conservation efforts.

Biogeographical patterns and dynamics emerging from low-level eco-evolutionary models

Juliano Sarmento Cabral[1],

[1] Julius-Maximilians-Universität of Würzburg

There has been an increasing effort towards developing predictive models for biodiversity to understand biogeographical patterns and biodiversity response to environmental change. This has led to a variety in mechanistic models that vary in their properties, processes implemented and in the ecological level of the agents. The simulation of lower ecological levels (e.g. individuals and populations) at biogegraphical scales has the ability to unify ecological and evolutionary first principles to generate emergent biogeographical patterns. However, such level of detail comes with a series of challenges, most notably computational feasibility. Still, constant improvement in computational power has already allowed important milestones in cross-scale mechanistic modelling. Here, I provide an overview on this recent development in biodiversity simulation models, focusing on applications of individual-based ecological and eco-evolutionary models across environmental gradients or long temporal extents. Presented models are able to depict plant metacommunity patterns across vertical, depth and elevation gradients as well as eco-evolutionary and diversification dynamics caused by natural or human-induced environmental change. These emergent patterns stress how the interplay of genetic and ecological traits, spatial processes and local interactions can cascade up to known biogeographical patterns. This is important, as causal relationships and ecological and evolutionary dynamics at large scales are difficult to address in real-world systems, but that can be tackled with mechanistic models. Popularizing the use of these models, many of which are publicly available, should be pursued for assessing biogeographical processes directly and for conservation assessments.

Global plant-frugivore trait matching is shaped by climate and biogeographic history

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Species interactions are influenced by the trait structure of local multi-trophic communities. However, it remains unclear whether mutualistic interactions in particular can drive trait patterns at the global scale, where climatic constraints and biogeographic processes gain importance. Here we evaluate global relationships between traits of frugivorous birds and palms (Arecaceae), and how these relationships are affected, directly or indirectly, by assemblage richness, climate and biogeographic history. We leverage a new and expanded gape size dataset for nearly all avian frugivores, and find a positive relationship between gape size and fruit size, that is, trait matching, which is influenced indirectly by palm richness and climate. We also uncover a latitudinal gradient in trait matching strength, which increases towards the tropics and varies among zoogeographic realms. Taken together, our results suggest trophic interactions have consistent influences on trait structure, but that abiotic, biogeographic and richness effects also play important, though sometimes indirect, roles in shaping the functional biogeography of mutualisms.

The drivers of global plant diversity

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Species richness varies massively around the world. Variation in rate of diversification (speciation minus extinction) is often hypothesized to explain this pattern, with alternative explanations based on time and ecological carrying capacities. Focusing on seed plants, the world's most important engineers of terrestrial ecosystems, we show that global patterns of species richness and diversification rate are entirely independent. Both species richness and diversification rates are driven by climate and environmental space (namely, soil diversity), but in contrasting ways. Species richness is highest in regions with many soil types, warm climate, and high cover of tropical rainforest, whereas diversification is highest in regions of low precipitation and in areas with many soil types (but independently from species richness). We conclude that species richness is driven by the antiquity of wet-tropical areas (confirming the "tropical conservatism hypothesis") and/or the high ecological carrying capacity of warm, wet and edaphically diverse environments. Meanwhile, our results suggest that diversification rates are driven by environmental variation allowing ecological speciation, in conjunction with selective pressures associated with the origin of ecologically demanding (dry-seasonal) environments during the Cenozoic. Importantly, by finding no relationship between temperature and diversification rate, or diversification rate and species richness, we reject the Metabolic Theory of Ecology, one of the dominant explanations for global gradients in species richness.

Integrating traits and networks: the geography of functional diversity in multitrophic assemblages

Gabriel Munoz[1,] W. Daniel Kissling[2,] Jean-Philippe Lessard,

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Trait-based ecology aims to reveal mechanisms underpinning biodiversity patterns. Biodiversity includes many species from distinct trophic levels and their interactions. However, multi-species approaches to integrate trait-based concepts across trophic levels remain scarce. In climatic gradients, the trait-based sorting of species from regional species pools can set boundaries to the presence and diversity of traits involved in species interactions. Using functional traits of interacting palms and mammalian frugivores in the Neotropics, we ask to what extent spatial and seasonal variability in temperature and precipitation shapes the functional composition of interacting palm and mammal frugivore assemblages. First, we created a trait-matching space scaling the variation of traits across trophic by a matrix of species interactions. We then built multitrophic assemblages at the 1×1 grid degree scale and computed the relationships between the representativeness of palms and mammals in multitrophic trait-matching space and synthetic variables of climatic variability. We found that climate shapes functionally asymmetric palm-frugivore assemblages, especially in the transition from tropical humid to tropical dry forests and with the associated increases in temperature seasonality. Specifically, the functional diversity of mammalian frugivores was less rich and more densely packed in tropical dry forests and savannas than that of palms. We show the extent to which climatic constraints on the functional composition of species assemblages may vary between trophic levels, resulting in functional asymmetries that can influence the structure of seed dispersal networks. Our work can help develop a more holistic outlook on the functional complexity of multitrophic assemblages along climatic gradients.

Mycorrhiza-mediated plant species interactions between forest layers in western USA

Corrina Thomsen[1,] Jason Pither[2,]

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Mycorrhizal fungi play an important role in plant recruitment, growth, and survival, and can result in positive or negative plant-soil feedbacks (PSFs) depending on the type of mycorrhiza formed: arbuscular mycorrhizal fungi (AMF) tend to produce negative PSF and ectomycorrhizal fungi (EMF) tend to produce a positive PSF (Bennett et al. 2017). This effect was initially demonstrated between conspecifics, but has since been shown to extend to heterospecific interactions among trees in natural forests (Johnson et al. 2018; Chen et al. 2019; Sasaki et al. 2019). However, whether such feedbacks extend to the understory remains unknown. For example, recruitment of understory herbs and shrubs could be either facilitated or suppressed depending on the mycorrhizal types of the neighbouring trees, which could result in non-random co-occurrence patterns among canopy and understory hosts of different mycorrhizal types. We explored this idea using the USDA's Forest Inventory Assessment (FIA) database. We first quantified the plot-scale relative abundance of AMF and EMF hosts within the understory and the canopy. We then used a null model analysis to determine whether encounter probabilities between like and unlike host types in canopy and understory layers were greater or less than what would be expected if hosts (with their respective mycorrhizal type) were randomly distributed across the landscape, considering potential environmental co-variation. We calculated standardized effect sizes, mapped these values across the western USA, and modeled their association with abiotic predictors.

Evidence of introgression, distributional shifts and selection in North Atlantic Asterias sea stars

Melina Giakoumis[1,] Dr. Michael Hickerson[2,]

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Sea stars (Asteroidea) have been shown to be keystone species in the intertidal community, creating incentive to understand their population dynamics. Asterias rubens and A. forbesi are a sister species pair of sea stars found across the North Atlantic with an area of co-occurrence along the northeast coast of North America. This study uses species distribution modeling, 48 low-coverage genomes, and RADseq from 178 individuals to reconstruct the demographic history, estimate timing of admixture, and uncover patterns of selection in this hybridizing sister species pair of Asterias seas stars. Species distribution models (SDMs) were built for each species using GBIF occurrence data and Bio-Oracle marine environmental layers, and subsequently projected into the areas confirmed as areas of active hybridization to better understand how environmental factors influence hybridization in Asterias. Analyses of population structure in the RADseq dataset are consistent with hypotheses that the two species are admixing in New England through Atlantic Canada. Given that Asteroids are understudied, ecologically important and threatened by climate change, habitat loss and sea star wasting (SSW) outbreaks, this study can be of importance to many stakeholders of the Northeast coastal region.

Virtual Talks

Virtual Session 01 (Island Biogeography)
June 3rd 1:15 pm – 2:45 pm

Climate controls plant life-form and functional trait patterns on the Canary Islands

Severin D. H. Irl[1], Dagmar Hanz[1], Pia Eibes,

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In the context of the emerging sub-discipline of functional island biogeography, applying the concepts of plant life-forms and PFTs to the flora of an oceanic archipelago might help us better understand the mechanism generating diversity on islands. Thereby, plant life-forms characterize key morphological strategies that enable large-scale comparisons of plant communities, while plant functional traits (PFTs) link to performance and fitness of individuals. Here, we use the diverse and endemic-rich flora of the Canary Islands as a model system to study how climate drives patterns of plant life-forms and PFTs. Plant life-forms, functional diversity as well as individual PFTs are strongly differentiated in climate and geographic space. Interestingly, endemic and non-endemic native plant species occupy similar functional trait space that often strongly reflect the main vegetation units of the islands. However, non-native species often express new trait combinations, thus expanding overall functional niche space. Interestingly, trait variation in endemic and non-endemic assemblages is driven by similar filtering mechanisms along environmental gradients, even despite their distinct evolutionary history. In large parts, the Canary Islands are quite arid. However, we find that positive co-occurrences (facilitation) decrease with increasing aridity, likely because of competition for water resources. We identify climate as an important driver of plant life-form patterns, PFTs and functional diversity. Thus, it is important to understand trait-climate relationships in order to assess how climate change will redistribute species, PFTs and life-forms on the Canary Islands.

Functionally equivalent? Birds of the world's islands say no

Ana Maria Bastidas Urrutia[1], Matt Biddick[2], Christian Hof,

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The equilibrium theory of island biogeography (ETIB) predicts that species richness results from the interplay of immigration and extinction, which in turn vary with island isolation and area. However, the rise of trait-based approaches has cast doubt on one of the primary assumptions of the ETIB: namely, functional equivalence. For example, we expect trophic and dispersal traits to influence the likelihood of colonization, regardless of how immigration rates vary with island isolation and area. To test this, we examined the dispersal and trophic trait spaces of 3278 terrestrial bird taxa inhabiting 2539 of the world's islands. Our results demonstrate that the non-endemic bird faunas of highly isolated islands exhibit greater dispersal ability than those of less isolated islands. We further found that large islands close to the equator housed bird faunas with more diverse feeding traits than did smaller islands at higher latitudes. Overall results suggest: (1) that the assumption of functional equivalence is overly simplistic and ignores important functional differences that affect colonization; and (2) that island area influences not only species richness per se, but also the trophic diversity of that richness.

Assembly of functional diversity of an oceanic island flora

Paola Barajas[1], Dylan Craven[2], Patrick Weigelt, Pierre Denelle[3], Rüdiger Otto[4], Sandra Díaz[5], Jonathan Price[6], José María Fernández-Palacios[7], Holger Kreft[3],

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Oceanic island floras are well-known for their morphological oddities and exhibit striking examples of trait evolution. These morphological shifts, whose peculiar biogeographical and evolutionary history have shaped island biota, are related to insularity. However, the pathways through which biogeography and evolution have shaped plant functional traits remain unclear. In this study, we sampled and described the functional trait space of an entire oceanic island (Tenerife) flora and related it to global trade-offs in ecological syndromes. We find that the island trait space is concentrated around a functional hotspot dominated by shrubs with a conservative life history strategy. By dividing the island flora into four species groups with distinct biogeographic ranges and species that diversified via cladogenesis our results reveal that long-distance dispersal, and prominently the complex interplay between speciation and inter-island dispersal at the archipelago level drive functional divergence and expand the island trait space. Conversely, speciation via cladogenesis has led to functional convergence, densely packing the island trait space around shrubbiness and succulence. Our approach is at the interface of ecology, biogeography and evolution and offers a step towards understanding, from a trait-based perspective, how dispersal and speciation jointly shaped the assembly of entire native flora.

Island Biogeography and Species' Pools

Jorge Soberón[1], Claudia Nunez Penichet[1],

[1] University of Kansas

In Island Biogeography, the pool of species from which an island sample is taken has been shown to be very important (in some cases, more important than distance or area) to determine the species number in the island. In this work we use two families of butterflies of the Greater Antilles to explore the role of pool composition and environmental similarity to predict the composition of species (not just the number) in different islands as a function of the similarity of climate between the pool, and the individual climatic preferences (“niches”) of the species. For a given island, we consider as its potential source pool all the species reported on the periphery of the mainland and all other islands on the archipelago, removing endemics to the island in question. From the literature, the list of butterfly species reported for the mainland and each island of the Greater Antilles archipelago was obtained. This list is regarded as the “observed” list. We downloaded the occurrences of those species from GBIF, cleaned the data, and using 3 WorldClim climatic variables we overlaid niche models to create hypothetical lists. We then compared the observed and the modeled lists a Jaccard Index. We conclude that a well-defined pool region and species-defined environmental filters allow, for a given island, excellent prediction of species present, but much less satisfactory prediction of species absent. We discuss this result in terms of factors determining species distributions.

Do subtropical montane cloud forests in Taiwan act as insular systems for woody species?

Yu-Pei Tseng[1,]

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Subtropical montane cloud forest (SMCF) distincts from from surrounding habitats due to frequent fog immersion. However, study focused on the insularity of fragmented montane cloud forests are lacking. Here, we aim to explore whether SMCF acts as an insular terrestrial habitat system by the theory of island biogeography. Theory predicts that the number of species at the true island is positively related to its area and negatively to its isolation. As a case study, we used SMCF distributed in Taiwan (1500–2500 m a.s.l.), which has been shown to be highly fragmented into isolated patches. We used the National Vegetation Database of Taiwan to calculate the species richness of each 20 m × 20 m vegetation plot and identified cloud forest specialists of woody species. The SMCF distribution map in Taiwan is used to estimate the area of SMCF around this plot (3 km radius buffer zones). We additionally assume a positive link between the richness of the entire island and the fixed area of a vegetation plot since the richness of each whole island is unavailable. Results showed a significant positive relationship between the species richness of cloud specialists in the plot and the proportion of the surrounding SMCF area around each plot, indicating that SMCF may act as an insular system. Surprisingly, the relationship became significantly negative if all species were considered, including habitat generalists. This may be due to smaller islands having a higher chance to gain species through dispersal from the neighboring areas since a larger proportion of other habitats surrounds them. In conclusion, our results indicate that the SMCF in Taiwan behaves as an insular system. This is important from a theoretical perspective (making SMCF a suitable system to study the effect of fragmentation) and also a practical perspective (e.g. for suggesting conservation strategies under foreseen increasing fragmentation). We plan to do more investigations on other island properties of SMCF.

Virtual Session 02 (Biodiversity Patterns & Maintenance/Species Distributions)
June 5th 3:30 pm – 5:30 pm

Tetrapod diversity hotspots in jeopardy under global change

Enrico Tordoni[1,] Aurèle Toussaint[1,] Meelis Pärtel, David Nogués-Bravo[2,] Spyros Theodoridis[3,] Carlos Pérez Carmona[1,]

[1] University of Tartu
[2] Center for Macroecology, Evolution and Climate
[3] Senckenberg Biodiversity and Climate Research Centre

Anthropogenic activities have eroded different facets of biodiversity, yet their impacts across biodiversity facets and the future exposure to global change is still poorly understood. Here, we synthesized taxonomic, functional and phylogenetic information (mu-Diversity) across more than 17,000 tetrapod species (terrestrial mammals, amphibians, reptiles and birds). We show that the global distribution of tetrapod mu-Diversity mainly results from water-energy dynamics and long-term climatic stability, but humans have influenced broad-scale diversity patterns since the agricultural revolution of the Neolithic. In addition, mu-Diversity hotspots (the 5% richest locations) mainly located in sub-Saharan tropical Africa and India will be vastly exposed to predicted mid-21st century climate and land use change. Specifically, in the less sustainable scenario, more than 50% of the cells in these highly diverse geographic areas will be exposed to severe land use change and reduction of primary vegetation, while regions characterized by lower mu-Diversity (e.g., temperate and boreal forests) will probably suffer an increase of mean annual temperature > 2°C. High levels of exposure have been observed also within the single taxonomic groups. Our findings show that human impacts are likely to extend in the near future, particularly in the parts of the world that host the highest diversity of tetrapods, which have been already influenced by past human activities and are disproportionally exposed to mid-21st global change. This calls for urgent actions to mitigate or at least delay the profound ecological disruptions facing natural ecosystems.

Sharks in the oceans of tomorrow – assessing shifts in habitat suitability under climate change

Catarina Pereira Santos[1,] Francisco O. Borges[1,] Catarina Frazão Santos, Rui Rosa[1,]

[1] MARE | Marine and Environmental Sciences Centre

One of the chief consequences of climate change is the worldwide redistribution of species in the pursue of physiologically and ecologically favorable conditions. While the scale and ecological consequences of these movements are difficult to ascertain, understanding the potential shifts in the distribution of key species should represent a priority, considering their potential influence over ecosystem dynamics. Sharks represent one of such groups, with their high trophic positions translating into an important role in the regulation of marine communities' structure and the potential to modulate the habitat use and behavior of other species. In this context, we implement species distribution models to assess global shifts in habitat suitability for several key shark species considering different climate change projection pathways (RCP2.6, 4.5, 6.0, and 8.5) and timeframes (middle and end of the century). Prediction models, relying on curated data from GBIF and environmental variables from Bio-ORACLE and MARSPEC, are implemented to create ensemble maps of habitat suitability and binomial presence-absence. Shifts in these metrics are then used to calculate net changes in habitat suitability and distribution, along with shifts in species overlap. As part of one of the most threatened groups of vertebrates, assessing how climate change may affect the potential distribution patterns of key shark species can further support efforts towards the preemptive design and implementation of conservation measures better tailored to the oceans of tomorrow.

Aridity emerges as the main factor driving variation in rodent diversity across 49 elevational gradients

Brooks Kohli[1], Reymond Miyajima[2], Marta Jarzyna,

[1] Morehead State University
[2] Ohio State University

Mountains harbor extraordinarily high biodiversity and have been essential to the development and testing of ecological and evolutionary theories on the mechanisms responsible for formation of biodiversity patterns. Patterns of species richness along elevation vary with geographic and environmental factors but evidence for similar variation in functional and phylogenetic diversity remains scarce. Here, we provide a comprehensive evaluation of elevational gradients in taxonomic, functional, and phylogenetic diversity of rodents—one of the most ecologically diverse groups of mammals—and test the effects of latitude and aridity on their variation. To accomplish this, we compiled occurrence and trait data for 374 species of rodents along 49 elevational gradients across 5 continents, of which nearly half have not been previously considered in large-scale comparative analyses. To assess how rodent diversity varies with elevation, we fitted a series of models that included either a linear or a quadratic relationship with elevation as well as their interactions with average latitude and aridity of each mountain system, while accounting for variation in study design and sampling effort. We uncover the critical importance of aridity as a determinant of variation in patterns of rodent functional and phylogenetic diversity along elevation. Specifically, we find that functional and phylogenetic richness and dispersion decline with elevation in wet mountain systems but increase with elevation in arid mountain systems. The deviation of patterns of functional and phylogenetic diversity from those of species richness is particularly pronounced in arid regions. Both wet-mountain lowlands and arid-mountain highlands harbor the most functionally and phylogenetically diverse rodent communities, suggesting that water availability is a strong environmental filter in structuring diversity of small mammals on mountain gradients.

Same process different patterns: pervasive effect of evolutionary time on species richness in freshwater fish orders

Ana Berenice Garcia-Andrade[1], Pablo Tedesco[2], Juan David Carvajal-Quintero, Fabricio Villalobos[3],

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Worldwide, tropical lands harbor the highest number of species, resulting in the ubiquitous latitudinal diversity gradient (LDG). However, exceptions to this pattern have been observed in some taxa perhaps given by the interaction between their evolutionary histories and the environmental factors related to their physiological and ecological requirements. Here, we applied a deconstructive approach to map the detailed species richness patterns of 16 orders of freshwater fishes (FWF) and disentangle their corresponding drivers using geographic ranges and a species-level phylogeny, comprising 12,556 fish species. To determine the drivers of the FWF species richness patterns, we evaluated seven hypotheses commonly posited to explain the diversity gradients of vertebrates and freshwater fishes into a structural equation modeling. Our results showed distinct diversity gradients across the FWF orders, including the traditional LDG, bimodal, as well as anti-tropical patterns. Despite these differences, patterns for the vast majority of FWF orders were mainly explained by the positive effect of evolutionary time, where species-rich regions are inhabited by older lineages compared to species-poor regions. Variation of current and past temperatures also had a considerable effect in several orders. Overall, the diversity gradient of each order has been shaped by a unique combination of factors, highlighting the importance of performing a combined evaluation of evolutionary, historical, and ecological factors to reach a comprehensive understanding on the causes driving the geographic distribution of diversity around the world.

Not all traits influence hummingbird diversification, but their evolutionary rates do

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Why some clades diversify dramatically faster than others remain largely unresolved. Here we investigate the relationship between hummingbird diversification and ecologically important morphological (body mass and bill length) and niche traits (temperature and precipitation position and breadth, and mid-elevation). We also explore the effects of trait conservatism and divergence on diversification by evaluating the relationship between the evolutionary rates of these traits and hummingbird diversification. Integrating diversification analyses, simulations, and GIS, we detected increased diversification rates among hummingbirds that are smaller, have shorter bills, live at higher elevations, and tolerate a wider range of temperatures. In contrast, we found no clear relationship between diversification and temperature position or precipitation niche traits, meaning that hummingbirds diversify at comparable rates irrespective of these climatic preferences. We also found that lineages with fast divergence in their morphological and niche traits rapidly accumulate species, suggesting that evolutionary divergence rather than conservatism explains the variation in hummingbird diversification. In sum, our results highlight that both the traits themselves and their capacity to evolve are associated with diversification in hummingbirds. However, not all traits relate to diversification. Our findings shed light on the complexity of mechanisms that ultimately yield current patterns of diversity.

Do animals influence the distribution of net primary productivity via mutualistic interactions with plants?

Lilian Sales[1], Jean-Philippe Lessard[2], Pedro Peres-Neto,

[1] Concordia University, Montreal
[2] Concordia University

Biodiversity affects several ecosystem functions and services, including carbon cycling and retention. While it is known that the efficiency of carbon capture by plant communities increases with species diversity, the diversity of plant-animal interactions in trophic networks could further influence this important ecosystem function. Moreover, while the diversity of plant-animal interactions is known to vary in space, how such variation affects the distribution of net primary productivity (NPP) remains undocumented. Here, we test if animal-plant mutualisms modulate the biodiversity-productivity relationships observed for plants. To test this, we quantify the effect of the potential diversity and the density of a mutualistic animal-plant interaction on regional estimates of NPP, while controlling for the underlying effect of the abiotic environment on plant and animal diversity. To do so, we combine field observations of fruit-frugivore interactions in a biodiversity hotspot – i.e. the Brazilian Atlantic forest, to spatial estimates of species potential distributions, in addition to satellite-based covariates. We also test for the spatial-scale dependency of this relationship, using spatially explicit structured equation models. Preliminary results show that the potential diversity and the density of interactions are positively correlated to NPP, especially at the local spatial scale. Overall, our results suggest that plant-animal mutualistic interactions scale up to affect the geography of ecosystem functioning, perhaps by facilitating plant dispersal, enhancing spatial complexity and/or preventing local extinctions. Our research supports the view that multiple dimensions of community complexity—including mutualistic interactions—drives ecosystem function in tropical systems. This is also the first evidence that animal-plant interactions imprint spatial signatures on the biogeography of zoogeochemical cycles via mechanisms other than consumption.

Camera trapping as an expanded view into global biodiversity and its change

Ruth Oliver[1], Fabiola Iannarilli[1], Walter Jetz,

[1] Yale University

The growing threats to global biodiversity demand understanding species status and trends in order to deploy efficient and effective conservation measures. Achieving this understanding requires detailed information on species occurrence and abundance across large geographic scales. Camera traps, combined with emerging computer vision models, provide a nearly autonomous method to survey species with higher spatiotemporal resolution and fewer resources than traditional survey techniques. Here, we demonstrate the potential of camera trapping to contribute to biodiversity science by assessing the "capturability" of terrestrial birds and mammals based on their traits to inform where and for what species camera trapping may be most important using publicly available data from the newly launched Wildlife Insights platform. We find that camera-trap data provides a large boost in data coverage in tropical regions of the world and therefore may assist in closing historical biodiversity gaps, especially in remote areas. Our findings demonstrate that mobilizing, sharing and aggregating camera-trap data collected by independent groups and organizations is set to be a key action in the upcoming years to provide a critical lense into our changing planet.

New species richness estimation methods help to clarify biogeographic patterns

John Alroy[1],

[1] Macquarie University

Although species richness is the most fundamental property of ecological systems, methods for estimating it remain unsettled. Face-value richness is often far too low. Therefore, much of the literature uses lower-bound estimators or statistics such as Hill numbers and Fisher's alpha. Lower-bound methods are severely biased whenever counts of individuals (= abundances) are very uneven, and abstract indices simply aren't about richness. Here I suggest that the best estimators should identified by showing which models of abundance distribution best fit the data. I propose two new, simple models that assume high unevenness. Estimators are derived mathematically from the models. When applied to a global data set of more than 3000 terrestrial animal and tree inventories, they outperform rivals such as the geometric series, Poisson log normal, and zero-sum multinomial in terms of fit to the data. Regression analysis of diversity estimates for these samples against climate and other environmental data show that the new methods improve model fit for a majority of study groups. The extrapolators ACE, Chao 1, and iNEXT do nothing to improve fit, whereas the Poisson log normal adds noise. Biogeographic effects are in general not very strong. Climate variables are good predictors for selected groups such as butterflies, mosquitoes, and trees, but most animal groups have idiosyncratic patterns. Anthropogenic effects are important for bats and large mammals, but rarely so for insects. The results suggest that within many groups, local diversity is not strongly controlled by simple factors that vary at the continental or global scale.

Virtual Session 03 (Anthropocene Biogeography)
June 4th 1:00 pm – 3:00 pm PT

Seafood biogeography: diversity, distribution and extinction risk of exploited marine bivalves

Shan Huang[1,] Stewart Edie[2,] Katie Collins, Nicholas Crouch[3,] Kaustuv Roy[4,] David Jablonski[3,]

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Bivalves underpin a global fishery supporting many businesses and households, and are under threat from overfishing, habitat destruction, and climate change like many other marine animals. We compiled a database of exploited shallow-marine bivalves and explored patterns of their biology and geographic distribution. Compared to the other ~5000 bivalve species, the 547 exploited species tend to have larger shells and live in shallower waters (controlling for phylogeny), presumably increasing their accessibility for harvest. Globally, the number of exploited species is highest in the tropical west Pacific where the overall bivalve species richness peaks, whereas the proportion of exploited species is highest along temperate western coastlines. We further assessed the intrinsic extinction risk of exploited species in relation to other bivalves using the Paleontological Extinction Risk In Lineages (PERIL) score (Collins et al 2018, Proc B), which is based on present-day geographic range size, realized thermal tolerance (from sea surface temperature), and lineage extinction history in the fossil record. Because exploited species tend to have wide geographic and temperature ranges, their overall intrinsic risk of extinction tends to be low, even when they belong to families with a history of higher extinction rates during the Cenozoic. Still, a number of exploited species are prone to extinction, and we find those to be distributed unevenly across the globe; for example, exploited species tend to be more extinction-prone due to their intrinsic biology than non-exploited species in several temperate and polar regions, including the polar Atlantic and the temperate northeastern Atlantic and northeastern Pacific. Collectively, our findings demonstrate how combining paleontological, biogeographic and ecological data can inform the management of global marine resources.

The Island Biogeography of Humans

Fabio Mologni[1,] Kevin Burns[1,]

[1] Victoria University of Wellington

For decades, biogeographers have sought a better understanding of how organisms are distributed among islands. However, the island biogeography of humans remains largely unknown. Here, we investigate how human population size varies among 486 islands at two spatial scales. At a global scale, we tested whether population size increases with island area, and declines with island elevation, nearest mainland and latitude, as is common in non-human species. At a regional scale, we test whether population sizes vary among islands within archipelagos according to the positioning of different cultural source pools. Results illustrate that on a global scale, humans increased in abundance with island area, and declined in abundance with island elevation, nearest mainland and latitude, similar to non-human species. At a regional scale, human populations often varied among islands within archipelagos relative to the location of different cultural source pools. Despite broad-scale similarities in the geographic distribution of human and non-human species among islands, results from this study indicate that the island biogeography of humans may also be influenced by archipelago-specific social, political and historical circumstances.

Evolutionary imbalance, colonial history, and the global biogeography of naturalized alien plants

Trevor Fristoe[1], Jonas Bleilevens[2], Nicole Kinlock, Qiang Yang[3], Zhijie Zhang[1], Mark van Kleunen[1],

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Geographic imbalances in the establishment of alien species have long been recognized. Darwin's explanation emphasized that natural selection only acts in response to selective pressures experienced by species across their evolutionary history. He suggested that geographic barriers divide Earth's biota into various evolutionary arenas, each with features that influence the intensity of selection. The outcome has been differences in competitive abilities among biogeographic regions and, by extension, species' capacities to establish in new areas when barriers are removed. This idea has been expanded as the evolutionary imbalance hypothesis (EIH), which proposes that invasion potential should be highest for species originating from 1) large areas able to support large populations and high genetic diversity, 2) regions of high biodiversity where lineages must compete with many others to persist, and 3) stable areas where selection is given ample time to optimize. To test the role of EIH mechanisms in shaping the biogeography of biological invasions, we compiled data on native and alien distributions for the global seed plant flora (n = 336,245, of which 14,461 are naturalized aliens). After accounting for environmental filtering and anthropogenic factors, we find support for the first two EIH mechanisms in driving plant naturalization success globally. Additionally, our results suggest important links between evolutionary imbalance, plant-human relationships, and the trajectory of human history. While association with humans is a key driver of success for plants in the Anthropocene, the ecology and evolutionary histories of plants have likewise shaped the fates of the human cultures that spread them.

Understanding the biogeographic patterns of Colombian edible plants.

Benedetta Gori[1], Mauricio Diazgranados[1], Tiziana Ulian, Henry Yesid Bernal[2],

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Despite being the second most biodiverse country in the world, Colombia is characterized by widespread poverty and food insecurity. According to recent analyses, between 40 and 50% of the Colombian population is affected by malnutrition. Considering the recent attention given to the economic and nutritional benefits of neglected and underutilized edible species (NUS), the present study unveils the diversity of Colombian edible plants as a potential resource for tackling these issues. By combining spatial and taxonomic analyses, this work answers three fundamental questions: What does Colombian edible plant diversity look like? What is the distribution of such diversity across different bioregions? And what are the taxonomic gaps in the current consumption and conservation of edible plants in Colombia? The cataloguing of edible plants of Colombia resulted in 3,864 species. However, only 198 of them are currently being commercialised in the country, revealing significant gaps in the exploitation of local resources and their potential contribution to the national food security. The biogeographic analysis of edible species distribution across Colombian ecoregions showed several diversity hotspots in the country, both in terms of species richness and conservation importance, such as the Andean region. Based on these results, along with further ethnobotanical exploration of the diverse regional culinary uses of the Colombian NUS, tailored prioritization and promotion initiatives may effectively be put in place in the country to diversity diets and support the creation of sustainable value chains.

Climate vulnerability of mountain biota revisited

Yi-Hsiu Chen[1,] I-Ching Chen[1,]

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Climate change has resulted in pervasive species redistribution to track thermal isotherm shifts across the planet, and such phenomenon is of particular concern in mountain ecosystems owning to the disproportional biodiversity. Mountaintop extirpation, range-shift gaps, and lowland biotic attrition, have been proposed as the major threats but empirical tests were sparse. Here we assessed the three mechanisms of climate vulnerability by re-analysis the changes in elevational extents of 734 terrestrial plant and animal species between historical (1849-1998) and contemporary times (2003-2017). Using Bayesian multivariate and univariate linear mixed models, we found that, mountaintop extirpation has been widely observed across taxonomic groups as species moving upwards; meanwhile, lowland and narrow-ranging species have significantly expanded their elevational extents upwards. As such, range-shift gaps may not be the pervasive threats; lowland biotic attrition is likely but also brought about strong community reorganization in the mountains. Importantly, the tropical species reduced the elevational range sizes more than their temperate counterpart. Species exhibited greater lower-limit contractions at lowlands in the tropics but at uplands in the temperate regions, which has seldom been reported before. Collectively, the thermal niches of temperate species increase in the lowland but decrease toward the uplands while thermal niches of tropical species being particularly diverse in the uplands. Our results modify the three mechanisms of vulnerability in that mountaintop extirpation was pervasive but likely threaten temperate species more; rage shift gaps may not be the major concern; the extend of reducing biodiversity at lowlands will be a balance between species' elevational expansion and contraction.

Diversity erosion of Neotropical mountain amphibian communities in the Anthropocene

Pablo Menéndez-Guerrero[1,] Sofía Carvajal-Endara[2,] Santiago Ron, George Vaca-Guerrero[3,] Mario H. Yánez-Muñoz[4,] Martín R. Bustamante[5,] David M. Green[6,] Jonathan Davies[7,]

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Human activities have caused alarming trends of biodiversity loss at a global scale. However, at regional and local scales, patterns of species responses to anthropogenic pressures are less clear. A better understanding of the contemporary re-shaping of communities and how these shifts might affect stability of ecosystems functioning is critical specially for some groups that are declining stronger such as amphibian and reptiles. Here we evaluated the response of seven anuran communities from the Neotropical highlands to human-caused environmental changes over the last 50 years. First, we found that most communities showed a substantial decrease in species richness, in average almost 52% of species were locally lost. Second, local species losses were strongly associated with species climatic niches and extreme warm temperature events. Third, we show that the reduction of local taxonomic diversity has resulted in larger phylogenetic and functional diversity reduction, which could hamper ecosystem functioning. Finally, we found that communities re-shaping has yielded an increase in functional homogenization across space. Our results suggest climate warming might have played an important role on amphibian montane diversity erosion and highlight the need to evaluate biodiversity shifts beyond species richness.

Main process driving functional diversity of urban avian assemblages varies among cities with different development levels

Yu Tsai-Chen[1], Chia Hsieh[2], Mao-Ning Tuanmu,

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Urbanization is a major threat to biodiversity, but how it reshapes biological assemblages is unclear because most studies only focus on a few cities and are highly biased to the cities in developed countries. Here we examined how niche differentiation and niche filtering shaped functional diversity of the avian assemblages in 106 cities worldwide, including 70 cities in developing countries. We integrated species occurrence records, expert species range maps, and information on foraging (i.e., diets and foraging strata) and breeding-related traits (i.e., nest site and structure) for 4,549 bird species breeding in the regions where those cities are located. We then examined (1) whether the urban assemblages showed functional over-dispersion (indicating strong niche differentiation) or functional clustering (indicating strong niche filtering) and (2) whether the functional richness pattern varied among traits or between cities in developed and developing countries. Our results showed that the urban assemblages generally showed functional over-dispersion, indicating strong niche differentiation among species, especially in the cities in developed countries. The strong niche differentiation was mainly shown in foraging-related traits, suggesting strong interspecific competition for food resources and foraging habitats. In contrast, niche filtering had strong effects on breeding-related traits in developing countries. This suggests that, as cities develop, the major process in shaping urban avian assemblages changes from strong filtering effects on breeding-related traits to strong differentiation in foraging niches. This mechanistic understanding of the assembly of urban bird assemblages provides essential information for urban planning to sustain urban biodiversity at different stages of city development.

Virtual Session 04 (Biodiversity Patterns & Maintenance/Species Distributions)
June 4th 4:00 pm – 5:15 pm PT

Inferring how regional features influence biogeographical diversification

Michael Landis[1], Ignacio Quintero[2], Martha Muñoz, Felipe Zapata[3], Michael Donoghue[4],

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Biological theory predicts that regional features of geography may influence the evolutionary tempo and mode for lineage dispersal, extinction, and speciation. Yet this fundamental link between regional features and evolutionary outcomes has not been fully integrated into phylogenetic models of biogeography. In this talk, we present a prototype for such a model that explicitly relates multiple types of regional features to biogeographical rates by building upon the GeoSSE framework. Our approach solves two major methodological challenges encountered when extending GeoSSE models to larger numbers of regions. First, we describe a hierarchical modeling framework to transform quantitative and categorical regional features into a parameterized geography that can ultimately be used to compute GeoSSE likelihoods, which facilitates biogeographical hypothesis testing while keeping the number of model parameters small. Second, we introduced a range split score to model how geographical barriers might impose a common mechanism for severing 'gene flow' edges between pairs of regions. To highlight the potential use of our new framework, we share results analyzing the historical biogeography of Anolis while allowing the sizes and distances among nine mainland and island regions to influence evolutionary rates.

Trait equilibria on islands

Julian Schrader[1], Holger Kreft[2], Ian J. Wright, Patrick Weigelt[3], Samuel C. Andrew[4], Mark Westoby[1],

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The Equilibrium Theory of Island Biogeography (ETIB) posits that species richness on islands is governed by a dynamic equilibrium of immigration and extinction. ETIB is an example of neutral ecology. It makes predictions about numbers of species, but not about their identity or functional traits. However, ecologists are interested in understanding the role of functional traits in the assembly of island biotas. Here we build on the principle that island communities are at an equilibrium of immigration and extinction and ask how these processes affect functional traits over time. We assembled a novel island-trait dataset from an archipelago in Western Australia and linked seed mass, plant height and leaf area of 156 species to their occurrences on 15 islands surveyed four times within four decades. Using community trait means and functional diversity we tested whether trait distributions remained at equilibrium over time and identified factors affecting trait equilibria on islands. We found strong evidence that ETIB can be extended to functional traits. Functional diversity and community trait means remained at equilibrium on islands similar to species richness irrespective of species turnover. Environmental characteristics had no strong effect in explaining trait turnover. Species most susceptible to turnover were on average smaller and had lower seed mass than persisting species. Integrating traits to island biogeography can greatly advance our understanding of immigration and extinction dynamics on islands.

Using Geographical Overlaps to Track Temporal Changes in Species Interactions and Community Coexistence Instability

Yin Zheng Lai[1,] Chih-Wei Tu[1,] Chih-hao Hsieh, Chia-Ying Ko[1,]

[1] National Taiwan University, Taiwan

Environmental and climatic changes are expected to redistribute species, altering the strengths of species interaction networks; however, long-term and large-scale evaluations remain elusive. One way to infer species interaction networks is by analyzing their geographical overlaps, which provides indices of species interdependence, such as mean spatial robustness (MSR), which represents the geographical impact of a species on other species, and mean spatial sensitivity (MSS), which indicates how a species is influenced by other species. Integrating MSR and MSS further allows us to assess community coexistence stability and structure, with a stronger negative relationship between MSR and MSS within a community at a given time suggesting a more stable community. Here, we assessed multidecadal changes in adult marine fish communities using bottom trawl datasets from 1982 to 2011 in the Eastern US Continental Shelf, North Sea, and Eastern Bering Sea. Consistent, significant long-term increasing temporal trends of MSR and MSS were found in all three large marine communities. MSR exhibited strong correlations with species' range sizes, especially in high-latitude communities, while MSS was strongly positively correlated with species' median proportion of overlap with interacting species. The relationships between MSR and MSS were generally negative, indicating stably coexisting fish communities. However, the negative relationships weakened over time, implying that the coexisting fish communities gradually became unstable. Our findings provide an assessment of changes in spatially geographical aspects of multiple species, for decades and at mid- to high latitudes, to allow the detection of global ecological changes in marine systems by alternative estimation of geographic overlaps of species interaction networks.

Areas of endemism of selected seed plant species in southwestern U.S.A.

Anna Saghatelyan[1,]

[1] McMurry University

Areas of endemism (AEs) are fundamental entities of analysis in biogeography and a key step for biogeographical regionalization. We attempt an endemicity analysis (EA) of 400 mostly desert species from SW U.S.A. Using digitized specimen data from IDigBio, we built a dataset with 81,851 point records for 400 species of angiosperms, Ephedra, and Juniperus, selected from the floras of southern TX, NM, AZ, S CA, and a few from adjacent floras in UT and SE USA. The dataset includes the species of 174 genera of 61 families of angiosperms and 2 genera of gymnosperms. We applied the method of endemicity analysis with NDM/VNDM to the raw distributional data under different grid sizes. The resultant sets of endemic species were combined to consensus areas (CAs) under various lowest endemicity scores (e). The overlapping CAs from different analyses are presented as AEs. We obtained 28 AEs, including the partially overlapping or nested ones. Many of the AEs form a western and an eastern group. Many of supporting the AEs endemic species are in the genera which are geographically split to the western and eastern clades.

SSE models for biogeography: prospects and challenges

Nicholas Matzke[1,] Wallis Bland[1,]

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Traditional model-based historical biogeography uses relatively simple probabilistic models to calculate the likelihood of observed geographic ranges at the tips of the tree. Popular models include DEC (Dispersal-Extirpation-Cladogenesis), DEC+J (adding jump dispersal/founder event speciation), and numerous modifications of these. These models have several limitations, such as ignoring lineage extinction, and only allowing paleogeography to change in discrete time-bins. Here we explore the potential of State-dependent Speciation/Extinction (SSE) models for including not only extinction, but various predictors of speciation, extinction, and dispersal processes. Major challenges result from the way the number of possible ranges/states explodes with the number of discrete areas in the analysis. We discuss methods to address the computational time for calculating the statistical likelihood, the explosion in the number of free parameters, and the potential mis-match between the observed ranges and the assumed state space.

Virtual Session 05 (Climate Change/Conservation Biogeography)
June 5th 1:00 pm – 2:45 pm

Marine biogeography is limited by available oxygen habitat

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The recent availability of oxygen data with depth for the world ocean enables calculation of how well oxygenated the ocean is and whether it is likely to significantly limit species' biogeography. Based on published assessments of the oxygen requirements of marine species we classified volumes of ocean as hypoxic if < 3 mg/l and oxic if > 6 mg/l. Between 3 to 6 mg/l oxygen levels can be fatal to marine species if temperatures are above 20 oC and may be stressful at lower temperatures depending on the species. Polar oceans are well oxygenated, with 95% of the Arctic and 41% of the Southern Ocean oxic, and 0% hypoxic. However, 21% and 33% of the Indian and Pacific Oceans are hypoxic, and only 16% and 14% oxic respectively. Of non-oceanic seas, their volumes are on average 33% hypoxic and 41% oxic. In contrast to these extremes, the Atlantic is 7% hypoxic and 29% oxic. Overall, 18% of the world ocean is hypoxic and only 26% oxic. Oxygen availability is thus already a major constraint on the distribution of marine species.

Highly heterogeneous data reveal the drivers of past occupancy changes in Central European insects

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Recent changes in climate and land-use are having substantial impacts on biological organization including population declines, range shifts, and changes in community composition. However, few studies have managed to compare these impacts among multiple taxa, particularly because of a lack of standardized time series data over long time periods. To make matters worse, existing datasets are typically of low resolution or poor coverage, thereby limiting what inferences can be made from their use. Here, we compare climate and land-use driven occupancy changes in butterflies, grasshoppers, and dragonflies using an extensive dataset of highly heterogeneous observation data collected in the central European region of Bavaria over a 40-year period. Using occupancy models, we show that the occupancies (the proportion of sites occupied by a species in each year) of cold-adapted species across taxa have already declined in past decades, while those of warm-adapted species have increased. In terrestrial taxa (i.e. butterflies and grasshoppers), habitat specialists also decrease, while in semi-aquatic dragonflies there was no difference between habitat generalists and specialists. Our findings illustrate not only why these taxa showed differing trends in the past, but also how we might mitigate the detrimental effects of human development on their diversity in the future.

Species distributions in the light of the Law of the Minimum

Sara Villén-Pérez[1,] Fernanda Alves-Martins[2,] Jennifer Morales-Barbero, David Palomino[3,] Ignacio Morales-Castilla[1,] Enrique Andivia[4,] Paulo De Marco[5,] Luis M. Carrascal[6,]

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Understanding the extant abundance patterns across climatic gradients can give useful insights into the potential impacts of global warming. Remarkably, the response of abundance to environmental gradients do not show line-shaped patterns as it would be expected. Instead, abundance-environmental relationships are characterized by polygonal-shaped point clouds scattered from zero to a maximum abundance limitation. We found that these patterns are widespread when analysing 187 trees and 114 birds in USA, 70 birds in peninsular Spain and 25 plants in Finland. Moreover, a literature review confirmed the generality of polygonal-shaped patterns across taxa and geographical regions, and called attention to the fact that they have been historically overlooked. We propose a novel theoretical framework to the study of limiting ecological relationships in biogeography based on Liebig's Law of the Minimum, which predicts that only one factor actually limits species' abundance at a specific point in time and space. We apply quantile regressions to assess the limitation imposed by climatic factors on the maximum abundance of species and use simulated species to demonstrate that this approach can be used to estimate the fundamental niche of species. Finally, we use quantile regression models to predict shifts on the maximum potential abundance of tree and bird species under future climate change scenarios. Our results highlight the interest of the Law of the Minimum in biogeography and theoretical ecology, and open new perspectives to studying limiting relationships in the context of global climate change.

Scale-dependence of climate change vulnerability of birds in the Western Hemisphere

Muyang Lu[1,] Walter Jetz[1,]

[1] Yale University

Climate change is threatening the life of millions of species on Earth. Evaluating the impact of climate change on species' survival is crucial for preserving biodiversity and mitigating the loss of ecosystem services. One of the biggest challenges in assessing species vulnerability to climate change is the issue of spatial scale. Specifically, a change of analysis grain might change the relative importance of climatic variables, and the rankings of species-level vulnerability, therefore impedes effective conservation planning. To assess the impact of grain size on climate change vulnerability analysis, we develop a new metric to partition the scale-dependence of total vulnerability into univariate components and an orientation component, and apply it to 1804 bird species in the Western Hemisphere using eBird data and CHELSA environmental layers. We find that temperature change is the primary source of total vulnerability and most subjected to the issue of scale-dependence. We further show that species-level scale-dependence of climate change vulnerability is mainly driven by the environmental autocorrelation, latitude and longitude of a species' range. In general, climate vulnerability of tropical species is more impacted by the choice of scale than temperate species, especially in the Andes, Amazonian forests and on Caribbean islands. Our results highlight the spatial variations and species-level drivers of the scale-dependence of climate change vulnerability, and call for more considerate sampling and modeling for highly sensitive species in the most affected regions.

Expanding Wallace species distribution modeling software to calculate biodiversity change indicators for conservation management and planning

Mary Blair[1], Matthew Aiello-Lammens[2], Samuel Chang, Peter Ersts[3], Peter Galante[3], Beth Gerstner[4], Valentina Grisales-Betancur[5], Ned Horning[3], Bethany Johnson[6], Jamie M. Kass[7], Cory Merow[8], Daniel López-Lozano[9], Erika Suarez-Valencia[9], Elkin Noguera-Urbano[9], Andrea Paz[10], Gonzalo E. Pinilla-Buitrago[11], Jorge Velásquez-Tibatá[12], Robert P. Anderson[10],

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Wallace is an open-source, instructive, and interactive R-based software application with a graphical user interface that supports reproducible, flexible, and expandable species distribution modeling (SDM) workflows. Our development team continually improves and advances Wallace in response to user-community feedback, such as new enhancements for metadata-reporting and to manage multiple species' models in a single session. Here, we describe an ongoing expansion of Wallace's functionalities for conservation biogeography applications. This expansion was co-developed between the Wallace team and the Colombia Biodiversity Observation Network (BON). We have developed two new R packages (maskRangeR and changeRangeR) and added their functionalities as new modules to a development version of Wallace. These packages enable quantifications of species' current geographic ranges by post-processing SDM outputs with remote sensing and other data. Specific quantifications include calculation of biodiversity change metrics such as range size, the upper bounds of IUCN's extent of occurrence and area of occupancy, percent suitable land cover, protected area representativeness, and projected trends under future scenarios. Users can also calculate estimates of potential species richness and endemism by combining SDM outputs across multiple species. Further, Wallace now interfaces with the existing Colombia BON tool BioModelos, which enables expert validation of occurrence records and species range estimates, to support conservation decision-making. The expansion of Wallace presented here was made possible by the modular design of the software, producing not only specific functionalities of Wallace for conservation biogeography, but also a proof of concept for the adaptability of the software to other subfields within biogeography.

Continental risk assessment for understudied taxa post catastrophic wildfire indicates severe impacts on the Australian bee fauna

James Dorey[1], Celina M Rebola[2], Olivia K Davies, Kit S Prendergast[3], Ben A Parslow[4], Katja Hogendoorn[5], Remko Leijs[4], Lucas R Hearn[2], Emrys J Leitch[6], Robert L O'Reilly[2], Jessica Marsh[7], John CZ Woinarski[8], Stefan Caddy-Retalic[9],

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The 2019-20 Australian Black Summer wildfires demonstrated that single events can have widespread and catastrophic impacts on biodiversity, causing a sudden and marked reduction in population size for many species. In such circumstances, there is a need for conservation managers to respond rapidly to implement priority remedial management actions for the most-affected species in order to help prevent extinctions. To date, priority responses have been biased towards high-profile taxa with substantial information bases. Here, we demonstrate that sufficient data are available to model the extinction risk for many less well-known species, which could inform much broader and more effective ecological disaster responses. Using an array of publicly-available collection and GIS datasets, combined with life-history data, we modelled the extinction risk from the 2019–20 catastrophic Australian wildfires for 553 Australian native bee species (33% of all described Australian bee taxa). We suggest that two species are now eligible for listing as Endangered and nine are eligible for listing as Vulnerable on the basis of fire overlap, intensity, frequency, and life-history traits: this tally far exceeds the three Australian bee species listed as threatened prior to the wildfire. The model demonstrates that it is possible to undertake a wide-scale assessment of wildfire impact on a poorly-understood group which can help to focus surveys and recovery efforts. We also provide the methods and the script required to make similar assessments for other taxa or in other countries.

Projecting the impacts of climate change on traditional food species for Arctic indigenous peoples

Zhixin Zhang[1], Jorge García Molinos[1],

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The Arctic is the region of the Earth exposed to more rapid and drastic anthropogenic climate change; a tendency expected to exacerbate in the future. Evidence demonstrates that these changes are threatening Arctic ecosystems and its biodiversity at unprecedented rates, yet no study have so far investigated what these changes may represent to the species of plants and animals that sustain the food systems Arctic peoples rely on. Here, we present the first pan-Arctic assessment of traditional food diversity in the Arctic spanning over 100 species of country food used by Arctic indigenous peoples encompassing marine, terrestrial and freshwater species of plants and animals. Using curated occurrence records and species-specific environmental predictors, we developed ensemble species distribution models (SDMs) for each food species and predicted potential impacts of climate change on their habitat suitability. Our preliminary results show that ensemble models had good predictive abilities for these indigenous food species. Model predictions suggest that climate change is likely to produce profound changes in habitat suitability and composition of many of these species even under future scenarios accounting for strong climate mitigation policies and sustainability-focused socioeconomic narratives.

Virtual Session 06 (Paleobiogeography & Historical Biogeography)
June 5th 3:30 pm – 5:15 pm PT

Pantropical plant dispersal out of Madagascar's forests

Jan Hackel[1,]

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Madagascar is renowned for its highly diverse and unique biota. Repeated immigration from other areas and diversification in isolation are thought to have generated its outstanding levels of endemism. We show that, conversely, a clade of c. 120 grass species has spread across the tropics from its Malagasy origin. Out of its ancestral forest understory habitat, the group has radiated into diverse niches and colonised areas as distant as the Neotropics. Timing as well as patterns of diversification on the island suggest a driving role of Miocene mountain uplift. This challenges the simplifying notion of Madagascar as a sink of immigrant lineages. Instead, our results suggest that its dynamic geological history also made it a source and laboratory of diversification, contributing species across the tropics. They also emphasise the highly threatened Malagasy forests as evolutionary cradles of diversity.

The Invasion Hierarchy: Quantifying long-term ecological and evolutionary consequences of invasions using the fossil record

Alycia Stigall[1,]

[1] Ohio University

Species invasions are pervasive in Earth's history, yet the ecological and evolutionary consequences vary greatly. Ancient invasion events can be organized in a hierarchy of increasing invasion intensity from ephemeral invasions to globally pervasive invasive regimes. Each level exhibits emergent properties exceeding the sum of interactions at lower levels. Hierarchy levels correspond to, but do not always exactly correlate with, geographic extent of invasion success. The ecological impacts of lower level impacts can be negligible or result in temporary community accommodation. Invasion events at moderate to high levels of the hierarchy permanently alter quantitative aspects of ecological communities, regional faunas, and global ecosystems. The prevalence of invasive species results in quantifiable evolutionary changes by fostering niche evolution, differential survival of ecologically generalized taxa, faunal homogenization, and suppressing speciation. These impacts can contribute to mass extinctions and biodiversity crises that alter the trajectory of ecological and evolutionary patterns of life. Examples are provided including ephemeral invasions in local strata, the regional Richmondian Invasion, the Great American Biotic Interchange, and the Late Devonian Biodiversity Crisis. The fossil record provides a long-term record of how invasion impacts may scale up through time, which can augment ecological studies of modern species invasions.

Climate- and extinction-driven ecological shifts in Onychomys grasshopper mice over 22,000 years at Hall's Cave, TX

Jonathan Keller[1], Seth Newsome[1], Kate Lyons, Felisa Smith[1]

[1] University of New Mexico

At Hall's Cave in Central Texas, the micromammal community persisted from the Pleistocene to the present with minor turnover despite considerable climate- and extinction-mediated ecosystem restructuring. To understand how these animals adapted in situ, we reconstructed ecological shifts in the superabundant micromammal fossil record over the past 22,000 years. We evaluated changes in microCT-derived 3D dental ecomorphology in relation to stable isotope analyses of bone collagen (δ13C and δ15N) and shifts in body size inferred from tooth row length. While prior work characterized mild responses by small herbivores, we report strong, climate- and extinction-driven body size, isotopic niche, and dental ecomorphology shifts in invertivorous Onychomys grasshopper mice. Consistent with Bergmann's rule, temperature best explained Onychomys body size variation over time. However, megafaunal extinction effects likely outweighed Onychomys' typical climate response immediately post-extinction because body size nearly doubled despite a warming climate. For these post-extinction Onychomys, body size positively correlated with elevated δ15N, suggesting increased carnivory for the larger individuals characteristic of this time. This hypothesis is corroborated by shifts in 3D dental ecomorphology. We document significantly greater occlusal convexity (OCC), a measure of tooth pointiness associated with faunivory, coincident with increased size and trophic level. This may reflect a temporary dietary shift from arthropods to other small mammals during a period of post-extinction resource abundance. Finally, post-extinction, hypercarnivorous Onychomys from Hall's Cave represent the largest modern or fossil specimens yet known. These results emphasize megafaunal extinction's transformative effects in light of modern anthropogenic extinctions in a warming world.

Magnetic reversals and their relationship with speciation and extinction events in bony fish

Mariana Ferrera[1], Francisco Correa-Sandoval[2], Alicia Abadía-Cardoso, Luis Malpica Cruz[1],

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The Earth's magnetic field generated by the activity and components of the nucleus acts as a magnetic compass in which two poles occurred. The process by which these magnetic poles reverse is known as a geomagnetic reversal (GM). In this period, registers showed that the Earth's atmosphere weakens, cosmic radiation and solar wind increases. The linkage between these conditions with mass extinction and speciation events is gaining bigger attention for some groups like mammals. In this study, we identified speciation events with GM events in bony fishes, particularly in Perciformes order. GM data was based on Ogg, 2021 data and divergency on Betancur et al. 2017 phylogeny. We also complement data with speciation and extinction events frame with Time Scale Creator 8.0 (TSC) program. From the complete phylogeny of bony fishes, 11% of nodes (43/383) were associated with a GM event considering ± 50,000 and 100,000 intervals after the GM event, so effects in differentiation could be at population level but not at species. For the 38 Perciformes families, 42% of nodes (144/33) were associated with a GM. Data from TSC showed 194 magnetic reversals in a 100 My time frame in which, 9.8% are associated with events of speciation and extinction. Changes in environmental condition as radiation and temperature, driven by multiple GM events that concur may lead to several adaptative strategies in bony fishes like habitat and food selection, also conditions on the different ocean basins, for example, diversity levels between Pacific and the Atlantic Ocean.

Plant migrations maintain climate fidelity in the face of dynamic climate change

Yue Wang [1]

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As climates change, a species can either track climate through migration or remain in place, experiencing climatic niche shifts. For future predictions of species responses, niche conservatism and climate tracking are typically assumed. However, this assumption is not confirmed, and the effects of migration on species niche dynamics are rarely studied. Here we examine the climate fidelity of 16 North American plant taxa over the past 18,000 years. Climate fidelity is defined as the ability of species to track climate change while maintaining niche conservatism. We reconstruct plants' niches using the Neotoma database, including 4,310 surface pollen samples and 13,240 fossil pollen samples from 337 sites. We calculate the niche overlaps of plants between six age bins in five transition periods: deglaciation (18-14 ka to 14-10 ka), early Holocene (14-10 ka to 10-6 ka), mid-Holocene (10-6 ka to 6-2 ka), late Holocene (6-2 ka to 2 ka – 1950 AD), and recent (2 ka – 1950 AD to after 1950 AD). We test the significance of niche conservatism/divergence in the transition periods using both niche equivalency and niche similarity tests. Most plants show high niche overlaps and niche conservatism during the past 18,000 years in North America under climate change, with the average niche overlap of 0.65 ± 0.13. Long-migrating taxa exhibit higher niche overlaps than short-migrating taxa during the periods that experience climate change. Our work implies that under the rapidly changing climate today and in the future, most plants need to disperse to track their preferred climates.

Uncovering the biogeographic history of the Neotropical Tillandsia subgenus Tillandsia

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Tillandsia is the most diverse genus in Bromeliaceae (Poales), with 754 Neotropical species distributed from Southern USA to Argentina and Chile. Tillandsias are known by their notable morphological and ecological adaptations to the epiphytic and saxicolous habitats, such as specialized roots for anchoring, reduced stems with leaves in compact rosettes, modified trichomes for water and nutrient uptake, and a Crassulacean Acid Metabolism. Recent phylogenetic studies have greatly improved our knowledge about the infrageneric classification of Tillandsia. Among the seven subgenera currently recognized for the genus, subgenus Tillandsia is the most diverse (270 spp.) and has its center of diversity in Mexico and Central America. Previous studies suggest that Bromeliaceae arose in the Guyana shield, later dispersing to the rest of the Neotropics. Tillandsia subgenus Tillandsia is thought to have dispersed from the Andes to Central and North America. However, a lack of phylogenetic resolution of previous studies, using conventional Sanger-sequenced markers, have hindered the reconstruction of this dispersal route in detail. The present work uses complete plastomes assembled from off-targeted Hyb-Seq and shallow sequencing data of a representative sampling of the subgenus Tillandsia and selected outgroups from the Tillandsioideae. We generated a phylogeny which we dated and used to perform ancestral-area reconstruction analyses. The additional phylogenetic resolution provided by the analysis of full plastomes allowed for a robust reconstruction of the biogeographic history of subgenus Tillandsia at a fine scale.

Regionalization and evolution of the West Palearctic ant fauna: tackling the Wallacean shortfall through integrative and collaborative approaches

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For centuries, biogeographers have proposed various regionalization systems mainly based on plant and vertebrate taxa, but classifications based on insects, which represent the overwhelming component of biodiversity, have been scant. One of the biggest barriers to such achievements is the lack of sufficient and reliable information about species distributions over a large geographic scale. Ants represent a good model organism for tackling biogeographic questions within insects due to their diversity and wide distributions across latitude and biomes but also thanks to recent taxonomic, phylogenetic and biodiversity informatics progresses. Through extensive collaboration with several European ant experts and the integration of a species distribution modelling approach, we're able to develop a novel database for over 750 ant species including their most comprehensive and finest spatial scale distribution information. This dataset allows testing how geological and climatic processes shape the biogeographical structure of West Palearctic ants and to integrate large-scale phylogeny to reveal their effects on the regional evolutionary history. Our results identified the higher uniqueness of ant fauna in Mediterranean regions in comparison to northern European continental regions, both taxonomically and phylogenetically. Geological processes and current climate explain the biogeographical structure of West Palearctic ants while climate change since the Last Glacial Maximum has strongly restricted ant distributions but also deeply eroded their evolutionary history. This study shows how collaborative and integrative approaches can help to improve the distribution knowledge for a diverse insect group and to recognize the rich historical signals detected in this regional fauna, highlighting the advantage of using insects as models in biogeography studies.

On-demand/Recorded Talks

On-demand talks (Anthropocene Biogeography)

A global assessment of human influence on niche shifts and risk predictions of bird invasions

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Estimating the strength of niche conservatism is key for predictions of invasion risk. Most studies consider only the climatic niche, but other factors, such as human disturbance, also shape niches. Whether occupation of human habitats in the alien range depends on the native tolerances of species remains unexplored. We assessed niche conservatism in climatic and human spaces for bird species showing different responses to humans in native ranges and evaluated whether considering anthropogenic niche variables affects invasion predictions. We assessed niche conservatism by comparing the native and alien distributions of 150 bird species. We differentiated “niche expansions” into environments new to the species and “niche unfilling”, whereby a species fills its native niche only in part. Global predictions of alien bird distribution were generated using species distribution models (SDMs). Climatic niche similarity was higher than random expectation in 56% of species, and human disturbance niche similarity in 43%. Only 34 and 15% of species had >10% of their alien distribution in climates or human conditions, respectively, different from those of native ranges. Climatic niche expansions mostly involved colonization of colder and less seasonal climates. Human niche expansions involved colonization of more disturbed environments by species not responding positively to human influence in native ranges. Climatic and human niche unfilling was more common than expansions and was lower for species introduced earlier and those responding positively to human influence. Models including human variables do equally well for all species. Alien birds tend to invade areas with similar climatic and human conditions to their native range, but niche unfilling and expansions occur and relate to species native tolerances to human-modified habitats and first introduction year. Incorporation of human-related variables in SDM results in more accurate predictions for all species.

Biogeography of human cultural diversity

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Our species inhabits virtually every part of the globe. Just like any other species, our ancestors adapted to different climates and environments. Therefore, our physical and biological features partly reflect past environmental conditions. Similar to human biological diversity, aspects of cultural diversity are affected by our environment as well. The spatial variation in human biocultural diversity is however seldomly studied by biogeographers. In this talk, we will explore how biogeographic approaches could contribute to a better understanding of how human biocultural diversity has been shaped by climate, topography and ecology. In turn, we will highlight how biogeographic studies of the human past might enhance our understanding of other species as well. We will present ongoing work on the environmental drivers of cultural diversity, and discuss some of the challenges and opportunities.

Fisheries enhance pressure on Mediterranean regions and pelagic species already impacted by climate forcing

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Marine species are widely threatened by anthropogenic activities, including fishing and human-induced climate change. However, geographically broad, spatially-explicit assessments on the simultaneous impact of major these threats are clearly lacking due to practical challenges of surveying vast geographical areas. Yet, these assessments are key for identifying highly and doubly impacted marine areas and species that should be prioritized for conservation through knowledge-based management strategies. Here, we analysed a 26-year time series of high-resolution remotely sensed environmental data to evaluate changes in optimal habitat availability (i.e. extent of marine areas encompassing optimal environmental conditions) for 15 species of small, medium and large pelagic fish inhabiting the Mediterranean Sea. We then developed a spatially-explicit risk assessment framework, in which fishing pressure and environmental data were combined, to identify areas at high risk of impact derived from human activities and shifting environmental conditions. Our analyses showed that, with few exceptions, most of the study species have gone through reductions of optimal habitat availability (i.e. worsening of environmental conditions), particularly in the western and central Mediterranean Sea. Worryingly, these environmentally impacted areas largely overlap fishing hotspots. Among fish species, small pelagics were the most impacted group, as they are the ones with a largest proportion of their distribution in highly, cumulative impacted areas. Redistributing fishing pressure and reducing it in highly impacted areas and for highly impacted species might become an achievable way for alleviating overall cumulative pressure on fish stocks, and contributing to the necessary shift to sustainable fisheries.

Biodiversity trends amidst intensification and abandonment of land around the world

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Human-driven land-use change is transforming the planet’s biodiversity. Concurrent with ongoing logging and conversion of natural habitat to agricultural and urban land, the abandonment of farmland and human settlements has nearly doubled in the last fifty years. While we know that land-use change impacts biodiversity, we lack understanding of the pace of biodiversity alterations and how the magnitude of resulting shifts varies across time, space and the tree of life. We tested the relationships between global change drivers and population and biodiversity change over time in over 6,000 population and community time-series from the BioTIME and Living Planet databases. We found that at sites around the world, forest loss accelerated both increases and decreases in biodiversity across plant and animal taxa, with lag effects extending up to half a century. In contrast, land abandonment in Europe favored specific groups of species, such as herbivorous mammals and carnivorous birds. Globally, land-use change occurs simultaneously with other global change drivers, such as climate change and pollution. We found that cumulative exposure to different global change drivers more often dampened versus amplified biodiversity change. Our findings suggest that global change drivers are producing a wide distribution of positive, negative and stable biodiversity trends. Future biodiversity will be shaped not only by human presence, but also by human disappearance. By incorporating the full land-use change spectrum in scenarios and projections, we can more accurately predict biodiversity change.

What predicts location and intensity of human impacts on global terrestrial ecosystems?

David Jenkins[1,]

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Human impacts on natural systems have been evaluated for ~50 years using the IPAT framework, where impact (I) is a function of population (P), affluence (A), and technology (T). Varied results have accrued, but problems remain: I is almost always CO2 emissions; anthropocentric IPAT does not include ecological predictors; vastly different countries are often treated as replicates; and alternative hypotheses beyond I as a function of P and A are rarely evaluated. Here we model I as human appropriation of net primary production (HANPP); like IPAT predictors, it is globally mapped as a 5 arc-min grid (~10 x 10 km at the equator). We also: include ecological predictors (plant biomass and climate); use greenhouse gas emissions to indicate T; evaluate countries (N = 168) and anthropogenic biomes (anthromes; N = 19) as study units; and compare all models. The most plausible models predict location and amount of HANPP well (R2 = 0.91 and 0.63, respectively) and use all IPAT terms, ecological variables, countries and anthromes. Ecological predictors and population are most important in both cases, consistent with a general, ecological predator-prey relationship modified by socio-ecological conditions. Results here demonstrate that human impacts on lands – with all those portend for biodiversity and climate change – depend on both socioeconomic and ecological predictors, and hence reflect determinants not usually considered in the classic IPAT framework. Understanding these relationships is a necessary step toward mitigating human impacts on land.

On-demand talks (Biodiversity Patterns & Maintenance)

A consistent hump-shaped pattern of diversity-elevation relationship observed at different grain scales: a case study using woody species in Taiwan

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Although the diversity pattern along elevation can have several different shapes, the hump-shaped one with a decrease in diversity toward both low and high elevation is surprisingly the most common. Studies describing this pattern and testing its explanations have usually fixed scale in terms of extent (the area across which the pattern is being described) and grain (the area of individual assemblage). Here we ask whether the hump-shaped pattern will consistently appear when using assemblage data on different grain sizes, from small (400 m2), intermediate (10,000 m2) to a large one (more than 3600 km2). We used non-cultivated native tree and shrub species occurrences across non-tropical parts of Taiwan island, East Asia. Three datasets were compiled: 1) small grain size, 1200 vegetation plots 400 m2 each, with numbers of individuals for each woody species; 2) intermediate grain size, 17 forest dynamics plots of at least 1 ha (10,000 m2) each, with numbers of individuals for each woody species, and 3) large grain size, ca 30,000 herbarium specimens' occurrences separated into fixed-width elevation bands. We standardized assemblages within the same dataset (vegetation plot, dynamics plot, elevation band) to the same level of completeness, calculated diversity of the three main orders ($q = 0$, 1 and 2), and regressed it against elevation. Results showed that while keeping the extent fixed (island of Taiwan), a hump-shaped diversity pattern with the highest diversity at around 1000 m a.s.l. can be consistently observed at all grain sizes. We argue that whatever is the mechanism responsible for the pattern, its effect propagates across the grain scales, from large to small or vice versa.

A critical review of current species distribution model methods to guide greater reproducibility and accessibility

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Species distribution models (SDMs) have increased >300% in the last two decades alone, with >11,000 published between 2017-2020. Despite their popularity, SDMs represent a relatively young and growing discipline with problems of reproducibility and methodological transparency from the numerous species-specific scenarios and choices in SDM details. Recent efforts have addressed reporting guidelines per SDM study regarding source information, response variables, predictor variables, model building, and model evaluation. However, these efforts lacked methodological guidance. Furthermore, SDM model choices and their consequences have yet to be summarized into an accessible baseline of strategies. We reviewed 200 randomly selected SDM articles from 2017-2020 (50/year) based on 27 methodological SDM decisions to: 1) assess the current state of the science; 2) quantify and summarize recent methods; and 3) highlight potential errors based on recent methods across all SDMs. Overall, SDMs provided wide-ranging results with excessive variations in sample sizes (e.g., 7-1 million presence data, 1-80 predictors, and 23 unique algorithms) and infrequent and/or inconsistent applications of common model strategies (e.g., only 41% mitigated for spatial autocorrelation and only 33% analyzed multiple algorithms). There were biases towards some model choices that often lacked justification (e.g., MaxEnt algorithm used 74% of the time but justified only 22%). The resulting methods baseline from our SDM review should be further developed into a robust framework that answers the what, why, and how of reproducible, accessible, and ecologically relevant SDMs. We also recommend future research topics to better address gaps in SDM methodology.

A decline in diversity explains the low species richness of dipodoid rodents

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Species richness across the tree of life is uneven, with clades harboring much more species than others. In particular, understanding why some clades are species-poor compared to their sister clades is a long-standing question in evolutionary biology. Here, we study the diversification of Dipodoidea (53 species), a clade of rodents mostly distributed in the deserts of the Northern Hemisphere, which is the sister lineage of Muroidea (1500+ species). Phylogenetic birth-death models suggest the dipodoid diversity dynamics experienced a two-phase pattern: an early radiation from the mid-Eocene to early Miocene, followed by a declining phase from the early Miocene to present. A decrease in species diversity was also detected with fossils confirming that the clade has been declining since 25 Ma. We hypothesize that the dipodoid decline was related to environmental variations, which may have shrunk the geographical extent of their ancestral habitats through time. This hypothesis is supported by diversification analyses showing that temperature variations and speciation rates are positively correlated, indicating lower diversification during cooler climate. In contrast, we found that the sequential evolution of locomotion (from quadrupedal, saltatorial to bipedal) did not lead to higher diversification, as these morphological adaptations were often proposed as key innovations to desert environment.

A tale of two trees: Contrasting growth patterns at opposing range margins for two North American pine species.

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Species range margins may not represent ideal, or optimized, conditions for survival or growth. Further, with ongoing climate change, conditions at a range margin may be becoming more or less suitable for a species depending on position (i.e., north vs. south). To study how species are dealing with climate change at their range margins, we assessed annual growth trends in two long-lived tree species, Pinus banksiana (jack pine) and Pinus rigida (pitch pine) which have opposing latitudinal range margins where they co-occur at the Altona Flat Rock pine barrens in northern New York State. We hypothesized that with warming climate, environmental conditions may be becoming too warm for jack pine at its southern limit, while warming temperatures may be facilitating pitch pine growth at its northern margin. Increment cores taken from 75 jack pine, and 75 pitch pine were measured and crossdated using standard dendrochronological techniques. Results show that jack pine growth has remained relatively constant over the past century, while pitch pine growth has been steadily increasing since the 1960's. Jack Pine showed a low correlation with both temperature and precipitation suggesting climate is not a determining factor for growth at this site. Pitch Pine showed a stronger correlation to climate, with fall temperature and annual precipitation having the largest influence on growth. This study will increase our knowledge of how tree species are responding to ongoing climate change, and inform management decisions in regard to species vulnerability and forest biodiversity along range margins.

Assessing the relation between fine-scale geodiversity and species richness in mountain heaths and tundra

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There is an urgent need to find complementary measures to tackle the current biodiversity loss. Geodiversity could be one such approach as its positive relationship with biodiversity is well established. There is, however, a lack of research that use empirical geodiversity data in explaining biodiversity patterns at finer scales. In this study, we investigated the connection between the fine-scale geodiversity and species richness of vascular plants, bryophytes and lichens in boreal mountain heaths and subarctic tundra environments located in Northern Europe. Using a recently developed field method to map fine-scale geodiversity, we assessed georichness, i.e. the occurrence of different geofeatures (geological, geomorphological, and hydrological features), within a radius of five meters from the inventoried vegetation plots (N=181). Our preliminary results show that the relationship between geodiversity and species richness is significant, but depends on context, area, and species group. The relationship was strongest in the subarctic tundra where georichness correlated positively with the richness of all species groups. Our results suggest that the inclusion of fine-scale geodiversity estimates may improve understanding and predictions of species richness patterns in the tundra. This further encourages to examine the geodiversity-biodiversity relationship at finer scales and could help to develop methods to fight against biodiversity loss in sensitive northern environments.

Asynchrony outweighs population stability and diversity in stabilizing terrestrial communities

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Because stability determines community responses to environmental change, the hypothesis that diversity stabilizes communities is central to biodiversity maintenance and conservation management. However, empirical studies are equivocal with respect to the stabilizing effects of diversity and typically suffer from limited spatial scale and taxonomic coverage. We employ data from 6,106 time series globally (BioTIME) for four terrestrial taxonomic groups to establish general patterns for how biotic and abiotic variables interact and regulate stability of terrestrial communities. We found that synchrony consistently showed the highest relative importance in reducing community stability. While diverse communities are often more synchronous, this effect could be obscured by other drivers altering synchrony. Our results highlight the importance of synchrony in generating broad-scale community stability patterns, suggesting that environmental drivers disrupting synchrony may have large ecological impacts compared to the effect of diversity itself.

Chorotypes and diversity patterns of human infectious diseases in Brazil

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Herein we described the spatial patterns of multiple human infectious diseases in Brazil. We obtained the geographic distribution of diseases from the SINAN database, a Brazilian information system of mandatory notifications, for the municipalities (2007-2020). We assumed the following operational taxonomic units (n = 13): Bordetella pertussis, Whooping Cough; Clostridium spp., Botulism; Corynebacterium diphtheriae, Diphtheria; Flavivirus sp.1, Dengue; Flavivirus sp.2, Yellow Fever; Hantavirus, Hantaviruses; HAV, Hepatitis A; Leishmania spp., Leishmaniasis, Rickettsia rickettsia, Rocky Mountain Spotted Fever; Salmonella Typhi, Typhoid Fever; Schistosoma spp., Schistosomiasis; Tripanossoma cruzi, Chagas Disease and Vibrio cholerae, Cholera. Chorotypes, groups of coincident distribution areas, were obtained by a fuzzy logic algorithm. Alpha diversity was spatially described for political and biome units, and values were statistically compared to bioclimatic variables (WorldClim) and to ‘human footprint’ (Earthdata). We obtained four chorotypes: C1 (S and SE); C2 (N and NE); C3 (Cholera); C4 (whole range). Higher values of alpha diversity occurred at SE region of Brazil, in the Atlantic Forest biome and part of Cerrado (C1 + C4), and lower values in the N region, Amazonia. Global analysis (OLS) showed no significant relation between diversity pattern and variables. Local analysis (GWR) showed a strong and negative relation with Bio5 (Max Temperature of Warmest Month) in central Brazil and a strong and positive relation in central Amazonia. This is the first study on multiple human infectious diseases in Brazil. The description of the geographic structure will help us understand the assembly and the dynamics of emergent patterns.

Divergent biogeographic trajectories: The need to integrate genetic, pollen, and occurrence data for robust inference

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Reconstructions of species’ biogeographic histories commonly rely on disparate types of data and analyses: occurrence data modeled with species distribution models (SDMs), pollen relative abundance models informed by fossil pollen records, and genetic data analyzed with scenario-based models. Using green ash (Fraxinus pennsylvanica) in eastern North America as a case study, we analyze the consistency of inference between the three data types and the most commonly used method associated with each data type. Genetic data were modeled using Approximate Bayesian Computation and a spatially-explicit forward-time demographic model coupled with coalescent simulations. Relative abundance of tree pollen, including ash pollen, across space and through time was estimated using a Bayesian hierarchical spatio-temporal model, and climatically suitable habitat was modeled using SDMs with multiple algorithms. We integrated pollen data and SDMs with genomic data through Approximate Bayesian Computation. We then compare estimates of the pace of range movement (biotic velocity) through time from these three datasets and corresponding approaches. Overall, biotic velocities estimated using fossil pollen were higher than those using either genomic data or SDMs, but biotic velocities rarely exceeded 150 meters/year for any method. We also found a temporal mismatch between methods detecting peaks in biotic velocity. Both integrated ABC-SDM and ABC-pollen analyses reduced the variance of biotic velocity estimates. Our results demonstrate the need for quantitative comparison of the results from different biogeographic reconstruction methods, and suggest that integration of these multiple lines of evidence in a unified framework may result in improved biogeographic inference.

East or West, nests are best: dramatically different dragonfly habitats have surprisingly similar nymphal nestedness

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Nested species distributions in patchy habitats are sometimes observed locally, but direct comparisons of analogous communities in distinct ecosystems are uncommon despite presenting excellent opportunities to test the generality of biogeographic theories. To determine if larval odonate (dragonfly and damselfly) communities in dissimilar ecosystems can exhibit similar degrees of nestedness, we collected exuviae (larval exoskeletons) from 27 saline sinkholes in New Mexico (U.S.A.) and 21 freshwater ponds in Rhode Island (U.S.A), then used NeD (Nestedness for Dummies, Strona & Fattorini 2014) to conduct our analyses. The analyses revealed that both systems support significantly nested larval communities and regression analyses suggested that species richness tends to increase with increasing pond size. However, the environmental mechanisms driving the observed nestedness appear to differ between the two ecosystem types. Species-specific larval water salinity tolerances and predation pressure or competition from larger larval odonates are important in the desert sinkholes, but in the temperate pond system the degree of surrounding urbanization appears to drive local species distributions. This study illustrates that superficially similar species richness patterns in analogous taxonomic communities may arise from idiosyncratic biotic and abiotic factors acting at the local scale, so a detailed scrutiny of these factors may provide more insight than would generalizations based solely on the varying numbers of species distributed throughout patchy systems.

Ecological processes and the biogeography of speciation among endemic lizards of Madagascar

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Although the genetic patterns produced as a result of population isolation during speciation are well documented, the biogeographic and ecological processes that trigger speciation remain poorly understood. Alternative hypotheses for the biogeography and ecology of speciation include geographic isolation combined with niche conservation (soft allopatry) or niche divergence along an environmental gradient (ecological speciation). In this talk we combine species' distributions, environmental data and two null models to test these alternative hypotheses among 28 sister pairs of micro-endemic lizards in Madagascar. Our results demonstrate bimodal peaks along a niche divergence-conservation spectrum, with at least 25 out of 28 sister pairs exhibiting either niche conservation or divergence, and the remaining pairs showing weak ecological signals. These findings provide strong evidence of a role for ecological processes driving speciation, rather than the classic expectation of speciation through geographic isolation, but demonstrate that the link between biogeography and ecology is complex and requires further analysis of a broader taxonomic sample to fully resolve.

Estimating and conserving patterns of grasshopper diversity and richness in Western Australia

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Conservation planning requires an understanding of how biodiversity is distributed over the landscape. Identifying every species, particularly in lesser-known taxa such as insects, occurring in a region and understanding their biology and ecology can be time consuming and may not be cost effective. Recent studies of global insect decline suggest that major issues of insect conservation are emerging (i.e., insect Armageddon). Here we investigated the richness and diversity pattern of grasshoppers in Western Australia (WA) to assess the representativeness of the protected area network for conservation of this invertebrate group. We collected grasshopper occurrence records from field notebooks based on historical surveys spanning 1942 to 1989 throughout WA. We developed generalized dissimilarity models (GDM) to identify species composition turnover and modelled species richness with regression analyses. The fitted GDM model explained up to 41.4% of the deviance in the compositional species turnover. Species composition derived from transformed environmental predictors suggested at least four distinct grasshopper communities are distributed over the north, north-west, arid-interior, and south-west of WA, respectively. Based on lognormal models, higher species richness was predicted at the northern half of WA and the lowest in south-west. Although high species richness was predicted in the Pilbara region the area remains underrepresented in the national reserve system i.e., <10% areas are protected. We found that endemic grasshopper species are distributed throughout the WA with only 26.8% are protected in national reserve system. Our analyses highlight areas requiring more targeted research and conservation efforts and demonstrate that field notebooks can be a valuable resource for planning invertebrate conservation.

Evidence of strong increase in demersal fish biodiversity across the Norwegian and Barents Seas in the last 31 years

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Climate warming constitutes one of the main faces of climate change and is having a direct impact on species, communities and ecosystems. In the Arctic Ocean, the effect of increased temperatures leads to northern limit expansions of boreal species, which are increasingly found at northern latitudes than in previous decades. However, the extent of these climate-induced changes in species composition remains little studied. Using flexible machine learning methods (Boosted Regression Tree models), we analysed the fish component of an open-access database composed of several thousand research bottom trawling surveys from the last 31 years in the Norwegian and Barents Sea and found a robust and continuous increase in species richness (alpha diversity) over our study period. Other measures of biodiversity also changed over time, with an increase in gamma diversity and a slight variation of beta diversity. We explored relationships between the changes in alpha diversity with environmental co-variates and results suggest that temperature is the main driver of the increase in species richness across time. Our results confirm previous findings and substantially increase the evidence of a redistribution of biodiversity towards higher latitudes.

Geographic patterns in artiodactyl richness and ecological diversity

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Understanding geographic patterns of species richness improves with information about ecological functions. We analyzed geographic patterns of ecological diversity in the most species-rich group of large terrestrial mammals today, the Artiodactyla, using occurrence data for 161 species from a global dataset of 328 faunal localities. We investigated the relationship between species richness and ecological diversity across continents, the climatic and physiographic distribution of species with different dietary habits, and environmental predictors of species richness and ecological diversity. Species were assigned to one of seven feeding categories and one of six body-size classes. Species richness patterns vary among continents and among ecological categories. The highest species richness of artiodactyls occurs in Africa and is achieved by accommodation of more species in all ecological categories. Excluding African localities, species richness exhibits no latitudinal variation, whereas Shannon index values for diet and size exhibit a latitudinal diversity gradient, reflecting more even distribution of species among ecological categories in low latitudes. Some regions of the world with similar richness levels have different evenness patterns in ecological diversity, suggesting different underlying processes of community assembly. We also analyzed diversity patterns in relation to climatic and topographic variables. Dietary extremes (frugivores and obligate grazers) show the most restricted climatic envelopes, reflecting their narrow dietary niche breadths. Seasonal extremes of temperature and precipitation are the most useful environmental predictors of species richness. Our findings highlight the importance of understanding the ecological dimensions of observed diversity patterns in relation to functional traits and the environment.

Identifying the drivers of spatial taxonomic and functional beta-diversity of British breeding birds

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Spatial variation in community composition may be driven by a variety of processes, including environmental filtering and dispersal limitation. While work has been conducted on the relative importance of these processes on various taxa and at varying resolutions, tests using high-resolution empirical data across large spatial extents are sparse. Here, we use a dataset on the presence/absence of breeding bird species collected at the 10 km x 10 km scale across the whole of Britain. Pairwise spatial taxonomic and functional beta diversity, and the constituent components of each (turnover and nestedness/richness loss or gain), were calculated alongside two other measures of functional change (mean nearest taxon distance and mean pairwise distance). Predictor variables included climate and land use measures, as well as a measure of elevation, human influence, and habitat diversity. Generalized dissimilarity modeling was used
to analyze the contribution of each predictor variable to variation in the different beta diversity metrics. Overall, we found that there was a moderate and unique proportion of the variance explained by geographical distance per se, which could highlight the role of dispersal limitation in community dissimilarity. Climate, land use, and human influence all also contributed to the observed patterns, but a large proportion of the explained variance in beta diversity was shared between these variables and geographical distance. However, both taxonomic nestedness and functional nestedness were uniquely predicted by a combination of land use, human influence, elevation, and climate variables, indicating a key role for environmental filtering. These findings may have important conservation

Insights into biogeographical patterns in the Indo-Australian Archipelago from beta-diversity of bird assemblages

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The uniqueness of flora and fauna in the Indo-Australian Archipelago has attracted biogeographers since the 1800s and lead to the demarcation of the IAA into three regions where biotic turnover is particularly marked: Sunda, Sahul, and Wallacea in between. Despite the amount of research that has been done in the region, there are still several areas of contention and the need to use more consistent quantitative assessment of. Using calculated beta diversity indices, we investigate the consistency of regionalization patterns between taxonomic levels in birds and investigate potential correlates (geographic proximity, sea barriers, land area, environmental distance) to turnover. We consistently found patterns of communities with high similarity between areas within a shared continental shelf. Furthermore, we found the avian biota of Java to ally with Sunda and Maluku with Wallacea/Sahul, whilst in contrast with past studies on plant communities, Melanesian birds are firmly allied with Australia rather than Asia. The islands of Wallacea that lie between Sunda and Sahul are less consistently grouped with either continental shelf, suggesting a complete lack of coherence to Wallacea. Additionally, analyses using multiple regression models suggest geographic distance, sea barriers, and land area as a significant correlate to turnover but not environmental distance. Overall, our results from various analyses agree that isolation – through space and time, has a stronger influence on turnover than dispersal capacity or environmental distance. Further analyses including using ancestral state reconstructions will shed further light on the processes that may drive these biogeographical turnovers and differentiation across the IAA.

Islands in the mist: a systematic review of coastal lomas ecosystems

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The Peruvian-Chilean desert, located on the western slopes of the Andes, is one of the driest on the planet yet it contains one of the most unique vegetation formations: coastal Lomas. Coastal Lomas are fog oases found from northern Peru (8°S) to central Chile (30° S), where water supply year-round is largely dependent on influxes from oceanic clouds and fog. We performed a systematic review of the literature related to the coastal Lomas, which revealed numerous shortfalls in the knowledge of biodiversity, ecosystem functioning and services, and conservation status. Our results show that there is no consensus on the period when coastal Lomas originated. The spatial and temporal dynamics of the marine fog that maintains the vegetation of coastal Lomas are not well understood. Yet, there is evidence that variation in the influx of marine fog is associated with the El Niño Southern Oscillation (ENSO), which increases the moisture supply, allow the persistence of Lomas vegetation. The taxonomic diversity of Lomas vegetation, and fog variability has been extensively studied at local scales, mainly in Peru, yet larger scale diversity patterns have yet to be explored, and how ecosystem services are shaped by ecosystem functions and the extent to which they are dependent on biodiversity is uncertain. Conservation efforts have been limited to establishing conservation areas, but their efficiency in managing and protection, including interactions between the atmosphere, soil, and plants, has not been evaluated. Our systematic review identifies key questions for our current understanding of coastal Lomas.

Macroecological patterns of biotic interactions and their consequences in prey communities: Insights from elevational gradients in the equatorial Andes

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Studies looking at macroecological gradients of predation have proposed a decrease in the ecological importance of the interaction at higher latitudes and elevations. These, however, have largely based their conclusions on predation rates which may not have a 1:1 correspondence with the ecological impact of predation. Instead, we studied the ecological impact of predation as reflected by the anti-predator investment in prey, particularly treehoppers, a group of insects relying on behavioral strategies involving maternal care and ant-mutualists to counteract predation. We did so along 4000-meter elevational gradients on western and eastern slopes of the equatorial Andes, where we studied the degree and type of anti-predator investment of treehopper communities in relation to predation rates and the activity of ants either as mutualist partner or sources of predation. We show treehopper anti-predator investment decreases only above 2500 m despite the steep decrease in predation rates. This pattern may arise as the negative effects of temperature and productivity on predators and prey cancel out up to the highest elevations where primary productivity can no longer sustain a predator trophic level. The drop of ants as the main predators at higher elevations, however, where associated with a shift from ant-mutualism to maternal care as the predominant anti-predator strategy, revealing that qualitative shifts in predation can have important consequences to prey populations.

Possible mechanisms explaining hump-shaped richness-elevation pattern of woody species in Taiwan

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Several patterns of richness-elevation relationship were reported for different taxa, with the hump-shaped relationship being the most common. Several ecological mechanisms were proposed to explain the richness-elevation relationship, such as the mid-domain effect (MDE), the effect of productivity, land area or environmental heterogeneity. We tested the relative importance of these mechanisms in explaining the richness-elevation pattern of woody species in Taiwan, using vegetation plots from the National Vegetation Database of Taiwan. We divided data into 17 equally wide elevation bands, and pooled vegetation plots sampled within each of them. Woody species richness of individual bands standardized to fixed completeness was then used to describe richness-elevation pattern. We performed simple linear regression to test how well different mechanisms can explain the observed richness-elevation pattern. The MDE was represented by a null model, the effect of land area by square-rooted values of surface area, the effect of heterogeneity by topographic ruggedness index, and the effect of productivity by potential evapotranspiration. We also tested the interaction between each two mechanisms by multiplying the values of the variables they are represented by. The results show that the pattern of woody species richness along elevation is hump-shaped, with the species maxima at lower middle elevation (1079 m a.s.l.). Interaction between the effects of land area and heterogeneity can explain the most variation in species richness. The MDE becomes significant only when interacting with the effect of land area or productivity. Our findings are also consistent with previous studies that none of the single mechanisms can perfectly explain the hump-shaped pattern by itself, and the interaction of two mechanisms is the more plausible explanation.

Regional co-occurrence patterns of Rhododendron species across spatiotemporal scales

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The coexistence of closely related species is a topic of enduring interest in ecology and evolutionary biology, involving intertwined considerations of biogeographic and evolutionary history and community ecology. Disentangling relevant factors will help us understand the nature of exceptionally rich biogeographic regions where in situ diversification has been a major contributor to species accumulation over time, and co-occurrence of ecologically similar congeners is prevalent. Interspecific competition is commonly assumed to be more intense for close relatives, and lead more often to competitive exclusion, or niche divergence that facilitates their coexistence. While physiological tolerances to local abiotic conditions constrain species occurrences through environmental filtering. With an integrative framework, we tested patterns of spatiotemporal coexistence of Rhododendron species at eastern Hengduan Mountains in southwestern China. We collected fine-scale data on abundance and phenology over a flowering season for 28 species across 128 sites. By null model tests, we found that abundance covariation tended to be spatially aggregated, whereas phenology showed a strong divergence pattern, especially along the elevational gradient. We also found that environmental variables, including climate and topography, could explain abundance covariance by a joint species distribution model, with no sign of significant species associations. Though there were signals of phylogenetic conservatism in both vegetative and floral traits, clustering patterns were found for floral traits and phylogenetic relatedness at high elevation. In summary, Rhododendron communities were mainly shaped by environmental filtering and evolutionary history. Our work also demonstrates that temporal divergence plays an essential role for species coexistence over both ecological and evolutionary time.

Species diversity habitat analysis of owl in Tolipir National Park, Azad Jammu and Kashmir, Pakistan

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The present study was conducted in Tolipir National Park, Azad Jammu & Kashmir. Field surveys were conducted fortnightly from February 2019 to May 2020 for documenting diversity of owl species. The study documents six species of owls, Asian Barred Owlet (Glaucidium cuculoides), Short-eared Owl (Asio flammeus) , scully's wood owl (Strix aluco), Eurasian eagle-owl (Bubo bubo hemachalana), (Athene brama) Spotted owlet, Glaucidium brodiei Collared pygmy owlet. These species were recorded from ten study sites: Ghorimar, Noor Kot, Kotari, Darak, Alisojal, Kahoo Kot, Dhahol Dhok, Hussain Kot, Pir Kot, and Panjal. The location of sub study sites were marked with GPS (Global Positioning System) Garmin arc 4.0.The study provides base line data for further studies.

The species (Asian Barred Owlet) was found in open forests with population density (30±12) while Short-eared Owl with population density (20±02). The population density of scully's wood owl (Strix aluco), (Bubo bubo hemachalana) were (5±01) while maximum population density of these two species were observed potted owlet, Glaucidium brodiei Collared pygmy owlet.

The major threats to the population of the recorded owl is deforestation and habitat fragmentation but alarming threats to decline of owl population are myth of local folks. The local populace consider the voice and presence of these species danger of death or big loss of economy if these are found near human vicinity so local people kill them. Only awareness with religious scholars, local wild life watchers and local admisntrative force collective can save these animals for proper function of ecosystem.

Temporally and spatially decoupled evolution of mimicry in an iconic system

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How do complex adaptive phenotypes arise in dynamic physical environments? Answers can be found studying the perfect mimicry between the Neotropical butterflies Heliconius erato and H. melpomene, which comprise a dazzling patchwork of 29 pairs of mimics, where each pair shares a protective wing pattern. This natural experiment in rapid diversification and repeated convergence was the subject of essential biogeographic studies by Bates and Müller. We revisit this classic system to ask: have the two radiations coevolved, is one of them the model for the other, and how were they shaped by the dynamic environments of the Neotropics? We leverage whole genome re-sequencing of 400 butterflies in 25 races of both species, including entirely novel genomic and chemical data from previously un-sampled diversity of the Brazilian Amazonia. Statistical cartography of genomic variation shows three million years of diversification of H. erato in the valleys of Andes and Central America, followed by a recent invasion of the Amazon basin 100,000 years ago, leading to the rapid emergence of the most complex phenotypes from a surprisingly uniform genomic background. In contrast, the apparent mimic H. melpomene shows a distinct pattern of steadier and earlier dispersal, with deep differentiation between the Upper and Lower Amazonia populations separated by major rivers. Coalescent demographic analyses reveal a staggering diversity of subspecies histories and complex patterns of connectivity between populations. Unexpectedly, we demonstrate that an animal trait under strong selection has evolved in a spatially heterogenous and temporarily decoupled manner.

Using a global dataset of country checklists to evaluate dragonfly data coverage

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Despite their great diversity, there has been relatively little global consideration of arthropod distribution in conservation. With increasing studies demonstrating a decline in diversity and populations of insects, early career entomologists are poised to both work through and act on these global declines. Leveraging the biodiversity informatics toolkit is key to identifying the dynamics of species distributional patterns. In a case study of the species occurrence coverage in Odonata, we find that spatially data-poor regions are among the most taxonomically diverse. These results can aid in establishing insect stewardship between regions and in confronting global biodiversity changes. Combined with monitoring and conservation programs, early career entomologists must confront these gaps in order to ensure that biodiversity research, policy, and management directly address insects.

On-demand talks (Climate Change Biogeography)

Addressing the challenge of applying climate change refugia in forest management

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As climate change alters the distribution and abundance of organisms, recent studies have highlighted the potential of climate change refugia (CCR; areas relatively buffered from contemporary climate change) to support the persistence of biodiversity in regions that may otherwise become unsuitable with climate change. In addition to providing insight into biological processes, CCR can also be used by natural resource managers. A key challenge in implementing management strategies based on CCR lies in defining and detecting refugia, as well as understanding their relationship with biodiversity patterns and management strategies. Here we address this challenge in the temperate coastal forests of the Pacific Northwestern United States where declines in the extent of old-growth forests have led some organizations to focus on restoring working timberlands to old-growth forest conditions by employing restoration strategies. We first used variation in remotely-sensed vegetation indices to identify and map climate change refugia in an experimental forest and found that biophysical variables were strong predictors of CCR presence/absence. We then assessed how CCR relate to forest characteristics and found that CCR can influence species presence and relative abundance. Finally, we examined the interaction between restoration strategies and landscape buffering capacity and found that currently applied restoration treatments, such as reducing the density of trees, on average, reduce climatic buffering capacity. Our study introduces a method of identifying CCR based on variation in vegetation responses to local climate and provides one way of including climate change adaptation into management decisions.

Beyond heat waves: Human cities may be incompatible with prolonged maximum monthly temperatures

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High urban population densities may not tolerate sustained heat wave temperatures. I examined patterns of population density classes and exposure to maximum monthly temperature to identify where high urban population density classes were more at risk for prolonged heat than other density classes and if heat may have influenced high urban population densities during the recent past (1970–2000) and the long-range future (2081–2100, under fossil fuel-driven ssp5-8.5). Population densities generally increased with increasing maximum monthly temperature by country. By temperature zone, the hypertropical zone inverted the order such that population densities increased with decreasing maximum monthly temperature, indicating that concentrated populations generally did not develop at high maximum monthly temperatures ≥ 36 °C. The 36 °C maximum monthly temperature threshold corresponds to heat wave warnings, which typically consist of a few consecutive days. Therefore, 36 °C maximum monthly temperature may indicate the start of an inhospitable tipping point beyond which human civilization may not flourish. Most land area will exceed 36 °C maximum monthly temperature under the CanESM5 ssp5-8.5 scenario by 2081–2100. Adaptation is not sufficient to moderate sustained unrelenting heat and migration of human populations would be less feasible than mitigation to reduce carbon emissions.

Biogeographic patterns of root carbon and nitrogen and their controls across U.S.

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Carbon and nitrogen concentration in plant roots is a vital parameter for ecosystem health and vegetation productivity. It is well known that roots are the organs for nutrient acquisition from soils; the carbon allocation to roots reflects the balance of aboveground photosynthesis and belowground nutrient uptake. Therefore, how root carbon and nitrogen shift is critically important for carbon and nutrient biogeochemistry in terrestrial ecosystems. We took advantage of the recently launched National Ecological Observatory Network (NEON) project by compiling data of carbon and nitrogen concentration and isotopic carbon and nitrogen in roots of major vegetations from the NEON dataset. Based on the reported carbon and nitrogen concentration and isotopic signals, we analyzed the carbon and nitrogen concentration in roots of major vegetation types in each of the 28 NEON core sites. There is a clear biogeographic pattern of carbon concentration, but no clear pattern was found for nitrogen concentration and isotopic carbon and nitrogen in plant roots. Carbon concentration in roots increases along latitude; the isotopic nitrogen was primarily controlled by mean annual temperature and soil pH value; the isotopic carbon was primarily controlled by mean annual precipitation; the root carbon concentration was predominately controlled by soil organic carbon, soil pH, and bulk density; while root nitrogen concentration was marginally controlled by soil clay content. Further analysis with a mixed generalized linear regression and structural equation models show that meteorological factors and edaphic factors concurrently control the root carbon and nitrogen concentration. A simulation with the CLM-Microbe model shows consistency with the latitudinal pattern of plant root carbon and nitrogen concentrations. The biogeographic patterns of root carbon and nitrogen are vital information for better understanding vegetation carbon dynamics and their roles in global climate change.

Biophysical effects of afforestation on land surface temperature in southern China

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A comprehensive understanding of the biophysical mechanism of afforestation in response to climate is conducive to coping with global warming more effectively. The planted forests in southern China are an essential carbon sink. However, the impacts of radiative and non-radiative processes on land surface temperature caused by converting open land (i.e., grassland and cropland) and natural forests into planted forests are not clear. We used satellite observations and intrinsic biophysical mechanism theory-based energy balance models to estimate the biophysical impacts of potential afforestation of open land and natural forests on surface temperature from 2000 to 2010 in Guangdong Province, southern China. The results revealed that the modeled land surface temperature due to afforestation had a net warming effect of 0.03±0.02 K. The afforestation's non-radiative and radiative processes led to a slight warming of 0.015±0.01 K and a cooling of −0.001±0.0003 K, respectively. The overall non-radiative forcing index is greater than 90%, indicating that the non-radiative process mainly drives the effect of afforestation on the surface temperature. While converting grassland to planted forests led to a substantial cooling effect in Guangdong Province, the most significant warming occurred when converting cropland to planted forests. Therefore, the conversion of cropland to forest is not advocated everywhere because it does not always lead to cooling. Consequently, it is necessary to obtain detailed spatiotemporal variation data for afforestation and a precise energy balance model to evaluate the climate response to afforestation. This strategy also provides a practical evaluation method for assessing the impact of afforestation on climate and the effectiveness of climate regulation.

Combining spores dispersal simulation and ecological niche models to evaluate climate change impact on Bryophytes in Europe

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Dispersal is a key evolutionary force that determines the survival, growth and reproduction of organisms, cycles of colonization and extinction of populations and globally drives species dynamic responses to their environment. In the context of ongoing climate changes, these dynamics take on even greater importance as the survivability of species depends on their ability to shift their ranges, find refugia or adapt to changes in local climatic conditions. We focus on bryophytes, whose documented long distance spores dispersal capacity, together with their lack of vascular system and high sensitivity to changes in humidity and temperature, position them as likely indicator species to monitor the effects of climate changes. In a recent paper we tackle the challenging task of simulating wind dispersal across a variable landscape (the whole European continent) in order to assess whether highly efficient wind-dispersed organisms like bryophytes can keep-up with projected shifts in their areas of suitable climate. Using a hybrid statistical-mechanistic approach accounting for spatial and temporal variations in both climatic and wind conditions, we simulated future migrations across Europe for 40 bryophyte species. The results highlights the importance of accounting for dispersal restrictions when projecting future distribution ranges and suggests that even highly dispersive organisms like bryophytes are not equipped to fully track the rates of ongoing climate change in the course of the next decades.

Monitoring the Treeline shift of Himalayan birch in response to climate variability using Remote Sensing and GIS in parts of North-Western Indian Himalayan Region

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The Himalayan birch (Betula utilis D. Don), also known as Bhojpatra in the Indian subcontinent, is one of the most important treeline species found in the high altitude areas of Indian Himalayan Region (IHR). Historically, Betula utilis is one of the most important treeline species used in various traditional medicine in India. But due to the over utilization and rapid climate variations have mounted pressures on the natural populations of Betula utilis in parts of North-Western IHR. Here, in this present study we have made an attempt to monitor the treeline shift of Himalayan birch over the period of 30 years (1990 to 2020) in response to regional climatic variation using both the field observation and satellite data in Lahaul and Spiti district of Himachal Pradesh. For this purpose, using multi-temporal LANDSAT and SRTM DEM data the change in treeline ecotone (TE) was monitored as a function of shift in altitude from the past (1990s) to the current (2020s) position. The shift locations were computed in ArcGIS 10.8. GIS queries were made to delineate the maximum shift zones to spot the direction and magnitude of the treeline shift. Also, the effect of climate variability (Precipitation, relative humidity, soil moisture, air temperature) over the forest cover in the study area have been monitored using correlation coefficient. Terra Climate monthly data and multi-temporal LANDSAT have been used for this purpose. The average elevation of the current treeline of B. utilis in the Lahaul and Spiti district is found to be 3672 m. Whereas the average elevation of treeline of B. utilis during the 1990s was of 3366 m. Thus, there is a mean upward shift of the treeline is about 306 ± 40 m. Outcome of the study, we believe, will be helpful in better assessing the impact of regional climate variability in alpine treeline shift in high altitude areas of IHR.

Natural niche truncation and the limits of our knowledge on of how species will respond and have responded to climate change

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Robust prediction of how a species has responded and will respond to climate change requires understanding how climate affects a species across the full breadth of its niche. When a species' realized niche is truncated relative to its fundamental niche, predictions from species distribution models and climate envelope analyses will be compromised. Niche truncation occurs through several means; here I investigate truncation arising from range edges abutting a natural barriers (e.g. coastline) or a species occupying the most extreme environments available to it. Specifically, I calculated the prevalence of niche truncation using species in the genus Asclepias (milkweeds) native to North America. Across all species, on average 36% (range: 0-80%) of species' present-day realized niche perimeters are truncated, meaning that they "face" climates that do not currently exist. When considering only climate that species will be exposed to under RCP6.0, from 2010 through 2070, I found that on average, 22% of species' current realized niche perimeters were truncated. Similarly, 26% of current realized niche perimeters 26% "faced" past climates (0 through 22 Kybp) that species are not currently exposed to. Future truncation and past truncation were positively related to each other (r=0.44), but neither was related to range size. When future or past climates surpass the point of truncation, models need to extrapolate beyond the range of the training data. Quantifying the degree of niche truncation is critical to understanding the limit of our ability to anticipate species' exposure to future climate change and reconstruct past biogeographic histories.

Predicting potential suitable habitat for Olea europaea in Eastern Mediterranean from Last Glacial Maximum to the Future

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The Mediterranean Basin is among the regions most affected by climate change and its effects in the world. 90% of the world's olives are produced in the Mediterranean Basin. Turkey ranks 4th in production. Olive which is bioindicator type of Mediterranean Climate is sensitive to high temperatures. The frequency and severity of extreme events such as high temperatures, drought, and floods, which are thought to be caused by human-induced climate change after the 2000s in the Mediterranean region, negatively affect olive cultivation. 2020 has been the year with the most extreme events in Turkey, with 984 extreme events. Extreme weather events have greatly affected olive yield. This study aims to determine how the distribution of Olea europaea has changed from LGM to the present and the future. For this purpose fossil pollen data taken from the Neotoma Paleoecology Database and occurrence data from Global Biodiversity Information Facility (GBIF) database, literature and field work. In this research bioclimatic variables taken from WorldClim 1.4 and CCSM4 model were used for LGM. Representative Concentration Pathway (RCP) 2.6, 4.5, and 8.5 scenarios and Community Climate System Model (CCSM4) model were used for future projection. The PCA method was applied to these variables, and 9 variables were determined for Species Distribution Models (SDM). Models were produced with MaxEnt 3.4.1, and ArcGIS 10.5. According to the obtained results, the most suitable distribution areas of Olea europaea in the Last Glacial Maximum (LGM) were Western Anatolia and Eastern Mediterranean. In the future, Eastern Mediterranean region is still very suitable habitat for olive trees in the future. However, the distribution of olive trees may shift to the Black Sea region according to RCP scenarios. Therefore, these results may be taken into account to improve conservation and management plans for Olea europaea and considering biodiversity, and model results will make an important contribution to the future distribution of olive trees habitat in Eastern Mediterranean realm.

Revealing ecological mechanisms of range contraction for reindeers over the last 21,000 years

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The distribution of the reindeer today is the result of dynamic changes and shifts that started many millennia ago. Global warming, following the Last Glacial Maximum through to the early Holocene, together with the spreading of Palaeolithic human populations produced a fiercely contested debate on the roles of human hunting and climate change, or a synergy of these impacts, on the ecological mechanisms of range collapse and extinction of arctic megafauna. We use fossils, modern occurrence records, and ancient DNA (in addition to contemporary DNA) to continuously reconstruct the range dynamics of reindeers over the last 21,000 years. Process-explicit ecological models for reindeers are being combined with high temporal resolution paleoclimate data and spatially explicit demographic simulations of anatomically modern humans. Model simulations are being validated against inferences of timing of extirpation from fossils and population decline from aDNA using pattern-oriented methods. We show that reconstructing spatiotemporal occurrences, and regional extirpation and colonisation events, requires process-explicit models with specific demographic and niche constraints, and a constrained synergy of climatic change and hunting by humans. This new process-explicit approach promises to provide not only a more informed understanding of the range dynamics of the reindeer through time, but information that will aid future conservation of this iconic species.

Thermal niche traits of terrestrial ferns along an elevational tropical Andean gradient

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The response of plants related to climate change has received much attention during the last decades. Accordingly, the characterization of certain traits of the species that are directly related to their thermal tolerance and their acclimatization capacity constitutes a fundamental aspect to evaluate the susceptibility of the species or communities to eventual climate changes in the planet. Thermal traits work as indicators of plant responses to changes in temperature and at the same time allow the identification of species and communities vulnerable to these changes. There are few studies on the impact of climate change on tropical plants and most of these focuses on trees. Here we estimated i) species thermal niche traits (minimum temperature, optimum temperature and breadth) from the temperature data of 80 terrestrial fern species from 13026 georeferenced occurrences, and ii) plant community-weighted scores using the thermal niches of each species. Our most compelling result is that community-weighted scores of thermal niche breadth at mid-elevations were broader than the communities' scores at the extremes of the elevational gradient. These results suggest that the most vulnerable communities could be at the highest elevations, since in a scenario of increased environmental temperature, the species of these communities will not be able to migrate to higher elevations.

Trends in Geographic Sensitivity of Marine Fishes Over Decades in the North Sea

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Accounting for biotic interactions is important for predicting species and ecosystem variation under changing climate but difficult to achieve in practice. The proportion of geographical overlap between species, called species geographical sensitivity (SGS), could be used to gauge the potential for species interactions. Species with increasingly high SGS could have the potential to experience more interactions with other species and vice versa, which might have important implications in ecological assessment, particularly at a community level, in the face of climate change. We compiled fish occurrences in the North Sea from 1983 to 2020 and calculated annual mean SGS (mSGS) to systematically evaluate their temporal changes and to estimate influences of species traits on the relative temporal changes in mSGS. The results showed that 36.3% of species significantly changed their mSGS over time, with high correlations between changes in species range size and overlap with other species. The species' averaged mSGS before warming was highly correlated with the relative change in mSGS. Depth range, body length, and age at maturity together explained most variation in mSGS among these species. Contemporary climate change is expected to reorganize species distributions and interactions and substantially alter marine ecosystem functioning. Our assessment opens a new avenue for evaluating climate change impacts on species geographical interactions, and such geographical changes may be contingent on species traits.

On-demand talks (Conservation Biogeography)

Amazonian areas of endemism for Pachira Aubl. (Bombacoideae: Malvaceae)

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The genus Pachira Aubl. belongs to subfamily Bombacoideae (Malvaceae) and has about 50 species, occurring mainly in the Neotropical region. To date, there are few studies using Pachira to delimit areas of endemism and, therefore, we aimed to develop the biogeography study of this genus for the Amazonian species and infer the possible areas of endemism. To find these areas, we used the PAE (Parsimony Analysis of Endemism) and NDM (Endemism)analysis, performed in TNT and VNDM, respectively. In addition, we plotted all Amazonian Pachira occurrences points in the software Qgis and using the Amazonian delimitation described by Morrone in 2017 under a grid with 3º and 4º. As a result, we found 4 to 12 areas of endemism, with the grid of 4º being the most representative. The area with most endemic species and the highest value in the VNDM was the consensus area named Amazonas, with 12 squares (score of 5.21 – 5,46). This area comprises the igapó and campinarana phytophysiognomies and the highest mountains of the Brazilian Amazon, which reach 3,000m in height, being P. yapacanae and P. robynsii the endemic species of this area. Another important area found in both size of squares, but only in the PAE analysis was the Ecuadorian Amazon, composed of one square and two endemic species: P. condorensis and P. punga-schunkei. Thus, this is the main work with biogeography in Pachira and will be fundamental to development of new public policies for the creation of new protected areas in the Amazonian territory.

Biological Spectrum and Phytogeographic Elements of the Wildlife Park Bansra Gali, Murree – an example from Moist Temperate Ecosystem

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The present study investigated the floristic composition, biological spectrum and phytogeographic distribution of Bansra Gali Park, Murree, Pakistan. Quantitative ecological techniques i.e., quadrat and transect methods were used for vegetation sampling and data collection. Through Raunkiaer's method leaf spectra and life size were calculated. Floristically it hosts 135 plant species distributed in 105 genera of 50 different families. Poaceae (14.07%) was dominant family followed by Asteraceae (11.8%), Lamiaceae (7.40%) and Rosaceae (6.6%). Biological spectrum signifies Therophytes as most foremost life forms with the percentage (38.05%), followed by Nanophanerophytes (17.91%), Hemicryptophytes (17.91%), Geophytes (11.91%), Megaphanerophytes (9.70%), Chamaephytes (5.22%), Mesophanerophytes (2.98%) and Microphanerophytes (1.49%). The dominancy of Therophytes indicates anthropogenic and grazing pressures. While leaf spectra, reveals Microphylls with 40 species were dominant leaf form followed by Nanophylls with 35 species (26.1%), Mesophylls with 34 species (25.3%) and Leptophylls having 17 species (12.6%). Phytogeographically plant species belong to 20 phytogeographic elements. The most dominant category of phytogeographic elements was western Himalayan (20%) followed by Irano-turanian (13%), Paleotropical (10%), Pluriregional (9%), Eurasian (7%), Cosmopolitan and Holoartic (5%), Mediterranean and Eastern Himalayan were respresented by 4%, Sinojapanese, Eurosiberian and pantropical by 3%, Central Asiatic sub region, Eastern Asiatic region, tropical element, Sub cosmopolitan and western Asiatic region by 1% while remaining elements by a single specie. Relationship between Biological spectrum and Environmental Variables and relationship of phyto geographical elements with Environmental variables such as pH, TDS and EC were determined.

The area hosting a rich floral diversity and could be a potential and basic source for the conservation and advanced studies.

Coloniality, conservation and Indigenous peoples: a critical exploration of the World Heritage programme

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The vital role of Indigenous peoples in conservation is acknowledged within academic research and by international conservation treaties including the CBD and World Heritage Convention. However in Canada, cultural genocide wrought by British colonial and Canadian federal governments sought to annihilate Indigenous cultures, place-based knowledge systems and relationships with ancestral territories. Resultantly, Canada's Truth and Reconciliation Commission and National Inquiry into Missing and Murdered Indigenous Women and Girls both assert the importance of Indigenous peoples' cultural revitalisation in healing from the effects of settler colonialism. Aside from biodiversity and landscape conservation imperatives, Indigenous leadership in conservation is therefore crucial in upholding rights, ensuring cultural continuity and resisting coloniality (i.e. the patterns of power that emerge from colonialism). As the foremost international instrument for cultural and natural heritage protection under a single legal framework, the World Heritage Convention is an important locus for critical exploration of the above-mentioned issues, along with examination of its implementation in Canada. This paper considers how World Heritage can reproduce colonialities of power and knowledge, especially in the constitution of "natural" heritage. It also examines potentials for rights-based approaches in World Heritage that interlink conservation with upholding Indigenous worldviews, cultural continuity and human rights. This paper supports critique by Whittaker et al (2005) of a "pristine environment" worldview within conservation. It follows Trisos, C.H., Auerbach, J. & Katti's (2021) call for decolonial and anti-oppressive approaches in ecological research and practice which include deeper examination of power structures within sciences and interlinkages between colonialism and conservation.

Comparison of benthic macrofauna sampling methods in the rocky intertidal zone of Guadalupe Island, Mexico.

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In the present study, modifications to a traditional method are proposed and the differences in its estimates are demonstrated. Through a photographic record, the method allows a quick and more detailed census of the composition of the macrobenthic community considering the heterogeneity of the substrate. This is relevant, especially when you are working in the lower intertidal zone, and you have no time. The comparison of the sampling methods was carried out on a rocky intertidal beach on Guadalupe Island, in the Mexican Northeast Pacific. Modification to the traditional method allowed the census and registration of higher values of species richness and abundance. According to the Wilcoxon test, these differences are significant in the three intertidal zones regarding the abundance estimates by taxonomic group, except for arthropods and echinoderms.

Factors influencing effectiveness of wildflower compensation areas in Schleswig Holstein, Germany

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Wildflower compensation areas are becoming increasingly common methods to attempt to conserve wildlife in agricultural landscapes. However, little research has been done to determine what factors influence their effectiveness for wildlife conservation and ecosystem services. In particular, the quantity of nearby permanent semi-natural habitat and the degree of habitat fragmentation may influence whether wildlife can recolonize or utilize these areas. We are using several methods, including bioacoustic recording, pan trapping, nesting traps, botanical surveys and pitfall traps to assess biodiversity at 37 wildflower compensation areas across Schleswig Holstein, northern Germany. This is combined with high resolution spatial data on semi natural habitats and modelling of habitat fragmentation (using the MESH and Connectance indexes). Our preliminary results indicated a significant positive relationship between bee (Apidae) species richness and both semi-natural habitat percentage and the two fragmentation indices. However, we have not yet detected a significant relationship between semi-natural habitat or either habitat fragmentation metric for the richness of hoverflies (Syrphidae), grasshoppers and bush crickets (Orthoptera) or bats (Chiroptera). The study will be repeated and expanded in summer 2022, and we will also implement an eDNA method for detecting insects visiting wildflower heads.

GIS Supported - Evaluation of the Interrelationship between Urbanization and Wildlife Species Loss in Osogbo, Nigeria

Akinleye Oyegbami[1],

[1] Federal University of Agriculture, Abeokuta

Rapid urbanization has contributed significantly to wildlife habitat loss due to land fragmentations over time. The changes in habitat pattern have affected biodiversity, urban-ecology, quality of life and sustainability. This study examined the effect of urbanization on wildlife habitat loss in Osogbo, Nigeria as indicator of improved environment in Osogbo, Nigeria. Changes in vegetation cover was examined by the Normalized Difference Vegetation Index (NDVI) and Land Use Land Cover (LULC) change of the study area derived from Landsat imageries of 1987, 1997, 2007 and 2017. The data obtained were subjected to descriptive statistical tools (mean ± SD). The LULC analysis revealed that 2017 had the highest amount of built up area (7.26 km2) compared to 1987 when built up area was 56.29 km2. Dense vegetation was highest in 1987 (113.40 km2) when compared to 2017 (53.80 km2). NDVI value for 1987 was highest (-0.206 0.418) due to presence of dense vegetation while the value for 2017 (-0.009 0.299) indicated loss of vegetation. There was rapid deforestation and fragmentation of the urban forest between 1987 and 2017. The study therefore discovered that the place where forest still exist and support wildlife habitat is Osun Osogbo Sacred Groove. A total of 21 tree species and 13 families were encountered in the city. Tree species with highest frequency in the study area was Moringa olifera with a frequency of 210. Indigenous trees such as Mangifera indica, Morinda lucida and Anacardium occidentales were more abundant (82.4%) in the study area. The study concluded that urbanization had negative effects on the wildlife habitat in the area.

Hotspots for the conservation of evolutionary heritage and their exposure to land use impacts and climate change

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Human domination of landscapes is a key driver of biodiversity loss, with the fingerprint of climate change becoming increasingly pronounced. Frameworks and tools for identifying threats to biodiversity are required to meet Post-2020 Global Biodiversity Framework targets for 2030 that call for, among other things, reducing or halting species extinction rates. Hence, we compiled a phylogenetic tree for terrestrial tetrapods, mapped hotspots of geographically restricted and evolutionarily distinct tetrapod lineages, and identified hotspots simultaneously facing the highest magnitudes of land use impacts and climate change. Across a quarter of Earth's surface, these hotspots contain the entire ranges of 45% of tetrapods, representing 39% of terrestrial tetrapod evolutionary heritage. By 2070, we estimate 8-13% of this heritage to occur entirely within hotspots highly exposed to climate change, with 13-29% of hotspots projected to experience high exposure to both stressors simultaneously. Most hotspots at highest risk occur in countries least able to take action. Our analysis highlights the need for global ambition and coordination to avoid catastrophic loss of tetrapod evolutionary heritage.

How much of the worldwide marine habitats are we protecting? Two reproducible indexes to monitor the extent of marine habitats within protected areas.

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[1] Senckenberg Biodiversity and Climate Research Center
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Protected areas and other effective area-based conservation measures are key tools to halt biodiversity loss. Ecological representation within these areas is critical to achieving adequate biodiversity protection, but marine and coastal habitats are often overlooked when targets are set within the international policy landscape. In this talk, I will present a standardized, open-source, and reproducible workflow and two resulting indexes that monitor the extent of six marine and coastal habitats within protected areas and other effective area-based conservation measures. The Local Proportion of Habitats Protected Index (LPHPI) pinpoints the jurisdictions with the greatest opportunity to expand their own protected or conserved areas. In comparison, the Global Proportion of Habitats Protected Index (GPHPI) showcases which jurisdictions contribute the most area to protecting these habitats globally. We found that Areas Beyond National Jurisdiction, Norway, and Papua New Guinea have the highest opportunity to contribute the most habitat globally within protected or conserved areas if they meet a target of 30% coverage. Although we focus on marine and coastal habitats, our workflow can easily be extended to terrestrial and freshwater ecosystems. These indexes are helpful to monitor aspects of the Sustainable Development Goal 14 and the emerging post-2020 global biodiversity framework to understand the current status of international cooperation on coastal and marine habitats protection and conservation.

Identifying conservation corridors with the aid of cloud climatologies

Michael Douglas

Many tropical and subtropical forests have been altered by human agricultural or ranching activities. In the future, some of these areas may be suitable for restoration of the original vegetation cover. However, it may be difficult to identify the best locations for restoration if the original forest cover has been removed and if high resolution climatological data is lacking for the region. Similarly, existing forest patches might be re-connected via corridors, but how does one identify the most suitable corridors when the land between the forest patches has been cattle pasture or agricultural fields for decades? In this talk I show how climatologies developed from high spatial resolution cloud imagery from polar orbiting and geostationary satellites can be used to identify corridors for potential conservation action. Examples from the Mata Atlantic of Brazil, the eastern Andes, and parts of Central America will be shown. Not surprisingly, the procedure should work best for identifying corridors connecting patches of cloud forest. However, the climatologies can also be used to identify areas of maximum and minimum cloudiness that may be suitable for further biogeographical investigation or sampling.

Identifying geographical hotspots to guide conservation action for Colombia's useful plants

Laura Kor[1], Cristina Lopez-Gallego[2], Carolina Castellanos-Castro, Mauricio Diazgranados[1],

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Colombia supports over 7,000 plant species with documented human uses, from food and medicine to spiritual and cultural significance. Meanwhile, global conservation strategies increasingly highlight the importance of the conservation and sustainable use of socially, economically, and culturally valuable species. Drawing on a Checklist of Useful Plants of Colombia (UPC) and using existing occurrence records, we identified national-level hotspots for native useful plant species in Colombia. Regionalisation based on a combination of ecosystem and municipality boundaries was undertaken to define the units of analysis, with hotspots identified through the application of three different approaches. We found that native UPC are distributed across all major ecosystems of Colombia and identified 78 units of analysis as hotspots (89,901km2). In this presentation, we will discuss our methods and results, current in-situ conservation gaps, and how these hotspots can contribute to the identification of Important Plant Areas for useful plant species in Colombia.

Mammal Species of the World Next: platform for curating taxonomic intelligence to extend biodiversity data *

(*moved to live-virtual presentation)

Nathan Upham[1], DeeAnn Reeder[2], Nancy Simmons, Joseph Cook[3], Connor Burgin[3], Prashant Gupta[1], Caleb Powell[1], Ángel Luis Robles Fernández[1], Laura Rocha Prado[1], Beckett Sterner[1], Nico Franz[1],

[1] Arizona State University
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Wild mammals are a bellwether taxon for both biodiversity conservation and zoonotic disease monitoring. The Covid-19 pandemic and previous outbreaks of Ebola and Hantavirus have underscored the essential value of mammal taxonomy for accurately linking host species to pathogens and predicting the risks of zoonotic spillover. However, several hundred one-to-many splits have occurred in global mammals since 2004, resulting in a >25% increase in recognized species diversity. Here we outline progress on new infrastructure, a community platform for taxonomic intelligence called Mammal Species of the World Next (MSWx), that aims to maximize the accurate linking of mammal data points derived from the same species (e.g., specimens, tissues, images, parasites, pathogens, and various measurements). MSWx is extending the traditional capacity of taxonomic authorities beyond species checklists to the digital extraction of published taxonomic evidence: (i) species' geographic range maps depicting their extent of occurrence; (ii) verified DNA sequences of barcode genes such as cytochrome-b; (iii) type specimens pertaining to given species names; and (iv) the text of taxonomic treatments depicting the diagnostic traits of name usages. As a proof of concept, we apply the digital representations of species' taxonomic concepts to exemplar North American rodents, successfully disambiguating the concept labels of ~95% of the records examined and training a machine learning model to label the remaining records. Scaling of this project's tools and workflows beyond mammals and across the Tree of Life has promise for enabling biodiversity databases to stay taxonomically updated in lockstep with future progress.

Phytogeographical element and vegetation of wildlife park Bansra Gali, Murree

Ateeqa Khalid[1],

[1] Quaid-i-azam university

Phytogeography is the distribution of plants on earth's surface. Plant are not randomly or evenly distributed on earth surface rather they are present in geographic units, governed so by the physical climate and environment.The present study investigated floristic composition and phytogeographic distribution of Bansra Gali Park, Murree, Pakistan. Quantitative ecological techniques i.e., quadrat and transect methods were used for vegetation sampling and data collection. Through Raunkiaer's method leaf spectra and life size were calculated. Floristically it hosts 135 plant species distributed in 105 genera of 50 different families. Poaceae (14.07%) was dominant family followed by Asteraceae (11.8%), Lamiaceae (7.40%) and Rosaceae (6.6%). Biological spectrum signifies Therophytes as most foremost life forms with the percentage (38.05%), followed by Nanophanerophytes (17.91%), Hemicryptophytes (17.91%), Geophytes (11.91%), Megaphanerophytes (9.70%), Chamaephytes (5.22%), Mesophanerophytes (2.98%) and Microphanerophytes (1.49%). The dominancy of Therophytes indicates anthropogenic and grazing pressures. While leaf spectra, reveals Microphylls with 40 species were dominant leaf form followed by Nanophylls with 35 species (26.1%), Mesophylls with 34 species (25.3%) and Leptophylls having 17 species (12.6%). Phytogeographically plant species belong to 20 phytogeographic elements. The most dominant category of phytogeographic elements was western H

Selection of sampling sites for biodiversity inventory: effects of environmental and geographic considerations

Marlon Cobos[1], Claudia Nunez Penichet[1], Jorge Soberón, Tomer Gueta[2], Narayani Barve[3], Vijay Barve[3], Adolfo Navarro-Sigüenza[4], A. Townsend Peterson[1],

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Biodiversity inventory is among the major challenges for conservation biology in the face of global change. Species exist in two spaces that are linked in the so-called Hutchinsonian Duality: distributions in geographic space and ecological niches in environmental space. Here, we explore the implications of using distinct methods to select locations for biodiversity inventories, based on this idea of two-space distributions. We combined empirical and statistical methods to facilitate selecting localities for biodiversity inventory based on either or both geographic and environmental considerations. These approaches were applied to select sites for inventory in four example countries. For one of our examples, we tested how effective distinct methods were in sampling biodiversity. Random and geographically uniform selections are generally biased towards the most common environments in the regions; selections aiming for uniform sampling of environments are concentrated spatially in areas of high heterogeneity in geographic context. Considering disparate geographic distributions of environments helped to cover geographic areas more broadly when selections were environmentally uniform. Generally, sets of sites selected considering environmental conditions perform better in sampling known biodiversity in regions of interest. Our results underline the benefits of considering environmental and geographic conditions when selecting sites on the effectiveness of resulting inventories. Our tools, implemented in the R package biosurvey, will help researchers to design biodiversity survey systems taking into account the Hutchinsonian Duality and the crucial considerations that it suggests.

Using recent baselines as benchmarks for megafauna restoration places an unfair burden on the Global South

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The potential for megafauna restoration is unevenly distributed across the world, along with the socio-political capacity of countries to support these restoration initiatives. We present new results showing that choosing a recent baseline to identify species' indigenous range puts a higher burden for megafauna restoration on countries in the Global South, which also have less capacity to support these restoration initiatives. We explore how the responsibility for megafauna restoration is distributed across the world according to four scenarios using various temporal benchmarks to define species' indigenous range – current, historical (1500 AD), mid-Holocene and Pleistocene. We test how the distribution of restoration burden across the world correlates with indicators of conservation funding, human development and governance. Using a recent or historical baseline as a benchmark for restoration puts a higher pressure on African and south-east Asian countries while lifting the responsibility from the Global North, where extinctions happened a long time ago. When using a mid-Holocene or Pleistocene baseline, new opportunities arise for megafauna restoration in Europe and North America, respectively, where countries have a higher financial and societal capacity to support megafauna restoration. These results contribute to the debate around benchmarks in rewilding initiatives and the ethical implications of using recent baselines to guide restoration efforts. We suggest that countries from the Global North should reflect on their responsibility in supporting global restoration efforts, by both increasing their support for capacity building in the Global South and taking responsibility for restoring lost megafauna at home.

On-demand talks (Functional Biogeography)

Extending nestedness to functional and phylogenetic perspectives: study on amphibian metacommunities within China largest archipelago

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[1] Nanjing Normal University

Taxonomic nestedness has been raised to explain the patterns of species assembly for over 50 years. However, previous studies generally considered all species as being ecologically equivalent, and hence overlooked the ecological or evolutionary roles of species in generating and explaining the nested patterns. Here, we sampled the occurrence of amphibians on 37 land-bridge islands and explored the nested patterns as well as the underlying processes through three aspects of biodiversity, i.e., taxonomic, functional, and phylogenetic diversity. We quantified functional and phylogenetic nestedness by incorporating how similar species are in ecological traits and phylogeny. Overall, amphibian metacommunities were significantly nested in these three aspects of biodiversity. When relating different predictors to nestedness, we found that area, habitat diversity, and certain species traits were highly correlated with taxonomic nestedness. For amphibians' incidences ordered by decreasing area and habitat diversity, they also exhibited significantly functional and phylogenetic nested patterns. Therefore, the nestedness of amphibians supports the selective extinction and habitat nestedness hypotheses. Interestingly, we didn't observe significant influences of isolation on taxonomic or functional nestedness, whereas the observed phylogenetic diversity was significantly higher than expected for the matrix ordered by increasing distance to the mainland. This inferred that there were more phylogenetically diverse species on less-isolated islands, reflecting an overlooked selective colonization process by the taxonomic approach. Our study thus emphasized that a framework that simultaneously considers taxonomic, functional, and phylogenetic nestedness contributes to a complementary understanding of nestedness processes. Besides, it also improves our ability to conserve insular biodiversity from different perspectives.

Patterns and drivers of avian taxonomic and functional α- and β-diversity in Quebec

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The variation in species composition (taxonomic β-diversity) and functional roles (functional β-diversity) reflect underlying ecological processes shaping community structure. Here, we used data of bird atlas of Quebec (time period: 2010-2014) and functional traits and estimated the taxonomic and functional α- and β-diversity (and its turnover and nestedness components). We explored the relationship between the different facets of α-diversity using Generalized Additive Models (GAMs), and also the effects of climatic variables and land uses on α-diversity with GAMs and on β- diversity with Generalized Dissimilarity Models. We found a significant unimodal relationship between functional and taxonomic α-diversity, while both were significantly affected by climatic variables and land uses. Taxonomic β-diversity was driven by turnover component and showed a relatively strong variation along the environmental gradient, but not along the spatial gradient. Thus, processes such as environmental filtering might structure the species composition. The effects of land uses had the strongest explanatory power, with differences in forest cover (primarily regenerated and of young or middle age) emerging as the strongest drivers of differences in species composition. On the other hand, functional β-diversity was driven by nestedness component and was weakly related to environmental and spatial gradient, suggesting that perhaps, stochastic processes might affect the functional composition.

This research work was supported by the Hellenic Foundation for Research and Innovation under the “First Call for H.F.R.I. Research Projects to support Faculty members and Researchers and the procurement of high-cost research equipment grant” (Project Number: HFRI-FM17-2024 -MAPFUN).

Variation in avian morphology with altitude in tropical montane systems

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Examining patterns of intraspecies phenotypic variation with geography and environment can illuminate processes of natural selection and adaptive evolution. Such phenotypic variation along altitudinal gradients in the tropics is of particular interest, as species can experience considerable variation in climate and habitat over a small spatial scale. We analyzed and compared morphological variation in a broad suite of birds along two elevational gradients in Western Ecuador: a 675m gradient in the coastal cordillera, and a 2800m gradient on the western Andean slope. These gradients occur in global biodiversity hotspots: the Choco and the Tropical Andes, respectively. The data set we analyzed includes measurements of between six and nine traits in more than 4000 individual birds from more than 40 species and 12 families. Using multivariate analyses, we found evidence for statistically significant variation in morphology with elevation within a number of species, and along both elevational gradients. We further investigated this dataset using phylogenetically controlled multivariate regression, and determined which aspects of species ecology predict the existence and form of intraspecies morphological variation. These data suggest that environmental variation might be driving adaptive trait divergence along these gradients, including at small spatial scales.

On-demand talks (Gradients & Range Limits)

Determinants of plant species richness along the Himalayan elevational gradient

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Along the elevational and latitudinal gradients climate strongly correlates with species richness, resulting from differences in in-situ speciation and dispersal. We evaluated the patterns of species richness for natives and aliens based on the overlap of elevation ranges of ~10,000 species of angiosperms in the Himalaya. We further used grade of membership models on distribution of the Himalayan plant to identify taxonomically and phylogenetically distinct biotas and conducted phylogenetic analysis to evaluate diversification rates. Natives (8,765 species) show a mid-elevation peak in the east and a low elevation plateau in the northwest. Alien species (842 naturalised and 662 naturalised) show a monotonic decline with elevation. Native species fall into four cohesive biotas, organized by climate. Species turnover between tropical and temperate clades occur at the consistent freezing line (~2000m), and at the elevation of occasional freezing (~1500 m) and these boundaries run throughout the length of the Himalaya. These patterns are retained for different life forms as well as when we consider whole clades rather than species. Assembly by colonization has likely to have been important to the build-up of the Himalayan flora. The high elevation biota has few species, but spans the largest area, implying lower species richness than carrying capacity, particularly with respect to allopatric forms. We attribute the high rate of recent speciation in temperate climates to high rates of turnover, creating ecological and geographical opportunities. This study thus links climatic restrictions of clades to differences in diversification rates, and by inference species numbers.

Exploring signatures of differential selection and local adaptation across climate and habitat in the chisel-toothed kangaroo rat (Dipodomys microps)

Keaka Farleigh[1,] Tereza Jezkova[1,]

[1] Miami University

Environmental conditions such as temperature, precipitation, or vegetation can be major drivers in determining the latitudinal or altitudinal boundaries of a species range as well as the continuity and patchiness within its range. Yet, many species occupy wide distributions that span a diverse suite of environmental conditions. Environmental heterogeneity across a species distribution creates a unique set of conditions and environmental pressures that individual populations encounter. As a result, local selective pressures will vary across a species range and may lead to individual populations becoming locally adapted to their environment. We investigate how the strength of selection varies across the species distribution and we searched for genetic signals of local adaptation in the chisel-toothed kangaroo rat (Dipodomys microps), a species that occupies two distinct habitats (saltbrush and blackbrush, respectively) and a wide range of climatic conditions in the American southwest. We used double digest Restriction Site Associated DNA sequencing to generate a dataset of 42,890 single nucleotide polymorphisms from 180 individuals belonging to 30 populations. We then used genome-environment association and gene ontology methods to understand how selection varies across the species distribution, to identify loci that are correlated with environmental variables, and to link these loci to specific genes. Our analyses identified 964 loci that are associated with temperature and 131 loci associated with habitat. Our analyses also showed more adaptive loci present in the saltbush habitat than the blackbrush habitat. We linked candidate loci to genes that are involved in vision, kidney development, and response to stress.

Floristic change along na ecological gradiente in a hummock campo- Brasília/Brazil using indirect gradient analysis

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This study analyses the floristic change along an ecological gradient in a hummock campo (campo de murunduns) in Brasília. The gradient is the levels of the microtopography from the ground between the hummocks, with wet campo (campo úmido) to the top of the hummock with pure cerrado vegetation, using direct gradient analysis, and also indirect gradient analysis utilizing the program DECORANA. In 20 transects, each going from wet campo to cerrado, were placed 6 quadrats 1/2 x 2m each (120 quadrats total). The levels were 1) lowest ground between two hummocks, 2) the slightly higher ground next to but not on a hummock, 3) the lower part of the slope of the hummock, 4) the middle part of the slope, 5) the upper part of the slope, 6) the top of the hummock. The families with the largest number of species for the campo as a whole were Gramineae, Myrtaceae, Euphorbiaceae, and Cyperaceae. In the wet campo, Cyperaceae, Xyridaceae, and Iridaceae had the largest number of species. The indirect gradient analysis showed that the floristic change from wet campo species to cerrado species, as one ascends the slope of a hummock, was gradual. This change was due to the depth of the water table from the soil surface at each level. There was no sudden change at an intermediate level.

Macroecology in Depth: Estimating Marine Fish Biodiversity in Three Dimensions

Hannah Owens[1,]

[1] University of Copenhagen

To date, broad-scale estimates of marine fish diversity have generally only considered species distributions in two-dimensional space and do not account for depth distribution, which may lead to mis-estimation of species distributions and subsequent diversity estimates, especially among pelagic and benthic species. This aspect of marine distribution modeling has, in general, been largely neglected due to a lack of widely accepted methodological pipelines for three-dimensional distribution inference. Here, I present a possible way forward: generating species distribution models based on environmental data extracted at the depths where individuals were observed. I tested this method on marine Atlantic representatives of three orders of fishes: Gadiformes, Scombriformes, and Beloniformes. My results show biodiversity estimates based on two-dimensional models may underestimate the latitudinal breadth of deep-sea fish distributions, an error compounded when maps of these distributions are stacked to estimate biodiversity. Three-dimensional models not only provide not only a likely more accurate picture of current species' distributions and broad-scale diversity patterns but may also allow for more accurate past and future distribution projections. These projections could infer not only changes in latitudinal and longitudinal distributions, but also track suitable habitat conditions via changes in depth distribution and identify putative deep-sea refugia.

Meta-analysis of local adaptation in spring phenology across Europe and North America

Alina Zeng[1], Elizabeth Wolkovich[1],

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Over 250 years of common garden experiments have shown that most studied trees exhibit local adaptation– having the highest fitness at their site of origin. Around the globe, researchers have observed similar patterns of adaptive differentiation in fall biological events (e.g., bud set, cold hardiness) along altitudinal and latitudinal gradients Spring phenological events, such as budburst and leaf flush, appear to show greater phenotypic plasticity and more variable patterns of variation, at least in North American studies. As research in this area has grown, alongside its importance to climate change forecasting, so has interest in predicting local adaptation across different traits and locations. While common garden studies are abundant in North America and Europe, no study has looked at the relationship between the two continents' spring phenology variations. Combining meta-analytic techniques with hierarchical Bayesian models, and daily climate data in Europe and North America, we provide the first cross-continental assessment of local adaptation in spring phenology. Across 59 common garden studies in Europe and North America, 21 published studies have examined spring phenology across latitudinal clines. We found a latitudinal cline of spring leafout in North America, but not Europe, with strong hierarchical effects of garden and species explaining much of the variation. Clines across gardens with mean annual temperature were weak. This lack of effect may be explained by the similar spring climate of most provenances and gardens but suggests diverging latitudinal patterns in each continent.

Habitat but not topographic heterogeneity constrains the range sizes of African mammals

Daniel Lauer[1], Benjamin Shipley[1], Jenny McGuire,

[1] Georgia Institute of Technology

A species' geographic range size carries critical implications for its extinction risk, as smaller-ranged species persist in fewer environments. Theoretically, heterogeneous landscapes can foster small-ranged species by facilitating the coexistence of taxa that are each constrained to particular abiotic conditions. Whether this process is more attributable to a diversity in habitat types (habitat heterogeneity) or physical elevations (topographic heterogeneity) across landscapes is largely unknown. Here, we disentangle the comparative influences of habitat versus topographic heterogeneity on mammalian range sizes in Africa, where habitat and topographic heterogeneity are weakly correlated ($\rho=0.14$). We optimized a phylogenetic generalized least squares model, incorporating ~1000 species' functional traits and abiotic conditions to predict their range sizes, while accounting for their evolutionary non-independence. We assessed how the inclusion of species' experienced degrees of local habitat, and separately topographic, heterogeneity into the model impacted the model's performance. We find that habitat heterogeneity significantly decreased the model's AICc and increased its likelihood, producing a significant model coefficient of -0.71. Habitat heterogeneity also enhanced the model's predictive performance, increasing the percentage of variance that it explained in unknown species' range sizes from 58.5% to 61.8%. Conversely, topographic heterogeneity had no impact on the model's AICc, likelihood, or predictive performance, while also yielding a non-significant coefficient. The results obtained at multiple spatial resolutions differed minimally. Our findings advance prior ecological theory by demonstrating that a landscape's habitat diversity, and not its elevational variation, relates inversely with mammalian range sizes and therefore fosters the existence of small-ranged mammals.

On-demand talks (Invasion Biogeography)

Dark diversity at home describes the success of cross-continent tree invasions

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Non-native species threaten ecosystems worldwide, but we poorly know why some species invade more. Functional traits, residence time, and native range size have been often used as invasion predictors. Here, we advance in the field by linking invasion success to native range parameters derived from dark diversity — regionally present but locally absent set of ecologically suitable species. We tested whether those parameters improve the invasion success description of tree species native in North America invading Europe and the Mediterranean Basin or vice-versa. We define invasion success for each species as the number of locations occupied at their non-native range. The probabilistic dark diversity was estimated based on the species co-occurrences in their native ranges. It specifies how suitable is a species for a location, even if the species is absent. We calculated two parameters: the sum of native location suitabilities (niche breadth proxy) and dark diversity probability (how often a species is absent from suitable locations, indicating limitations in niche realisation). We compared the performance of models using the dark diversity parameters with a common species range measure, the number of locations occupied. We accomplished our models by adding functional traits, residence time, and invasion direction. Invasion success increased with the sum of native location suitabilities and decreased with dark diversity probability. This model with dark diversity parameters outperformed an alternative using the number of native locations occupied. Our best model included invasion direction, functional traits (including mycorrhizal status), and residence time, but dark diversity parameters remained important predictors. The dark diversity parameters can contribute to invasion ecology by linking the species performance in the non-native range to its niches parameters, derived from the native range.

The influence of fire and land use on breaking the grassland-tree barrier in North America, creating novel assemblages of eastern and western tree species

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Historical accounts documented tree density increases initiated between approximately 1860 and 1890 in the central North American grasslands bordering forests. This created the potential for new associations of eastern tree species with western species, given that the Great Plains grasslands historically prevented tree expansion and intermixing during the past 10,000 years. Land use change but not precipitation change corresponded with historical tree changes based on timing, magnitude and direction of change, and mechanism. Modern tree surveys (years 1966 to 2013) indicated range intersection of eastern redcedar and western Juniperus species totaled 200,000 km2 and increased by 31,600 km2 over time, representing a novel, viable assemblage of eastern and western species. Tree migration and novel assemblages are expected to form under current climate change. Nonetheless, tree migration and novel assemblages also can develop due to land use change rather than climate change.

Transboundary range expansion, spatial structure in abundance, and the influence of environmental filtering on a marine invasive species

Kevin C.K. Ma[1], P. William Froneman[1], Christopher D. McQuaid,

[1] Rhodes University

Acting as weak or strong barriers, biogeographic boundaries can affect the rate and extent of spread of species undergoing range shift. Novel ecosystem engineers can have profound effects on an ecosystem when they spread by competing with local species and, over time, re-engineer the newly invaded habitat. Marine bioregions are clearly defined in southern Africa and we tested the influence of their boundaries on the spread, spatial structure, and environmental filtering (the abiotic exclusion of species persistence) on an alien ecosystem engineer, the mussel Mytilus galloprovincialis. We compiled historical records and made field observations to reconstruct its invasion history and to determine structures in abundance across multiple bioregions. Specimens collected from its range centre to margins were used to determine the effects of environmental filtering on endolithic shell infestation and barnacle epibiosis. For this quadragenarian invasion, we found a pattern of saltatory spread; initial breaching of boundaries was associated with rapid spread, but other boundaries encountered decades later acted as barriers to further spread. Repeating spatial patterns in abundance were found at intra- (120–160 km) and inter-bioregional scales (400–990 km). Further, environmental filtering had a direct effect on population dynamics by affecting abundance and recruitment success. However, environmental filtering was a more limited determinant of endolith-induced shell damage and epibiont load, suggesting weak indirect effects. Overall, we demonstrated the influence of biogeography in driving temporal patterns of spread, spatial structure on the distribution and abundance, and increasingly negative effects (endolithic infestation and epibiosis) of an invasive species.

On-demand talks (Island Biogeography)

Extinction drives a discontinuous temporal pattern of species-area relationships in a microcosm system

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Despite the species-area relationship (SAR) having high potential to be an ecological law, its formation mechanism has not been tested directly. Species extinction may represent a breakthrough in SAR research because of its inclusion in most hypotheses regarding SAR formation. We propose the hypothesis that extinction can shape SARs under the same biodiversity background and total resource conditions without migration and species generation. Furthermore, since the extinction rate in a community has temporal dynamics, the corresponding occurrence of SAR should also have temporal dynamics. In this study, an independent and airtight microcosm system containing uniformly mixed Chinese pao cai (fermented vegetables) soup and airtight closed culture flasks was constructed. The biological diversity of the microcosm system was monitored at 26 time points over 60 days. We found that the SAR was temporally discontinuous. Small-scale extinctions in the community modified community structure to promote ecosystem stability and thus an SAR, while mass extinction pushed the community into the next successional stage, and the SAR disappeared. SAR loss should serve as an indicator of ecosystem stability. The role of extinction in communities has reference significance for the sustainable development of human societies.

Historical biogeography of Maesa (Primulaceae) with an emphasis on Malesian archipelago

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The Malesian archipelago is recognized as one of the world's most geologically and biogeographically complex areas with exceptional floristic diversity. These islands are situated between mainland Southeast Asia and Australia, acting as an area of floristic interchange. However, the pathways of plant dispersal across the region are still unclear. Although west-to-east dispersal into the Pacific is detected in several plant groups, the generality of this pattern remains to be tested. Maesa is a genus of shrubs, trees or woody scramblers in the family Primulaceae distributed in the palaeotropics from Africa to the Pacific. It comprises approximately 192 species which 39 species recorded in New Guinea as the area harbouring the richest species diversity of the genus. Most of the Maesa species found in the Malesian archipelago have narrow distributions, usually on a single island. In this study, we used Maesa as a model to reconstruct dispersal events between Malesian islands and the connection to continental Asia, Australia and the Pacific islands. In addition, we investigated the factors that made New Guinea the hotspot of species richness. We used a species-level phylogeny generated from genomic (target sequence capture) data for molecular dating and ancestral range estimation. Our investigation into the biogeographic history of the genus reveals the events that shape the current distribution of Maesa and shed the light on the connectivity between the complex Malesian archipelago and neighbouring islands and continents.

Impacts of forest fire on understory species diversity in Canary Pine ecosystems on the island of La Palma

Frank Weiser[1,] Carl Beierkuhnlein[1,]

[1] University of Bayreuth

Forest fires are a frequent occurrence in the Pine forests of the Canary islands. The dominant tree species, the endemic Pinus canariensis C. Sm. is well adapted to the fire regime and is able to resprout from all aboveground parts. Throughout the last decades, the fire regime has been changing due to both climate change and anthropogenic influence, which leads to more frequent large scale fires. We investigate species diversity patterns in the understory vegetation 1.5 years after the large 2016 wildfire on the western slopes of Cumbre Vieja, La Palma. Fire intensity was derived from Sentinel-2 satellite images and linked to measured environmental variables and species composition data from 79 sites along an elevational gradient of 654 meters. We use GLMs, distance-based redundancy analysis (dbRDA), bray-curtis dissimilarity and variance partitioning to investigate the drivers of both alpha and beta diversity patterns in the burned area. Elevation was the most important driver for both alpha and beta diversity. The high abundance of the endemic Lotus campylocladus ssp. hillebrandii (Christ) Sandral & D.D.Sokoloff in many of our sites was also an important influence on the investigated species composition. While the long term effects are unclear as Lotus fixes nitrogen and reduces erosion, the dominance of Lotus likely reduces the ability of other species to establish due to its water and nutrient uptake.

Island ontogeny, endemic species and the missing link between climatic rarity and functional traits

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Understanding the origin and maintenance of functionally rare species can help us to understand their contributions to overall species diversity. Functional rarity measures the distinctiveness of species traits and gives an indication of a species' role in an ecosystem. We used island biogeographic theory to develop three hypotheses to predict, over the life cycle of an island, how the functional distinctiveness of endemic and non-endemic species changes and how this is influenced by shifts into climatically rare habitats. We used plant trait data to measure functional distinctiveness of endemic and non-endemic species for each major island in the Canary Island archipelago. We used temperature and precipitation to quantify climatic rarity at a resolution of 500m, from which we estimate the mean climatic rarity of each species' range. Using phylogenetically corrected analyses, we compared functional distinctiveness between endemism groups and across islands. We found that functional distinctiveness is similar between endemics and non-endemics, as well as between islands. In contrast, endemics tend to be found in rarer climates than non-endemics, particularly in the younger islands. Furthermore, single island endemics show a strong decrease in their occupancy of rare climates on islands of increasing age. Overall, island endemics do not diverge from the community trait space, despite being found in rarer climates.

Land use change through the lens of macroecology: new insights from Azorean arthropod communities

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Land management practices, in particular land use change, have resulted in the global loss of biodiversity. These types of disturbance affect macroecological patterns, and therefore analyzing them can provide insights into how ecosystems are affected by land use change. We use arthropod census data from 96 sites in the Azores archipelago across four different land uses of increasing management intensity: native forest, exotic forest, semi-natural pasture, and intensive pasture, to examine the effects of land use type on three macroecological patterns. The Maximum Entropy Theory of Ecology (METE) has successfully predicted these patterns in undisturbed ecosystems, and thus provides a null expectation for their shapes. We find that the forest habitats are the best fit by METE predictions, while the semi-natural pasture is consistently the worst fit, and the intensive pasture is intermediately well fit. We show that the direction of failure of the METE predictions at the pasture sites is likely due to the presence of hyper-dominant introduced spider species. We hypothesize that the particularly poor fit for the semi-natural pasture is due to the mix of arthropod communities out of equilibrium, leading to greater heterogeneity in composition and complex dynamics that violate underlying assumptions of METE. The comparative better fit for the intensive pasture plausibly results from more homogeneous arthropod communities that are well adapted to intensive management. Analyzing deviations from theoretical predictions across land use type provides useful information about how land use and disturbance affect ecosystems; such comparisons could be useful across other habitats and taxa.

The northern Philippines is characterized by ancient colonization and persistent diversification by small mammals

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Island communities are often characterized as governed by equilibrium processes of colonization and extinction influenced by island area and distance from other landmasses, often with resultant high species turnover. The Philippine archipelago, comprising oceanic islands that vary extensively in age, area, and elevation, provides an ideal natural system to understand the importance of these equilibrium processes over longer, evolutionary time scales. We use time-calibrated phylogenetic trees of extant species to illustrate that the rodents and shrews of Luzon, Mindoro, Sibuyan, and Lubang Islands show a history of early and repeated colonization beginning roughly 18 million years ago, followed by lineage persistence and speciation across evolutionary time. Rates of colonization and species richness accumulation appear to be either constant or increasing through time, with younger islands increasing in species richness faster than older islands. Our results show that the northern Philippines challenges the expectations of colonization and extinction acting rapidly and in equilibrium, and therefore high in species turnover. The northern Philippines may, in effect, be unbounded by equilibrium island biogeographic processes due to the islands' consistent geographic growth over geologic and evolutionary time.

The biogeography of island elephants: when does Jumbo shrink?

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Before humans colonised the islands, many islands worldwide harboured at least one species of proboscidean, endemic to their island. Several genera are represented, including elephants, mammoths and stegodonts. Several of these island proboscideans evolved spectacular dwarfism to less than 10% of their ancestral size. In general, proboscideans exhibited far more extreme cases of dwarfism than extant insular mammals, which is consistent with the substantially more extended period of deep geological time that the selective pressures could act on these insular populations. We investigated the factors that influence the direction, degree and speed of body size evolution in fossil insular proboscideans worldwide. We assembled data on the geographical characteristics (latitude, island area, isolation), dispersal time and body size evolution of palaeo-insular species for 28 insular species of fossil elephants across 19 islands. Island area and body size are positively correlated, contrary to the trend in large mammals in general. We found a threshold of about 6-10 km distance between the island and the mainland, below which no dwarfism evolved. Presumably, this is due to continuation of genetic contact with the mainland population. Time in isolation is correlated to the degree of dwarfism exhibited. The presence of hominids as predator does not predict the occurrence and degree of dwarfism, contrary to earlier predictions.

Reconstructing pre-anthropic vegetation patterns of St Helena island, South Atlantic Ocean

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St Helena is one of the most isolated oceanic islands of the planet, with a unique and highly endangered endemic flora. In this study my aim is to reconstruct the pre-anthropic vegetation patterns on the island by using historical records together with current vegetation patterns, climate- and geographical data. I contrast the historical vegetation patterns to the current situation. The study shows that although a similar zonation along the altitudinal gradient exists in both the historical and current vegetation, the species composition has completely changed. St Helena's current vegetation is heavily dominated by introduced species while the endemic vegetation is reduced to small, isolated fragments. I further hypothesize that the refugia for the endemic vegetation are mostly cliffs and slopes over 60 degrees that have been inaccessible to the introduced goats. The findings of my study are important for the conservation and restoration planning of the highly endangered island flora of St Helena.

On-demand talks (Marine Biogeography)

Changing latitudinal distribution and body size of marine fishes across Norwegian waters

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The majority of marine species are water-breathing ectotherms, or organisms that breathe water and track their thermal affinity via the ambient temperature and/or dissolved oxygen concentration of their preferred environmental niche. As global oceans may continue to warm and lose oxygen concurrent to climate change, such changes will immediately affect the availability of suitable environmental conditions for water-breathing ectotherms. Species have been observed to shift their distributions geographically and decreases in maximum body size have been observed in warmer or less-oxygenated waters. Such changes will likely result in significant alterations to marine communities and food web interactions. Here, I report our research on changes to maximum body size and geographic range of teleost fish communities in relation to environmental covariates across Norwegian waters, from temperate to Arctic latitudes, throughout the past three decades. First, using generalized additive models, our results predict the asymptotic limitation or truncation of maximum size of fish species with increasing temperatures across their observed range. Second, we report an increase in the weighted abundance of 'warm' versus 'cold' water species across Norwegian waters, correlated to increases in temperature using the mean temperature of the catch index. Lastly, throughout the same observation period we report an increase in biodiversity of fish communities within the Barents Sea and southern Arctic Ocean. In concert with one another, these results suggest a changing ecological landscape for teleost fish communities across Norwegian waters, and prompt further research regarding subsequent impacts on marine communities and food webs throughout future climate change scenarios.

Diversity and dynamics of bull kelp niches in the Salish Sea

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Nereocystis luetkeana (also known as bull kelp) is a kelp species adapted to varied environmental conditions in the Salish Sea. Using very high-resolution imagery from 2004-2021 over the Southern Vancouver Islands and the Gulf Islands area, we discovered that bull kelp canopies emerge on the surface on repeated and predictable areas (hereby called 'kelp niches') that can be traced back to nautical charts elaborated in the decade of 1850. Additionally, the rocky and mixed substrate along the area of study was characterized according to environmental variables such as wind density, summer and spring sea surface temperature (SST), fetch, tidal amplitude and total suspended matter (TSM). Similar coastal environments were grouped in clusters, facilitating the analysis of kelp niches according to their similarities. The identification of niches and clusters have helped the identification of dynamic patterns of resilience for this foundation species.

Evidence of depth partitioning in Provanna (Gastropoda: Provannidae) from the Costa Rica Margin

Melissa Betters[1], Erik Cordes[1],

[1] Temple University

Range limits are an observable expression of species' ecology and are influenced by both abiotic and biotic factors within an organism's environment. While range limit research has historically focused on terrestrial and shallow-water marine realms, expanding investigations across depth represents a vital extension to this literature. In the present study, hydrocarbon seeps along the Pacific Costa Rica Margin (CRM) were explored and sampled during three research cruises from 2017-2019, in which 1,817 specimens of Provanna (Dall 1918) snails were collected, representing four species across six sites. This study aimed to investigate the potential factors affecting the distribution, genetic diversity, and morphological variety of these specimens. Our results expand the ranges of several known Provanna species and suggest that depth partitioning has allowed these species to maintain genetic, ecological, and morphological distinction in close proximity. The two dominant species at these sites were found to exhibit a parapatric distribution across depth, where the shallower species inhabits conditions likely intolerable to the deeper species, while the deeper species seems to competitively exclude the shallower species from settlement within its range. These results support well-established range limit hypotheses and suggest distinct evolutionary trajectories: one maximizing competitiveness within a preferred depth range, and one maximizing environmental tolerance, allowing individuals to avoid competition altogether. This study is the first to characterize, in detail, the distribution and diversity of Provanna at the CRM, and uses these data to present novel insights into their life strategies and resultant biogeography across the Pacific Ocean.

On-demand talks (Models & Methods in Biogeography)

Biogeographical modelling of the species competitive interactions: a fuzzy logic approach

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The environmental conditions of a territory determine to what degree the species are related to each other and to the environment. Species distribution models are used to establish relationships between the environment and the species distribution. Models based on fuzzy logic through the Favourability Function also allow the analysis of relationships between distributions of different taxa. By considering how the environment influences competition relationships between two species, we proposed the biogeographic analysis of three possible scenarios: i) sympatric coexistence; ii) environmental segregation; and iii) competitive exclusion. In order to identify these scenarios in different pairs of species with overlapping distributions, the Favourability Function and fuzzy logic tools were applied. Specifically, for each case, the favourability for each species and the fuzzy intersection between them, or "shared favourability", was calculated. For each case, the relationship between the favourability for each species and the shared favourability was analyzed, highlighting the areas where either environmental segregation, competitive exclusion or sympatric coexistence is predicted. The results showed that the Favourability Function is a useful tool for analyzing large-scale biogeographical outcomes of ecological interactions between species.

Detecting spatially-dependent trait evolution in biological communities

Pedro Henrique Pereira Braga[1], Pedro Peres-Neto[1], Steven Kembel,

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Evolution is a process not only structured in time, but also in space. Evolutionary processes, such as natural selection, variation and drift, act over time to determine species adaptations – reflected by their phenotypes and genotypes – that allow them to occupy and persist across different environment. Because environments are spatially structured, species' geographical ranges often accumulate phenotypical and genotypical variation. However, spatial variation is not only reflected in the environment and species phenotypical features, but also in the direction and how accelerated or decelerated traits change through evolutionary time. While evolutionary models have been useful in revealling patterns of evolutionary changes in phenotypical variation, they rarely incorporate spatial processes, hampering our understanding of how phenotypic evolution depends on spatial structure. In this study, we propose a quantitative framework that estimates how spatial and evolutionary signals, and their interactions, are associated to trait variation. Specifically, we apply sets of eigenfunctions to species phylogenetic relationships and their spatial distributions and then use the corresponding eigensystems to model species phenotypes. We assess the robustness of our framework using simulations of trait evolution under different strengths of selective pressure, contrasting different scenarios of spatially-dependent and spatially-independent phenotypical evolution. Finally, we also apply our framework to empirically test hypotheses of spatial non-independence in the evolution of climatic niche breadth in bats.

DynamicGrids.jl: fast, concise and extensible spatial modelling in Julia.

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The Julia language gives a unique opportunity to improve how we write models in biogeography: it makes models easy to understand while highly performant. Here we introduce a powerful and extensible Julia framework for concise spatial models: DynamicGrids.jl.

Designed to be generic and open-ended, DynamicGrids.jl has a wide range of current applications, including dispersal, dynamic SDMs, species interactions,
metacommunity dynamics, spatial genomics, management feedbacks and landscape or land-use changes. Its utility for agriculture, ecology and biogeography have been demonstrated in the Julia packages built on it like Dispersal.jl and MetaCommunityDynamics.jl, and a growing list of case-studies in biosecurity and organism dispersal.

We demonstrate the philosophy and applications of this novel package, and its potential to revolutionize spatial biogeographic modelling.

Fauxcurrence: simulating multi-species occurrences for null models in species distribution modelling and biogeography

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[6] Sam Ratulangi University
[7] Tadulako University
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Defining appropriate null expectations for species distribution hypotheses is important because sampling bias and spatial autocorrelation can produce realistic, but ecologically meaningless, geographic patterns. Generating null species occurrences with similar spatial structure to observed data can help overcome these problems, but existing methods focus on single or pairs of species and do not incorporate between-species spatial structure that may occlude comparative biogeographic analyses. Here, we describe an algorithm for generating randomised species occurrence points that mimic the within- and between-species spatial structure of real datasets and implement it in a new R package - fauxcurrence. The algorithm can be implemented on any geographic domain for any number of species, limited only by computing power. To demonstrate its utility, we apply the algorithm to two common analysis-types: testing the fit of species distribution models (SDMs) and evaluating niche-overlap. The method works well on all tested datasets within reasonable timescales. We found that many SDMs, despite a good fit to the data, were not significantly better than null expectations and identified only two cases (out of a possible 32) of significantly higher niche divergence than expected by chance. The package is user-friendly, flexible and has many potential applications beyond those tested here, such as joint SDM evaluation and species co-occurrence analysis, spanning the areas of ecology, evolutionary biology and biogeography.

How species range size affects distance-decay shape and a novel test for parameters comparison

Ramiro Martín-Devasa[1], Sara Martínez-Santalla[1], Carola Gómez-Rodríguez, Rosa Mª Crujeiras[1], Andrés Baselga[1],

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Distance-decay of similarity, i.e. the decrease in community similarity with spatial or environmental distance is a widely studied pattern in biogeography. Modeling the distance-decay of community similarity is a useful tool to assess how community variation is structured in space. This is because model parameters inform about the shape of the pattern and the rate at which communities change with spatial distance. Therefore, to be effective distance-decay models have to accurately capture the shape of the pattern. Once the shape of the pattern is accurately fitted, the comparison of distance-decay model parameters (i.e. intercept and slope) allows assessing differences in the role of dispersal limitation across biological groups. However, the pairwise autocorrelation of community similarities and spatial distances causes the inflation of degrees of freedom, affecting the estimation of the variance of parameters, which can bias such comparison of parameters. Here, we (i) assess how the size of species distribution size influences the shape of distance-decay patterns, and (ii) provide a test statistic (t_{dep}) for the equality of parameters between distance-decay models. This test estimates the variance of distance-decay model parameters using a block-resampling procedure to avoid biases associated to the inflation of degrees of freedom. We evaluate the type I and type II errors of t_{dep} through a simulation study in which we created three null and three alternative hypothesis scenarios of distance-decay relationships (equality and difference of parameters, respectively), considering different shapes of the distance-decay pattern.

How well do available methods quantify the importance of assembly processes in ecological community data: a simulation approach

Ching-Lin Huang[1], David Zelený[1],

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Understanding how different assembly processes influence the species composition and diversity in ecological communities is one of the main goals of community ecology and biogeography. Several methods were proposed to quantify the importance of dispersal and niche assembly processes and were applied widely in systems such as microbial, marine or plant communities. However, only a few studies attempted to compare the methods' performance systematically. As a result, ecologists lack knowledge of how to choose a method suitable to their specific system. In this study, we used a simulation approach to evaluate and compare two available methods: (1) variation partitioning (VP), and (2) dispersal-niche continuum index (DNCI). We used a comprehensive simulation model to generate scenarios with a known proportion of individual assembly processes, namely dispersal and environmental filtering. These scenarios include several metacommunity archetypes, such as species sorting, patch dynamics and neutral theory, and their interfaces. We then applied VP and DNCI to evaluate how well they recover the given proportion of individual processes in each simulated scenario. At our presentation, we will summarize how VP and DNCI methods perform in each archetype and how their performance differs from each other. From a practical perspective, our results highlight the limitations of individual methods and offer more detailed guidelines for applying them.

Inferring Evolutionary Rates in a Geographic Context: Incorporating Region Features

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Current methods for inferring evolutionary rates in a geographic context allow rates of dispersal, extirpation, and speciation (both within and between regions) to vary depending on the set of regions occupied by a lineage. It is hypothesized that the features of these regions may contribute to evolutionary rates. For example, a region's area may impact the rates of speciation and extinction within that region. Also, characteristics of region pairs such as distance or similarity may affect rates of dispersal and speciation between them. However, analyzing the potential effects of numerous features for each region or region pair presents a problem: how can the number of parameters be reduced so that the model is computationally tractable? Here, I present a Feature-Informed GeoSSE model that can be expanded to include numerous potentially-relevant features, allowing for the simultaneous inference of biogeographic history, evolutionary rates, and feature importance. I also apply the model to the South American lizard clade Liolaemidae, analyzing the effects of area, altitude, and distance on evolutionary rates.

How far can I extrapolate my specie distribution model? Comparing established and novel methods

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Species distribution modeling (SDM) is a common tool in biogeography, conservation biology, and ecology and is often used to predict distributions for different regions or periods. However, when the environmental conditions used for prediction are too dissimilar from those used for fitting models, models can extrapolate and predict unreliable habitat suitability values. Here we (i) compared the patterns of analog data within environmental space of widely-used extrapolation evaluation methods (MESS, MOP, and EXDET) and a novel method (SHAPE), and (ii) evaluated their contribution to improving the predictive capability of models outside the calibration conditions. To do so, we used 100 virtual species, which allows for comparisons between model predictions and the species' known fundamental niche. Species suitability values were predicted based on three algorithms (GAM, SVM, and RAF). The species niche and predicted suitability corrected for each extrapolation approach were compared using the RMSE metric. We found that despite MESS, MOP, and EXDET using different calculus to measure extrapolation, all of them detect analog data delimited by an envelope in environmental space. However, SHAPE could delimit complex shapes in environmental spaces that fit the calibration data. In terms of model improvements, we found that all extrapolation methods improved models prediction (i.e., they reduced the RMSE) independent of the algorithm. Previous extrapolation methods presented similar degrees of model improvement. Nevertheless, the versatility of SHAPE may outperform previous methods depending on the algorithm and extrapolation threshold used to assume analog areas.

Using experimentally measured temperature limits of Orthoptera in Bavaria (Germany) to inform a mechanistic range model and predict the impact of future climate change on them

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Mechanistic or process-based models offer greater insights into the future range dynamics for species facing complex threats from climate and land-use changes by focusing on ecological processes that can be applied to non-equilibrium conditions and by generating output which can be important for conservation such as abundance distributions and migration rates. The two limiting factors in the application of these models to real-world system are the computational demand and the data necessary to parameterize them. Taking advantage of data availability for selected species of Orthoptera native to Bavaria (Germany), we present how a spatially explicit, niche-based and metabolic constrained mechanistic model for range dynamics that includes local population dynamics and dispersal between populations can be informed using a combination of publicly available distribution and literature data as well as experimentally measured functional data of the species, including size and temperature limits. Important biological parameters that are considered in the model, as the reproduction rate or the carrying capacity, can be informed by the data while being also influenced by the local environmental conditions in the landscape. Our results indicate that the Alps and to a certain degree also the Bavarian Forest will act as refugia for cold adapted species, while thermophile species may be able to extend their range and metapopulation size if future land use decisions are able to conserve the areas with suitable habitat.

On-demand talks (Neotropical Biogeography)

Bioregions and regional biotic interchanges of New World monkeys

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Here we estimate the direction and timing of regional biotic interchanges of extant and fossil New World monkeys (Platyrrhini). Based on current geographic distribution, we elaborated a bioregional scheme, and then we reconstruct the biogeographic history of the clade. We used recently published platyrrhine phylogenies (n = 116) that explicitly acknowledge that living species and fossils are part of the same macroevolutionary process (FBD). Then we estimated ancestral ranges considering topological and age uncertainty by inferring dispersal and extinction events over a sample of trees from the posterior distribution and by replicating biogeographic stochastic mappings (BSM). We analyzed the most frequent events of dispersal (d) and range-switch (d + e) between source and sink bioregions. Geographic display of bioregions were very congruent with neotropical biomes, and Amazonia was split into western and eastern portions. Western Amazonia (WAM) was the main source of platyrrhine lineages (in situ speciation and origin of dispersal events) and the most frequently events occurred from WAM to Eastern Amazonia (EAM), to Choco (CHO), to Patagonia (PAT) to South Atlantic Forest (SAF) and to Caribbean (CAR). Dispersal events showed very high frequencies during Oligocene/Miocene boundary (~22 Mya); low frequencies during mid-Miocene (~13 Mya) and then a progressively increase until the end of Pliocene (~2 Mya). Dispersals from WAM to PAT occurred during Oligocene-Miocene and they were congruent with the climatically-linked geographic expansion hypothesis. These results demonstrate that several events of dispersal were necessary for species to expand from Western Amazonia towards their current distribution.

On the relationship between environmental suitability and habitat use for three neotropical mammals

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Recent studies have used occupancy models (OM) and ecological niche models (ENM) to provide a better understanding of species distributions at different scales. One of the main ideas underlying the theoretical foundations of both OM and ENM is that they are positively related to abundance: higher occupancy implies higher density and more suitable areas are likely to have more abundant populations. Here, we analyze the relationship between habitat use measured in terms of occupancy probabilities from OM and environmental suitability derived from ENM in three different Neotropical mammal species: Leopardus wiedii, Cuniculus paca, and Dasypus novemcinctus. For ENM we used climatic and vegetation cover variables and implemented a model calibration and selection protocol to select the best models. For OM, we used a single-species, single-season model with site covariates for camera-trap data from six different sites throughout the Neotropical realm. Covariates included vegetation percentage, normalized difference vegetation index (NDVI), normalized difference water index (NDWI), and elevation. For each site, we fit OM using all possible combinations of variables and selected the most competitive ($\Delta AICc < 2$) to build an average occupancy model. We explored relationships between estimated suitability and occupancy values using Spearman correlation analysis. Relationships between ENM and OM tended to be positive for the three Neotropical mammals, but the strength varied among sites, which could be explained by local factors such as site characteristics and conservation status of areas. We conjecture that ENM is suitable to understand spatial patterns at coarser geographic scales because the concept of the niche is about the species as a whole, whereas OM is more relevant to explain the distribution

locally, likely reflecting transient dynamics of populations resulting from many local factors such as community composition and biotic processes.

On-demand (Paleoecology and Paleobiogeography)

"Out-of-India" or "In-to-India" dispersal of tropical flora? Biotic interchange between India and Asia in deep time

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Peninsular India was once the part of the supercontinent Gondwana and got separated from Africa around the mid Jurassic. At the time moving towards the Eurasian plate the Indian subcontinent started drifting away from Madagascar, carrying some of the Gondwanan elements, acting as a bridge for dispersal. A subsequent biotic exchange took place after the collision of the Indian subcontinent with Eurasia pouring the Gondwanan elements into Southeast Asia and Asia referring as "Out-of-India" hypothesis whereas some elements entered into the India from Asia referring as "In-to-India" hypothesis. The fossil records from the India foreshadow the ancient Gondwanan origin of Asian biotic elements that had arrived in Asia by rafting on the Indian plate viz., Alphonsea Hook. f. & Thomson (Annonaceae), Aporosa Blume (Phyllanthaceae), Kleinhovia L. (Malvaceae), Uvaria L. (Annonaceae). Climatic condition during the paleoequatorial position of India was similar to current perhumid climatic conditions of Southeast Asia suggesting strong dispersal in both directions. However, sparse fossil records from the Southeast Asian region emphasizing the fact that none of the main angiosperm families that characterize the region today actually evolved in that area. Therefore, suggesting the origin of most of the Southeast Asian taxa had occurred outside Asia indicating their ancestral lineages having Gondwanan origin.

Ancient DNA of narrow-headed voles reveals common features of Late Pleistocene population dynamics in cold-adapted small mammals.

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Narrow-headed voles, alongside collared lemmings, were the most important small mammal species of steppe-tundra environments during the Late Pleistocene. Previous ancient DNA studies of the latter revealed a very dynamic past population history shaped by climatic fluctuations. To compare the Late Pleistocene history of these two species we generated a dataset comprising mitochondrial genomes of 139 ancient and 6 modern narrow-headed voles from multiple sites across Europe and Western Asia and covering last ca. 100 thousand years (ka). We applied molecular dating approach to estimate the age of undated specimens by inferring Bayesian time-aware phylogenies with the ages of the radiocarbon dated samples used for the molecular clock calibration. We estimated the divergence time of European and Asiatic narrow-headed voles to ca. 240 ka ago, during Marine Isotope Stage (MIS) 7, very similar to the published divergence time of Palearctic and Nearctic collared lemmings. Further diversification within each lineage took place around 100 ka ago suggesting the impact of MIS 5 warming on the narrow-headed vole populations. In Europe we identified multiple time structured mtDNA lineages, implying multiple population turnovers. Timing of some of this turnover was synchronous with those of collared lemmings allowing us to identify periods which had wider impact on Late Pleistocene ecosystems.

Gondwanan origin of Dipterocarpaceae and the rise of lowland rainforests of Southeast Asia

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The origin, speciation and dispersal of plant family Dipterocarpaceae is important to understand the rise of Dipterocarp lowland rainforest of SE Asia. The scant deep time record of the family has been a limitation to comprehend its complete evolutionary history and palaeobiogeography. The present study describes Dipterocarpus type pollen from the Maastrichtian of Sudan and eight pollen types referable to extant genera, Dipterocarpus, Dryobalanops, Monotes, Shorea, Vatica and Vateriopsis, of Dipterocarpaceae, from the Paleocene-Eocene of India. The morphological character matrix of the eight fossil types and 64 extant pollen of different species of Dipterocarpaceae were examined based on light microscopy, scanning electron microscopy and confocal laser scanning microscopy. The morphological data together with the DNA sequences of 309 extant species of Dipterocarpaceae was analysed under a phylogenetic framework in order to evaluate the divergence age estimates and ancestral areas of the family. The study suggests that the family originated in tropical Africa during the mid-Cretaceous (~102.9 Ma) and probably evolved as an adaptation to changing climatic state (semi-arid to perhumid) of the Late Cretaceous. The representatives of the family dispersed to India during the early Maastrichtian (~70 Ma) via Kohistan/Ladakh Island Arc, ascertaining the presence of an ephemeral land connection between the two landmasses. The study further suggests the dispersal of dipterocarps from India to similar climatic zones in Southeast Asia. Overall, our study provides the first reliable evidence for the west Gondwanan origin of the family and “Out-of-India” biogeographic hypothesis for the dispersal of dipterocarps to Southeast Asia.

Re-examining moisture balance control of forest-grassland boundaries in North America

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Moisture balance is generally believed to control forest-grassland boundaries, but wind-spread fire may have defined the Great Plains grasslands of central North America. I re-examined moisture balance control of forest-grassland boundaries, by modeling 17 precipitation and potential evapotranspiration variables at 1 km spatial resolution, along with wind speed as a proxy for the alternative fire option, to determine comprehensible class rules with the C5.0 classifier that differentiate the North American Great Plains grasslands from surrounding regions, as an in-depth extension of previous work. Potential evapotranspiration variables were more influential than precipitation variables and wind speed was more influential than potential evapotranspiration variables. Mapped grasslands following class rules for potential evapotranspiration and precipitation variables demonstrated major extensions of grasslands across the western or eastern U.S., Canada, or Mexico. In contrast, commission error for the grassland rule of >3.99 m s-1 and <=6.38 m s-1 wind speed resulted in modest extension of the Prairie Peninsula into eastern forests. These results helped establish the robustness of wind speed, as a proxy for fire spread, to delineate Great Plains grasslands as opposed to moisture control, although an unidentified climate moisture index or systematic weather pattern may better define the Great Plains.

Taxonomic composition, and biochronologic framework of Tragulidae from the Napak region

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Chevrotains or mousedeer (Tragulidae) are non-pecoran ruminant artiodactyls that nowadays live in two distinct areas in central Africa (Hyemoschus) and South plus Southeast Asia (Moschiola, Tragulus). In the fossil record, they have been reported to appear much more widely on both continents and in addition Europe. However, the palaeobiography of tragulids is still far from being revealed. Debatable taxonomy accompanied with limited data and biochronological controversies hamper the reconstruction of tragulid evolution. This study provides a revision of the taxonomy of tragulids from the late Early Miocene (ca. 20.5 Ma) to early Middle Miocene (ca. 16 Ma) sites of Napak in Uganda, which have yielded one of the oldest records of ruminants on the African continent. Dental morphometric analysis indicates the presence of three Dorcatherium species including the bunoselenodont Dorcatherium iririensis, Dorcatherium chappuisi and the selendont Dorcatherium n. sp. All the Dorcatherium species exclusively appear in the lithostratigraphical Napak Member (ca. 20-19Ma) followed by an extinction. Further documentation includes three small sized selenodont species: Siamotragulus songhorensis, Siamotragulus n. sp., and the very small sized selenodont Siamotragulus aff. songhorensis. Siamotragulus songhorensis occurs in the strata of the successive lithostratigraphical Iriri Member (ca. 20.5), Napak Member (ca. 20-19Ma), and Akisim (ca.16Ma) Member. The very small Siamotragulus aff. songhorensis spans the Iriri Member to Napak Member.

Trinidad and Tobago (Caribbean-South American) geogenomics: reconciling and synthesizing published genetics data into a comprehensive geologic, paleogeographic, and geomorphic model

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Geogenomics is an emerging field that links genetics and genetic clocks of key biota to geology, paleogeography, and landscape development. Over the past several decades, detailed genetic studies have been published for many endemic and cosmopolitan extant species (n = # of species) on the Caribbean islands of Trinidad (a continental island) and Tobago (an oceanic island) near mainland South America. These include studies on freshwater guppies (1), frogs (5), snakes (6), toads (1), lizards (1), and mammals (1) in this archipelago. These case studies link in time (genetic clocks) and space (paleogeography) evolutionary and paleogeographic events in the archipelago to those in mainland South America. We synthesize and assemble the Cenozoic- Recent geology including, tectonics, paleoclimate, and landscape development in the archipelago and on the mainland into a comprehensive geological model that highlights key geological events (e.g., rise and fall of the coastal Cordillera, rise of the Andes, inception and deflection of Orinoco River, STEP fault migration, glacial and interglacial sea level change, inception of Gulf of Cariaco and Gulf of Paria pull-apart basins, etc.). We synthesize the key published genetic (e.g., divergence, vicariance, common ancestor, etc.) events into this geological framework for the: Holocene-Pleistocene, Pliocene, and Miocene. Highlights to-date include: 1) A link in Trinidad between Holocene-Pleistocene differential coastal cordillera sinking and rising, headward stream erosion during glacial low stands, and a major discontinuity in freshwater guppy (Poecilia reticulata) genetics. 2) Symmetric sinking of Trinidad and Venezuela's coastal mountains into the intervening Gulf of Paria pull-apart to isolate (on Cerro Humo, Paria, Venezuela; El Tucuche- Cerro del Aripo, Northern Range, Trinidad)

amphibian subpopulations into two separate gene pools. 3) Common snake ancestors that reach back into the Miocene and variably migrated to the islands.

Taxonomic and Functional Beta Diversity of North American Mammal Paleocommunities are Decoupled Across the Cenozoic

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Taxonomic beta diversity has been widely used to examine the spatial structure of mammalian communities. More recently, functional beta diversity, a taxon-free approach, uses traits to more directly evaluate how ecosystem functioning varies across space. Taxonomic and functional beta diversity are often decoupled at local scales in the modern, but not consistently. Furthermore, changes in spatial structure in response to climate over time are not well understood. The North American fossil record of mammals over the last 65 million years encompasses several major environmental and ecological events making it an ideal system to evaluate functional beta diversity of mammals on a geologic timescale. We compiled 237 mammal paleocommunities spanning the Cenozoic. Functional diversity was calculated using four traits that are reflected in morphology: locomotion, body mass, life habit and diet. Paleocommunities were binned into 5-million year intervals to calculate functional and taxonomic beta diversity using a pairwise approach. In order to determine if the results were affected by the arbitrarily chosen bins, we employed a sliding window approach and adjusted bins by 1-million years. A breakpoint analysis was used to identify significant shifts in beta diversity. Functional and taxonomic beta diversity of mammal communities are decoupled over the Cenozoic. The Paleocene has high functional diversity and low taxonomic diversity suggesting differences in community assembly during this time. In addition, major shifts in functional beta diversity occurred during the early Eocene and mid-Miocene. This study provides important information on how abiotic and biotic factors can influence mammal paleocommunity spatial structure through time.

FAMM: A database of Fossil Arctic Marine Mammals for use in Pattern-Oriented Modeling

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The Arctic is currently experiencing the greatest amount of warming on Earth. The effects of this climatic change and associated loss of permanent summer sea ice threatens the diets and population structure of many Arctic native marine mammals. Future warming is projected to continue at even a faster rate, highlighting a need for more informed conservation strategies to safeguard this fragile ecosystems from future harm. However, future projections alone are insufficient for characterizing the vulnerability of species to future abrupt climate change. To better characterize how Arctic marine mammalian megafauna respond to abrupt climate change, we can use information from the recent fossil record to inform our understanding of climate-driven range and extinction dynamics. Here we present FAMM, a fossil database of 11 species of Arctic marine mammals (including seals, walrus, cetaceans, and polar bears). The database includes information about locality, taphonomy, age of occurrence, dietary information from stable isotopes, and genetic patterns from ancientDNA. These inferences of past species range dynamics can be used in statistical and process-explicit models to better understand ecological responses of Arctic megafauna to climate change.

Volcanism and Rodent Evolution: hypotheses and results from a workshop.

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Terrestrial biodiversity is higher in topographically complex regions than in low relief ones; this diversity evolved over millions of years along elevation gradients with disequilibrium of climatic conditions and biological interactions. The mountainous complex is heterogeneous, consisting of orogenic and volcanic mountains with different geological and climatic features. However, there is not investigation whether ecosystem or faunal evolution may have a particular influence due to a volcanic environment. Rodents are an excellent model to explore these questions because they are the most speciose clade of mammals and many species live in montane regions. Hypotheses and ideas were discussed during the Workshop on Volcanism and Rodent Evolution organized by the Research Group “Mammal diversification about dynamic landscapes of the North American Rodents Landscapes, Evolution & Ecology”. This meeting discussed rodent evolution in two North American volcanic provinces-- Basin and Range and Trans-Mexican Volcanic Belt. Workshop consisted of three modules: 1) origin and evolution of volcanic provinces of North America; 2) current ecosystems in volcanic provinces, with emphasis on faunal diversity; 3) rodent fauna paleontology in volcanic provinces of North America. Multidisciplinary group of geologists, biologists, and paleontologists discussed how speciation, endemism, extinction, geographic-range shifts, environmental sorting, and sky-island processes have shaped the diversity of rodents in volcanic regions.

On-demand talks (Phylogeography)

A time−calibrated multi−gene phylogeny of key groups of aquatic insects for assessing global patterns of phylogenetic diversity

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Aquatic insects are a highly diverse group of freshwater invertebrates with unique features and adaptations, thereby allowing answering comparative questions in ecology and biogeography. However, until now, the lack of a global molecular phylogenetic reconstruction with the potential to connect deep–time and present–day ecological mechanisms has precluded macroecological and eco–evolutionary questions for most groups of aquatic insects at broad scales. Here, we present the first global and well–supported phylogenetic analyses for monophyletic and mostly aquatic lineages of dragonflies and damselflies (Odonata), mayflies (Ephemeroptera), stoneflies (Plecoptera) and caddisflies (Trichoptera). Among various potential applications of these phylogenies, our strategy in the context of the ongoing GloBioTrends Project (https://www.largescaleecologylab.net/), comprising more than 50 collaborators worldwide, is to date phylogenetic trees based on available molecular and fossil information, and then use harmonised, fine–resolution community data to determine the eco–evolutionary mechanisms that generate and maintain stream insect biodiversity across the globe and at different spatial scales. After downloading sequences from GenBank for 9 independent gene portions (i.e., mitochondrial COI, 12S rRNA, 16S rRNA, nuclear small subunit 18S rRNA, 28S rRNA, Histone H3, EF–1α, RNA Pol II, and the protein–coding CAD) and correcting for nucleotide composition bias in protein–coding genes, our combination of best–scoring likelihood, Bayesian and quartet sampling routines revealed consistent and robust subordinal and familiar relationships, producing statistically congruent results and resolving previously controversial phylogenetic relationships. Overall, our dataset is the most phylogenetically diverse and taxonomically comprehensive reconstruction of aquatic insect evolution to date, comprising more than 1,200 genera and 127 recognised families.

Genome-wide SNP data unraveled phylogeography and cryptic divergence of living fossil coral across the Indo-West Pacific

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Species delimitation of corals is one of the most challenging issues in coral reef ecology and conservation. Morphology can obscure evolutionary relationships, and molecular datasets sometimes reveal greater within-species diversity than currently understood. Most phylogenetic studies, however, have examined narrow geographic areas and phylogeographic analysis covering a wider geographic range is required to obtain more robust interpretations of within- and among- species relationships. In the case of blue corals Heliopora, there are currently two valid species (H. coerulea and H. hiberniana) as evidenced by integrated genetic and morphological analyses in northwestern Australia. There are also two distinct genetic lineages of H. coerulea in the Kuroshio Current region that are morphologically and reproductively different from each other. To obtain a more complete picture of phylogeographic patterns within the genus Heliopora, we applied genome-wide analysis on > 1287 colonies across the Indo-West Pacific. Maximum likelihood phylogenetic trees indicated the examined Heliopora samples comprise three genetically distinct groups: H. coerulea group, H. hiberniana group, and a new undescribed Heliopora sp. group with further subdivisions within each group. Geographic structuring is evident among the three species with H. hiberniana group found in the Indo-Malay Archipelago and biased toward the Indian Ocean whilst Heliopora sp. was only found in the Kuroshio Current region and Singapore, indicating that allopatric speciation with different geographic origins across the Indo-West Pacific. Heliopora coerulea has a wider distribution both the Indian and western Pacific, being partially overlapped with other two groups. The different Heliopora groups and subclades in sympatric habitat had reproductive isolation or physiological differences, suggesting that allochronic and ecological divergences are possibly associated with species boundaries and speciation of blue corals.

Podocarpus in the palaeogeographically complex island of Hispaniola: a stepping-stone colonization and conservation recommendations

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Hispaniola is the second largest island in the Caribbean and a hotspot of biodiversity. The island was formed by the fusion of a northern and southern palaeo-islands during the mid-Miocene (15 Ma). The historical split of Hispaniola together with repeated marine incursions during the Pleistocene are known to have influenced lineage divergence and genetic structure in animals, but the effect on vascular plants is less understood. The conifer genus Podocarpus has two species, P. hispaniolensis and P. buchii, that are endemic to the mountains of Hispaniola (both IUCN endangered). The former occurs in the mountains of the north, and the latter in the south, with a region of sympatry in the Cordillera Central. Here we evaluate the historical split of the two palaeo-islands, and repeated marine incursions as dispersal barriers to the geographical distribution of genetic diversity, genetic structure, divergence patterns, and the historical demography of the two species. We used genotyping-by-sequencing in 47 Podocarpus samples and conducted a phylogenetic and an approximate Bayesian computation analysis to test different evolutionary hypotheses. Podocarpus showed a population genetic structure that corresponds to the geographic distribution of the species and fit a stepping-stone colonization model with bottlenecks at each mountain colonization event, and speciation in Cordillera Central. Our results suggest that Podocarpus seems to have been influenced by the current geographic barriers, rather than by the historical events. The clear divergence between species together with the elevated within-population genetic diversity and significant genetic structure call for a multi-population in situ conservation of each species.

Geomagnetic reversals and speciation in marine gastropods

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The phylogenetic divergence databases of littorinid and conid gastropods (http://www.timetree.org/) are analyzed and compared with the dates when the Earth's polarity changes occurred. From the comparative analysis, it is observed that the dates at which the taxa diverged partially agree with the dates at which the polarity changes occurred. Of the 184 littorinid species, the formation of 91 species is probably associated with polarity changes within 0 ≥100,000 years of the geomagnetic reversal. These species, which correspond to 49.45 % of the total, were probably formed by mutation derived from a higher incidence of cosmic radiation and from the solar wind, as the atmosphere thinned due to the decrease in the Earth's magnetic field. Of this group, 58 species (31.52 %) originated in the interval from 0 ≥50,000 years after the reversal occurred; the remaining 33 species (17.93 %) presumably originated between 50,000 ≥100,000 years after the polarity change occurred. The remaining 93 species (50.54 %) are those that formed not associated with reversals. In the conid gastropods, species probably associated with geomagnetic reversals within the + 0 ≥100,000-year range constitute 74.57 %. Of this group, 36 are associated with the 0 ≥50,000-year interval. When considering littorinid and conid species as a whole, that species likely to be associated with reversals in the 0 to 100,000 interval is over 55%. This is the first study to document a probable effect of polarity changes promoting or inducing speciation by mutation. This concordance between genetic and polarity chron data is likely to be the "imprint" or record of the history of the Earth's geomagnetic reversals in species' genome.

On-demand talks (Species Distributions)

Biogeography of Monopelopia Fittkau, 1962 (Chironomidae: Tanypodinae)

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Fittkau, 1962, established the genus Monopelopia as a member of the tribe Pentaneurini. He (1962) described the genus Monopelopia from the Holarctic area. The genus is divided into two subgenera Cantopelopia Roback, 1971 and Monopelopia s.str. (Cranston & Epler 2013; Silva & Ekrem 2016). According to the Chironomidae world catalogue (Ashe & O'Connor 2009), this genus comprises 11 species; however, Oliveira et al. (2010) and Dantas & Hamada (2012) described six new species from the Neotropical region (2017). Additionally, two new species from the Oriental region were found (Paul et al. 2014; Duan et al. 2021). Worldwide, a total of 19 species have been described (15 belonging to Monopelopia s.str. and 4 to Cantopelopia). In India, just three species have been discovered thus far. The genus has been categorised into two categories based on their habitats, phytotelm species and non-phytotelm species. Several tanypod specimens were collected in West Bengal's deep forested areas with deciduous foliage and Himalayan foothills. A molecular phylogeny for the genus Monopelopia was constructed using around 15 cytochrome oxidase I data from GenBank. The biogeography was deduced from the phylogeny, which was performed using the MEGA X software with the Maximum Likelihood approach and the GTR+G+I model. Additionally, a cladistic analysis including all 21 species was conducted utilising morphological data from both pre- and post-imaginal stages. The biogeography of Monopelopia was deduced using both morphological and genetic data.

Biogeography of Oriental species of Polypedilum Kieffer, 1912 (Diptera: Chironomidae)

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Polypedilum Kieffer, 1912, one of the most speciose genera in the Chironominae subfamily, comprising nine subgenera (Lin et al. 2019) has a worldwide range, found in all zoogeographical areas except Antarctica. Polypedilum larvae are found primarily in shallow, eutrophic waterways, with certain species tolerant to contaminated conditions (Armitage et al. 1995; Pornichu & MacDonald 2003). The male of the genus Polypedilum can be distinguished by the presence of a basally constricted eighth abdominal tergite and longitudinally divided pulvilli (Sæther et al. 2010). Studies on the systematics and biogeography of Polypedilum midges are not adequate. To date, 150 species of seven subgenera have been recorded from the Oriental region, including Atopipedilum Yamamoto, Yamamoto & Hirowatari, Cerobregma Sæther & Sundal, Pentapedilum Kieffer, Polypedilum s. str., Tripodura Townes, Uresipedilum Oyewo & Sæther, and Probolum Andersen & Sæther (Hazra et al. 2016). In India, 36 species belonging to only three subgenera have been reported (Mukherjee et al. 2020). Seven species of the subgenus Cerobregma have been described from the Oriental China and Japan. Around 70 to 65 million years ago, the Indian plate, a part of Gondwana supercontinent, moved north wards and collided with the Asian plate, resulting in the development of the great Himalayan mountain range. The formation of mountain ranges created a land bridge connecting the Palaearctic and Oriental regions. Overall the fauna of Oriental realm is an admixture of autochthonous Oriental forms supplemented by frequent Afrotropical, Australasia, and Palaearctic elements.

Butterfly Communities in China: Distribution, Diversity, and Environmental Correlates

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Abstract: The development and utilization of indicator organisms for biodiversity monitoring is one of the focuses of nature conservation. Butterflies are often used as indicator taxa. They have wide range of distributions and flourishing species diversity. In addition, they are easy to be observed and sensitive to environmental changes. The temporal and spatial dynamics of butterfly populations and the evolution of community structural characteristics can quickly and effectively mirror various ecological and environmental conditions such as environmental quality and human activity interference. Diversity observation data of the species is widely utilized in biodiversity monitoring and environmental quality assessment. This study summarized the butterfly species resources in different regions of China, and analyzed the butterfly communities and species diversity characteristics. Based on biodiversity theories and analytical models, we aimed to summarize the species data of butterflies and reveal environmental factors driving butterfly communities. The results can provide a theoretical basis for the conservation and sustainable use of butterfly species, and offer the basic data for China's ecological environment monitoring.

Diversity of wasp species (Hymenoptera: Vespidae) from the Hazara Region, Pakistan

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The present study describes the fauna of vespid wasp species found in the Hazara region of Northern Pakistan. The investigation was based on morphological characteristics. Morphological identification of 4500 samples was carried out, which represented 19 species from 3 sabfamilies including: subfamily Eumeninae: six species, Polistinae: six species and Vespinae: seven species. Among the identified samples, nine species: Delta conoideum D. esuriens, Anterhynchium abdominale bengalense, Rhynchum qunquecinctum, Antodynours flavesens, Ropalidia brevita, P. olivaceus, P. stigma and V. mandarinia are new for Hazara region during 2011-2013.

Estimating the fundamental climatic niche of species with occurrence data, physiological tolerances and accessible areas

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The fundamental niche of a species is the set of environmental conditions that allow the species to survive in the absence of biotic interactions and dispersal limitations. Estimating the center (i.e., the optimal environmental conditions for the species) and the extent of the fundamental niche is of great importance when the fitted models are used to predict the effects of climate change on the geographic distribution of the species. However, most of the existing approaches to estimate niches use occurrence samples that are biased, and often fit models that are not a biologically realistic representation of the fundamental niche' border. Occurrence samples come from the realized niche (a subset of the fundamental niche that includes biotic interactions and dispersal limitations) and may not represent the full environmental potentiality of a species; samples may be biased towards well-represented regions of niche space. I will present two new models to estimate the fundamental niche of a species that use occurrence data and assume a simple, biologically realistic shape for the fundamental niche. I will show how to incorporate known tolerance ranges for the species into the models and how to account for environmental biases in the samples.

Old Messinian modelled landscape still shapes the distribution of short-lived Mediterranean grasses

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The current distribution of Mediterranean plants is the result of entangled ancient and modern ecological and geological processes. Processes during the Miocene Age (23-5.33 Mya) played a key role in the diversification and the evolutionary trajectory of organisms. The initial cool temperature stages in this Age, coupled with events such as the Messinian Salinity Crisis, including the dissecation of the Mediterranean Sea and the opening of the Gibraltar Strait, followed by the onset of the Mediterranean climate, and the Quaternary glacial and interglacial periods, shaped dramatically the current species composition of the Mediterranean region.
To evaluate the effect of landscape features as the Strait of Gibraltar or the older Messinian Betic corridor (currently the Guadalquivir Valley) we used as a model the genus Aira L., which is a relatively small genus including c.12 taxa within the tribe Poeae, subtribe Airinae within the large Poaceae family. The genus Aira diversified across the Mediterranean Basin, and includes only slender, short-lived annual plants, which are usually occurs in dry pastures. The species concept for Aira has been the object of controversy. In order to understand taxa relationships in this species complex, and the impact of the biogeographical barriers in the distribution of Aira, we applied molecular markers (plastid and nuclear), and analysed morphological characters in Aira taxa found in the west Mediterranean. Therefore, because of an exhaustive review, two new taxa have been distinguished in the Iberian Peninsula and Balearic Islands, and their speciation processes are discussed.

Soil effects on plant distributions and migration in Eastern North America

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Many plant species are supposed to migrate to higher latitudes in response to climate warming. Species distribution model (SDM) has been widely used to quantify species future suitable habitats and extinction risks. Although soil properties can change greatly along latitudes, most of previous SDM studies have neglected soil properties in their models, which can lead errors when modelling species-environmental relationships and projecting species' future suitable habitats. In this study, by building two SDMs - one only with climate predictors (SDMclimate) and one with both climate and soil predictors (SDMsc) - for 1870 plant species in Eastern North America (ENA), we investigate the relative importance of soil properties in determining plant distributions at a continental scale and potential soil effects on plant migration under climate change. We found that although lower than the importance of climate predictors (mean relative importance = 0.573), soil properties still had non-negligible influences on the plant distributions at a continental scale (mean relative importance = 0.369). Meanwhile, SDMsc predicted much less changes in plant latitudinal distributions under climate change than SDMclimate, suggesting that high-latitude soils may impede ongoing plant migration. Our findings highlight the necessity of incorporating soil properties when modelling plant distributions and migration.

The animals of the concrete jungle: urban fauna of the Metropolitan Region of São Paulo, Brazil

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The Metropolitan Region of São Paulo (São Paulo State, Brazil) is one of the largest metropolitan regions in the world and its growth in the Atlantic Forest area changed its natural landscape into a cultural landscape. This region presents native flora and fauna and species that were introduced for different cultural reasons. The first step in the urban biogeographic study is to identify areas where both plants and animals are located. Since 2010, an educational project has been developed with students from the discipline of Biogeography, undergraduate degree in Geography, from the Department of Geography, from the Faculty of Philosophy, Letters and Human Sciences University of São Paulo, to obtain the location and identification of species found in the neighborhood of your home. In 11 years, 571 students participated and 266 species of 126 zoological families of annelid, molluscs, fish, crustaceans, chilopod, diplopod, arachnids, insects, amphibians, reptiles and mammals have already been identified and registered. Of the total, 29% of the species are exotic, 71% are Brazilian. The largest number of species belongs to the class of birds.
Keywords: urban fauna, urban biogeography, education, urban cartography, Brazil

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What controls species distributions? A demographic test and a new hypothesis

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Estimates of the percentage of species “committed to extinction” by climate change range from 15% to 37%. The question is whether factors other than climate need to be included in models predicting species’ range change. We created demographic range models that include climate vs. climate-plus-competition, evaluating their influence on the geographic distribution of Pinus edulis, a pine endemic to the semiarid southwestern U.S. Analyses of data on 23,426 trees in 1,941 forest inventory plots support the inclusion of competition in range models. However, climate and competition together only partially explain this species’ distribution. Instead, the evidence suggests that climate affects other range-limiting processes, including landscape-scale, spatial processes such as disturbances and antagonistic biotic interactions. Complex effects of climate on species distributions - through indirect effects, interactions, and feedbacks - are likely to cause sudden changes in abundance and distribution that are not predictable from a climate-only perspective.

Dissonance in predictions from species distribution models and pollen density models across the previous 21,000 years

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Historic shifts in species’ distributions reveal telling factors of their response to climate change. Ecological niche models (ENMs) are used to represent habitat suitability for a species in response to climate variables. Pollen density models (PDMs) use fossil pollen data to estimate spatiotemporal patterns of species abundance around lakes. Here, we compare the ENMs and PDMs of trees in the genus Fraxinus in their ability to predict past glacial refugia and rates of migration in North America since 21 Kybp. Specifically, we constructed individual ENMs for common species in Fraxinus and compared the output to a PDM at the genus level. Our PDM predicted the glacial refugia distribution along a north-south axis, aligning with the Mississippi River Valley up to the Great Lakes, with a disjunct portion in the southern part of the Florida peninsula. The ENMs for individual species were different from the output from the pollen model. For example, in the last glacial maximum, green ash was predicted to have had a large southern refuge oriented in an east-west direction. Additionally, Fraxinus’ rate of migration predicted by the PDM was greater than the rate of migration of some individual species modeled with ENMs. While both of these methods are often used independently to reconstruct species’ biogeographic histories, this comparison shows that they produce varying results. Each of these data types have their own strengths and weaknesses, thus an integration of these techniques combining pollen and occurrence data could harness the most robust results.

POSTERS (GROUPED BY CATEGORY)

Poster (Biodiversity Patterns & Maintenance)

Area vs. Environmental Heterogeneity: Scale-Dependence in Simulations

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Area and environmental variation are entwined in explanations of diversity. A simulation model may separate the shared contributions of area and environmental heterogeneity to the diversity of regions. We parameterized a composite gradient of environmental heterogeneity using climate, soils, and topographic data from alpine grasslands in 23 ranges of southern Europe. The grassland area was identified within above-treeline delineations using NDVI from Landsat. The environmental gradient was initialized on a simulation grid in a fractal pattern; cells represented the total area of each range with random cells excluded to leave grassland area. 100 virtual species were distributed to cells based on Gaussian responses to the gradient. Reproduction and mortality were iterated in Monte Carlo procedures. Diversity across the simulated ranges was correlated with their observed patterns. Simulation experiments were run with 6 levels of grid size, 3 of heterogeneity, and 3 of a limit on individuals per cell. Area was defined as the product of the number of cells and the limit to account for resolution. The variance in gamma diversity was explained more by area per se in small areas and by environmental heterogeneity across large areas. This scale-dependence may have sustained ambiguity in area and heterogeneity explanations ever since the Theory of Island Biogeography.

Arkansas Pimple Mounds as a Study System to Test How Plant Community Assembly Mechanisms Change across a Landscape.

Ben Benton[1,] Scott Mangan[1,] Travis Marsico,

[1] Arkansas State University

Understanding why plant community composition changes across the landscape is key to effective habitat conservation and restoration. Traditionally, competition for resources such as soil nutrients and water has been used to explain plant community assemblage; however, there is mounting evidence that demonstrates that pathogenic and mutualistic soil microbes also serve as strong forces to plant community assembly. However, the extent to which differing landscape features shift the relative importance of these two community assembly mechanisms is poorly understood. Pimple mounds of southwest Arkansas provide an ideal system to investigate the relative roles of biotic and abiotic soil factors to community assembly. These one-meter-tall relic dunes create islands of drier, sandier soil compared to the surrounding landscape and harbor unique vegetation that differs from the surrounding prairie. The goal of this study was to provide the first known characterization of the soil microbial communities and soil nutrient profiles of pimple mounds at Cherokee Prairie Natural Area. Soil samples collected from the mounds were used to compare soil nutrients and mycorrhizal fungal abundance with those collected from surrounding prairie matrix. These baseline data will be used as a first step to gaining insights about how nutrients and mycorrhizae interact with plants and how they combine to serve as regulating mechanisms for plant communities.

Bayesian biogeographic analysis of squirrel evolution suggests and Asian origin

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Squirrels have an incredibly diverse lineage with a global distribution and have dispersed over millions of years from a common ancestor approximately 40-50 MYA. The assumption since the 1980's has been that squirrels originated in North America and evolved from North American tree squirrels about 34-39 MYA, but in a more recent study, the oldest giant flying squirrel fossil was found in Oregon, suggesting a possible eastward immigration from Asia. This study made us question the previously accepted hypothesis that squirrels originated in North America and led to an exploration of squirrel evolution and origins. We used an R package called BiogeoBEARS with Bayesian biogeographic analysis and a DEC+J model to get a better picture of where squirrels were located at different points in their evolution. To run this analysis, we input a phylogenetic tree file, representing 225 modern Sciuridae species, and a biogeography file with each of their locations sorted into eight regions. Our analysis resulted in a few noteworthy findings regarding major biogeography changes and their timing: (1) we believe that squirrels originated in Asia, (2) North American and Southern African squirrels came from Asia, and (3) we found one long South American branch, genetically distant from all other South American Sciuridae species and stemming from near the oldest common squirrel ancestor, leading to just one species, Sciurillus pusillus, a modern species that has resided in South America for about 37 Myr.

Complex structure creates complex communities: How 3D vegetation drives understudied patterns in avian communities.

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Understanding how habitat structure relates to patterns of biodiversity is key to predicting how anthropogenic changes to habitat structure might affect species and community level patterns in the future. Most studies to date have examined the impacts of habitat configuration on biodiversity in 2-D. Recent increase in the availability of LiDAR data have enabled large-scale assessments of the relationship between 3-D vegetation structure and biodiversity, but most studies remain focused on simplistic metrics of vegetative structure (i.e., canopy height) and biodiversity measures (i.e., species richness). These metrics, however, might not fully capture how internal configuration and composition of vegetation drive diversity of different avian functional groups that take advantage of different parts of vertical and horizonal niche space. Thus, there is a gap in the research to compare more complex measures of vegetation structure to measures of functional diversity, such as functional richness, evenness, and divergence. Using organismal and LiDAR data from the National Ecological Observatory Network (NEON), we examine associations of species richness and functional and trait diversity with different aspects of vegetation structure. Using distance sampling methods and hierarchical Bayesian modeling framework to account for species' imperfect detection, we estimate the relative influences of vegetative structure, along with other environmental factors (temperature, precipitation, elevation, latitude), on avian diversity. We find that avian functional diversity is strongly predicted by 3-D measures of composition and configuration of vegetation. Our results help elucidate the relative influence of 3-D forest arrangement and volume on comparatively understudied measures of biodiversity.

Global drivers of mountain plant biodiversity

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Large databases and natural history collections have shown that plant diversity varies greatly across the mountain ranges of the world. It is generally known that geological, climatic, and environmental variables jointly influence the global and regional plant species richness. Yet, their relative influence across different mountain systems of the globe have not yet been comprehensively disentangled. Only few studies have evaluated multiple competing hypotheses and the complex interplay of the different processes. A general lack of available data on vascular plants in mountains has long prevented a robust characterization of variations and evolutionary origins of the global mountain plant diversity. As a consequence, there is no consensus on the processes involved in the assembly and maintenance of plant biodiversity across different mountain systems. In order to detect general and specific plant biodiversity patterns, we selected six mountain systems across six continents to study the relative influence of different biodiversity drivers. The selected ranges in this project include: the Central Rockies, the Northern Andes, the Alps, Eastern Madagascar, the Hengduan Mountains, and the South Island of New Zealand. By integrating multiple data sources and a novel downscaling approach, the plant species distribution is mapped at a 1 km spatial resolution for each mountain region. Phylogenetic metrics, geological, climatic and other environmental drivers hypothesized to be relevant for shaping species richness of plants within and among mountains are assessed with regards to their relative contribution. The importance of these factors was ranked both regionally and globally, shedding light on mountain plant diversity.

Influence of seasonal flooding on plant reproductive phenology on Buck Island, a Lower Mississippi River island

Caity Sims[1], Grace McCartha[1], Brendan Kosnik, Mathew Jones[1], Ben Benton[1], Scott Mangan[1], Travis Marsico[1],

[1] Arkansas State University

Plant reproductive phenology is sensitive to environmental factors such as temperature, precipitation, soil moisture, nutrient availability, light duration, and flooding. The influence of flooding on reproductive fitness is understudied in temperate systems. The Mississippi River experiences an annual flood cycle and islands in the Lower Mississippi River are subjected to higher river levels in the winter and spring, which may inundate entire islands or leave only the highest island elevations unflooded. We hypothesize that (1) plants at lower elevations that experience longer periods of flooding have later average peak flowering and fruiting periods compared to plants at higher elevations and (2) plants at higher elevations will produce more fruits than plants at lower elevations (i.e., have higher fecundity) due to a longer reproductive season. In spring, summer, and fall 2021, six native, herbaceous dicot species were monitored on Buck Island Wildlife Management Area, outside of Helena-West Helena, Arkansas. Patches were established throughout the elevation gradient of the island and in areas of the same habitat type and elevation. The number of reproductive structures in a phenophase (e.g., flower buds, open flowers, developing fruits) were counted twice per week on individually marked and tracked plants, and mature fruits were collected for all tracked individuals. As of October 11, 2021, 502 individual plants were tracked in 61 habitat patches ranging in elevation from 54-60 m. The three annual plant species have a wider elevation range than the 3 perennial species, and the annuals are more strongly shifted in peak flower and fruit phenology.

On modeling susceptibility of host parasite interactions through machine learning from only presence data.

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Understanding what pathogens and diseases can be transmitted across taxa and the specific geographic locations where these may occur is relevant for several purposes, including wildlife management, human risk, emerging infectious diseases. The likelihood of susceptibility to different pathogenic taxa among hosts of different taxonomic groups can be influenced by their geographic, environmental, and phylogenetic context, which relative importance changes depending on the epidemiological system. Here we used machine learning to analyze how such variables influence pathogen incidence for multi-host pathogen assemblages, including one of direct transmission (coronaviruses and bats), and two vector-borne systems (West Nile Virus and birds; avian malaria and birds). We show that this methodology is able to provide reliable global spatial susceptibility predictions for the studied host-parasite systems, even when using a small amount of incidence information (i.e., $<$ 20\% of information in a database). We found that avian malaria was mostly affected by environmental factors and by an interaction between phylogeny and geography, WNV susceptibility was equally affected by environment, phylogeny and by interactions between geography and phylogeny, whereas coronaviruses' susceptibility was mostly affected by geography. We provide maps that summarize the geographic locations where these interactions are more likely to occur, and use empirical data to measure accuracy of our models. Our analysis demonstrates that incidence of different host-pathogen systems can be predicted at global scales with high accuracy, as corroborated by independent test data. The predicted hotspots of these pathogenic interactions could be used as proxies to conduct field work and testing under different biodiversity dimensions (i.e., geographic, environmental and/or phylogenetic spaces).

Plant community composition of six Lower Mississippi River islands

Grace McCartha[1], Caity Sims[1], Brendan Kosnik, Richard Abbott[2], Mathew Jones[1], Ben Benton[1], Scott Mangan[1], Travis Marsico[1],

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The Lower Mississippi River (LMR) contains unique river islands that are isolated from the mainland for all or most of the year. These islands experience intense flood regimes that result in the receipt of a constant supply of organic materials from upstream, such as sediment and seeds. Moreover, the islands are some of the last remaining floodplain habitats in the Delta region, and surveying their botanical biodiversity is the first step to learning more about plant community structure and ecosystem function in the Mississippi River. From June 2020 through August 2021, we conducted a flora of six LMR islands from Helena-West Helena, Arkansas, to south of Greenville, Mississippi. Over 1,900 plant specimens were collected for a total of at least 461 species across all six islands. We found thirteen species that are putative state records (never before recorded in the state) in Arkansas and three in Mississippi. The six islands span four counties and of the three Arkansas counties, approximately 106 species were found that are county records. From mid-July to late-August 2021, we surveyed plant community composition in 59 100-m2 plots on these six islands following Carolina Vegetation Survey protocol. These plots were established across a range of elevations and habitat types (e.g. sand dunes, swamps, mesic forests). Data are being analyzed to relate abiotic factors (elevation, soil, proximity to tributary confluences, island size, island age, latitude) to plant communities on LMR islands to understand species distribution patterns in these seasonally flood-disturbed habitats.

Roots in the tundra - belowground plant traits under varying environmental conditions at multiple Arctic and Alpine sites

Laura Turner[1,] Franziska Schrodt[1,] Richard Field, Gabriela Schaepman-Strub[2,]

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Temperature and precipitation are changing rapidly in the Arctic, strongly affecting vegetation dynamics, yet less is known about belowground impacts, despite their importance for carbon storage and other ecosystem processes. Here, we investigate community-level root traits and how these vary with abiotic and biotic variables at several Arctic and sub-Arctic sites. Samples were taken at multiple sites on Disko Island, Greenland, and near Kilpisjarvi, Finland, with varying elevations, soil moisture conditions and vegetation types represented. I analyse key root functional traits and mycorrhizal colonisation alongside microclimate and plot-level data including species composition and aboveground plant traits. Similar methods have been employed in the Cairngorms, UK, and by collaborators at other Arctic and alpine sites, and in-growth cores installed to examine new root growth over the year. This poster describes methodologies, presents preliminary results, and outlines next steps. My research integrates belowground, aboveground and remotely sensed data, aiming to improve predictions of how Arctic ecosystems will respond to environmental change.

Synchronous populations as signals of biodiversity change

Katherine Hébert[1,] Dominique Gravel[1,]

[1] Université de Sherbrooke

Although population synchrony is a well-documented phenomenon and a foundational idea in ecology, the correlated fluctuations between distinct populations are only beginning to be incorporated into our understanding of biodiversity change. Synchrony provides valuable spatial and temporal information about ecosystem resilience and stability, and, importantly, adds nuance to assessments of biodiversity change based on average trends by directly reflecting population dynamics. Synchronously fluctuating populations are notably at a higher risk of extinction compared to asynchronous populations. Asynchrony can instead signal greater ecosystem resilience, due to a greater diversity of responses to environmental change among species within the ecosystem. As such, a mean trend showing average declines in populations is much more severe if these declining populations are also fluctuating in synchrony, as this could signal some correlated environmental change, disrupted interactions between species, or some altered dispersal dynamics which threaten the ecosystem, rather than some isolated population. Here, we assess the magnitude and direction of synchrony in abundance fluctuations between populations across the globe. We then identify species groups and regions that show stronger synchrony or asynchrony, to highlight the temporal and spatial signatures of ecosystem stability. In doing so, we hope to direct attention to synchrony "hubs" which merit closer attention, and asynchronous populations that may be capable of maintaining ecosystem resilience, to provide a more nuanced portrait of population-level biodiversity change.

The geography of metacommunity assembly: landscape heterogeneity and species pool attributes mediate the relative importance of assembly mechanisms

Gabriel Khattar[1,] Pedro Peres-Neto[1,]

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Theories of metacommunity ecology traditionally assume that landscape characteristics and species pools represent two independent axes that govern metacommunity dynamics. This simplification is at odds with ecogeographical hypotheses that posit a strong influence of landscape heterogeneity on the level of ecological specialization and dispersal of species in the regional pool. To reconcile the two perspectives, we propose a framework representing the assembly process as a mediation model wherein: (i) landscapes characteristics select for the attributes of species pools and (ii) both (simultaneously) mediate the relative importance of different core assembly mechanisms (e.g., selection, dispersal, drift). We used metacommunity simulations to illustrate how our conceptual model can generate predictions about the relevance of assembly mechanisms along broad-scale ecological gradients, including biogeographic regions. In these simulations, species pools with similar initial characteristics (i.e., number of species, environmental tolerance, dispersal ability, among others) were set to colonize and coexist in landscapes with varying levels of physical connectivity, seasonality, and spatial distribution of environmental conditions. We found that a negative covariance (trade-off) between environmental specialization and dispersal capacity emerges as different optimal strategies that increase species' abilities to persist along seasonality and connectivity gradients. We also derived a series of predictions regarding how the attributes of landscapes and species pools determine the effects of landscape heterogeneity and spatial factors (including dispersal) on metacommunities. We finalize by discussing how our findings compare with previous empirical and theoretical studies in macroecology and biogeography, highlighting predictions that remain to be tested.

Poster (Climate Change, Conservation & Invasion Biogeography)

A comprehensive framework for modeling freshwater mussel invasion

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[1] Simon Fraser University

Zebra and quagga mussels (Dreissena polymorpha and D. rostriformis bugensis) are a pressing threat to freshwater biodiversity in North America. Arriving in the Great Lakes in the 1980s, they have since spread across the continent via boats and natural watershed dynamics to rapidly colonize and alter lakes and rivers. These mussels have steadily marched westward and are poised to invade British Columbia. A comprehensive approach is required in order to predict the pathways through which zebra and quagga mussels will arrive, where they might be able to establish themselves and what impacts they will have. Here we present the results of just such a comprehensive modelling effort, which aims to build a replicable and biophysically-grounded series of models to predict each step of a possible invasion. Through a meta-analysis we have identified the environmental variables most likely to contribute to the large-scale patterns of the invasion and have extracted response curves from the literature for each variable in order to build a mechanistic niche model for dreissenid mussels. We then used the information extracted from these analyses of the literature to gather environmental data to evaluate the niche model against, providing us with a stepwise model of establishment success at the larval and adult life stages. These results represent an important step forward in our ability to understand the constraints on zebra and quagga mussel invasional success, and the framework as a whole is an important step forward in our ability to model the invasion of other species.

Biogeographical insights into hitchhiking plant propagules on the exterior of refrigerated shipping containers at the Port of Savannah, Georgia, USA

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As frequency and volume of trade increases, biotic risks associated with exchange of nonnative, potentially invasive, plant species must be measured to inform effective policy implementation. Additionally, nonnative plants arriving to new environments via global trade routes present a novel system for studying how organisms may expand their distribution to new continents. We conducted an industrialized flora at the Port of Savannah, Georgia, USA, and demonstrated that the proportion of nonnative plant species richness was higher at this industrial site than any of the 19 comparison floras conducted in Georgia and South Carolina over the last 30 years. Further research taxonomically classified and quantified hitchhiking seeds that accumulated on the exterior air-intake grilles of refrigerated shipping containers that were transported inadvertently from overseas to the USA. Over two years, we identified thirty taxa hitchhiking on shipping containers carrying a single agricultural commodity, primarily wind-dispersed members of the grass (Poaceae) and sunflower (Asteraceae) families. The most abundant species collected was the Federal Noxious Weed, wild sugarcane (Saccharum spontaneum) or its hybrid, which is not yet widely established in the USA. We estimated propagule pressure from these collections and further conducted controlled viability and survivorship trials. Based on these empirical data, process-based simulation models indicated high invasion risk for hitchhiking species, even with exceedingly low escape rates from containers. We will expand this research by including additional commodities from a variety of global sources to better understand risks associated with invasive species introduction through global trade and to inform strategic management efforts.

Effects of delayed mowing on plant species diversity in cultivated grasslands

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Grasslands for biomass and fodder production are omnipresent in our cultural landscapes in Central Europe. For Bavaria, over one third of grassland species can be found in those cultivated grasslands. With the ongoing intensification in agriculture, grasslands are more and more streamlined to species poor high-performance grasslands. To act against this, europe-wide measures have been taken to subsidize efforts of low intensity farming in grasslands, by e.g. restricting the fertilizer use and financially compensating farmers that agree to not mow before a certain date. We investigate the effect of delayed mowing on species richness and composition for grasslands under such conservation contracts (VNP1 and VNP2, no mowing before the 15th of June or 1st of July respectively) compared to “good farming practice” (GFP) grasslands with a regular mowing regime. We find, that VNP1 and VNP2 are higher in number of species encountered compared to GFP grasslands, however, the difference between restricting the first cut to the 15th of June (VNP1) or the 1st of July (VNP2) was not significant. The changes in species compositions was analysed with an NMDS, where a clear distinction could be made between the VNP grasslands and the GFP grasslands, where the communities in GFP grasslands are more dominated by grass species rather than herb species.

Nannorrhops ritchieana (Griff.) Aitch. is a gregarious Palm; shedding light on its associated chorotypes

Abdullah Abdullah[1], Shujaul Mulk Khan[1], Yaseen Khan, Shakil Ahmad Zeb[1],

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The distribution of Plant Species is not even nor random over the earth's crust. Phytogeographers classified plants species into various chorotypes. Phytochorionomic classification of a geographic region helps in understanding the center of origin for a species. In this study, we assess various chorotype with different environmental and edaphic drivers.

We allocated each native plant species as a chorotype, Irano-Turanian, American, North American, Holarctic, Holoantarctic, Mediterranean, Saharo-Sindian, Saharo-Arabian, Eastern Asiatic, Western Himalayan, Eastern Himalayan, Sudano-Zambezian and Euro-Siberian as well as Eurasian. We sampled the associated plant species of N. ritchieana Palm across 508 plant species. Plots of herbs 1x1m2, shrubs 10x10m2 and trees 10x10m2 were taken. We used Two Way Cluster, Correlation and Canonical Correspondence Analysis to assess the impact of different environmental and edaphic drivers. We analyzed the Important Value Index (IVI) of each chorotype under the influence of different environmental and edaphic drivers. A total of 254 plants belonging to 18 phytogeographic classes were documented. Irano-Turanian was the dominant phytogeographic class with 35chorotypes followed by Holarctic 34, Saharo-Arabian 24, Medititerriean 23, Paleotropical 22, Pantropical 5, Pluriregional 9, Western Himalayan 19, Sudano-Zambezian 5, Holoantarctic 7, Saharo-Sindian 6, Eastern Asiatic 3 and the others comprised of one species each. The relationship of different chorotypes with various climatic i.e., Maximum temperature, minimum temperature, wind speed, precipitation and edaphic variables such as pH, TDS, EC, Mg, K, Na, Ca and Fe were determined via canonical correspondence analysis. We determined that with an increase in nutrient concentration and precipitation i.e., Mg, Ca, Fe, Na and K the number of Irano-Turanian, Mediterranean, and Holoarctic chorotypes increases. On the other hand, chorotype abundance and IV

Severe recent bioclimatic shifts in the world′s biomes

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Biodiversity and climate a are tightly linked, and this interaction be described by bioclimatic variables important for physiological and ecological processes. Examples include evapotranspiration that affects the water budget of plants, solar radiation that influences photosynthesis, or soil water availability that limits many physiological and ecological processes. Despite the known importance of such key bioclimatic variables, a major focus in biogeography and macroecology has been on bioclimate described by temperature and precipitation alone. This is likely due to a lack of available information at biologically relevant spatial scales in the past. We now have filled this gap by developing a global bioclimatic time series that includes biologically relevant parameters at yet unpreceded spatio-temporal detail. These allow us to improve our understanding of biogeographic patterns and processes, including the impact of recent climate changes on the world's ecosystems. Here, we present the new bioclimatic predictors and how the major biomes globally were exposed to bioclimatic shifts over the last four decades. We explored the known distribution of species clades and assessed which, and how many species and families have been experiencing shifts in bioclimates. We can demonstrate that bioclimate has seen severe shifts in all major biomes worldwide with a strong increase in shifts in recent years. Not all bioclimatic parameters have shifted as strongly and equally in all biomes. However, for several key bioclimatic parameters, a majority of organisms has experienced shifts at the beginning of the 21st century that far exceed the variabilities experienced in preceding decades.

The nonrandom introduction of alien species is largely reflected in the pattern in the naturalized flora of Southern Africa.

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Most studies on biological invasions focus on the later stages of the invasion process, i.e. after species have already become naturalized. It is frequently overlooked, however, that patterns in origin, phylogeny, and traits of naturalized alien species might largely reflect which species have been introduced in the first place. Here, we quantify and account for such introduction biases by analyzing 5,317 plant species introduced for cultivation in Southern Africa (including 10 countries). We show that this cultivated alien flora represents a non-random subset of the global flora and that this bias at the introduction stage largely drives patterns in origin, growth form, and phylogenetic composition of the naturalized flora. For example, while species from Australasia are, compared to the global flora, disproportionally overrepresented in the naturalized cultivated flora of Southern Africa, this pattern is solely driven by their higher likelihood of having been introduced for cultivation. The same is true for the overrepresentation of free-standing woody species in the naturalized cultivated flora. The strong phylogenetic clustering of the naturalized cultivated flora is also to a large extent driven by phylogenetic clustering of the species introduced for cultivation. Thus, despite strong biases in which species have been introduced to Southern Africa, there are significant patterns in the species characteristics related to naturalization probability. Our quantification of introduction biases demonstrates that they are huge and that accounting for it is essential to avoid over-or under-estimation of the characteristics of successfully naturalized alien plants.

Poster (Functional Biogeography)

Deciphering the geographic and climatic effects on North American mammalian functional diversity

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Previous studies analyzing North American mammalian diversity have revealed the presence of a latitudinal taxonomic diversity gradient, however comparatively little research has examined the functional diversity of North American mammalian communities. As a metric of ecosystem function, functional diversity may provide a more nuanced understanding of these communities and their resilience to ecological disturbances. We quantified several metrics of functional diversity (functional richness, functional evenness, functional divergence, and functional dispersion) across the continent in order to determine their relationships to geography and climate. Our data consist of terrestrial mammal taxon lists, elevation, topographic relief, and several climatic variables representing temperature and moisture availability for 2040 grid cells from Canada to Panama, each 100 by 100 km. For each of the 749 species in the dataset, we recorded three ecological variables: size based on log10 of body mass in grams, diet, and locomotor mode. We then used the FD package in R to calculate each functional diversity metric for each grid cell. We find that functional richness has positive relationships with increasing elevation, relief, temperature, and moisture availability; functional evenness is high at high latitudes and low at high elevations and where moisture availability is high; functional divergence and dispersion are high in grid cells with high elevation and relief, with functional dispersion at its highest in grid cells with moderate and high temperature and moisture availability. These results indicate the presence of functional diversity gradients related to the latitude, topography, and climate of North America.

Functional diversity of native bird communities on oceanic islands shows no evidence of preventing establishment of non-native bird species through competitive exclusion

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Biological invasion is considered one of the main drivers of global biodiversity decline. Non-native species has the potential to cause significant decline in native community abundance and increase extinction risk. Island ecosystems seem particularly vulnerable to impacts of non-native species and are overrepresented in the proportion of highly threatened species and species extinctions. Biotic Resistance theory predicts that species rich native communities have higher resistance to invaders through mechanisms of competitive exclusion. However, empirical evidence yields contradictory results. Through the construction of a global database of island bird communities, we investigated the functional niche of locally interacting native and non-native species on oceanic islands using functional richness. Functional richness was seperately calculated for traits related to resource acquisition and morphology due to the potential for diverging mechanisms responsible for community assemblage. We demonstrated that successfully established non-native species contribute less functional richness than expected by the increase in species richness, and that the probability of establishment success is positively correlated to morphological diversity. Thus, providing no support for competitive exclusion of non-native birds on oceanic islands. However, it is uncertain whether this pattern of Biotic Acceptance will be equally prevalent for highly saturated communities. This study further demonstrates the importance of trait selection for interpretation of studies using a functional traits approach to determine underlying mechanisms of community composition. Due to the well-established impact of non-native species on global biodiversity, knowledge on the processes leading from introduction to impact is needed to prioritise future conservation efforts.

Persistent and cumulative impacts of drought on forest growth across a moisture gradient

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Circulation models forecast dramatic changes in global temperature and precipitation patterns that will likely alter forest function. North America is expected to experience increases in intensity and frequency of hot days and nights, and is already experiencing severe and frequent drought and forest fires. Current widespread forest dieback has been attributed to climate regime changes, however, forest resilience is not well understood.

Tree ring records can be used to assess forest resilience to climate variability. Trees exhibit delayed, persistent, and cumulative growth responses to disturbance, and physiological feedbacks may exacerbate their impacts on growth. Previous studies have identified North American Douglas fir as drought tolerant making it an ideal candidate for understanding impacts of drought. However, they found that trees in the southern range exhibit greater tolerance than trees in the northern range, suggesting local adaptation to drought and consistency with the moisture index latitudinal gradient. However, spatial variability in drought tolerance has only been examined at coarse scales, and ecological memory to drought events has not been quantified.

Here, we quantify the spatial variability in drought resistance of Douglas fir using tree ring records from 349 sites from the International Tree Ring Data Bank that extend across the species' range, and PRISM climate data. Using several moisture indices, we identify the magnitude and persistence of drought impacts on tree growth across a latitudinal gradient. This work advances understanding about impacts of disturbance on tree growth, improving our ability to predict forest function in future environments.

Where are tropical birds more colorful? The eco-evolutionary drivers promoting color diversity in tropical bird assemblages.

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Synergies between ecological and evolutionary processes influence the color diversity of species assemblages. Species color determines important aspects for mating, species interactions, and survival. With our research, we search to answer a seemingly simple question, where are birds more colorful? Although, it is evident that birds are colorful taxa, the underlying causes of varying plumage color patterns in birds are not well understood. Research in sexual and adaptive selection has provided answers for the differences in plumage coloration among tropical bird species. However, few have been the searches for broadscale patterns in the plumage color diversity of multispecies bird assemblages. Whether there are spatial patterns of multispecies color diversity or what are the mechanisms driving them remains largely unexplored. Here, to answer this question, we explore the global biogeography of plumage coloration in multispecies assemblages of tropical passerine birds. Using data on color obtained from digitized species illustrations we project bird species pool into an RGB color space. We use distance-based approaches to compute indexes of color diversity and color disparity at the scale of 1×1 degree grid cell. With this approach, we a) map patterns of plumage color diversity of passerine bird tropical assemblages for all tropical regions. b) identify color diversity hotspots, areas where the color diversity of bird assemblages significantly differ from neutral models of ecological assembly, c) identify whether color hotspots represent recent adaptive responses to climate of whether color hotspots represent older assemblages where color among species has had more time to differentiate. Knowing why birds can be more colorful between geographical regions can help gain a more mechanistic understanding of community-level phenotypic adaptations to climatic change.

Poster (Island & Marine Biogeography)

Eurymixis: Chaos and Determinism in the Sea in the Age of Genomics and Big Data

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Marine species show a wide variety of patterns of diversity at multiple spatial and temporal scales. The well-appreciated technical challenges to documenting patterns in the seas and the ability of the patterns that we could measure to defy and confound explanation contributed to the widespread adoption of “chaotic genetic patchiness” — genetic heterogeneity that does not follow a simple consistent pattern, but forms a shifting, ephemeral patchiness among sites and between years — as an acceptable description of genetic patterns in marine species. Introduced in the early 1980s, the term was popularized as larval life-history became part of a bigger bio-physical picture of marine dispersal in the 2000s, and particularly as papers claimed there was no or weak evidence for a relationship between dispersal potential and gene flow. However, recent years have seen great advances in our ability to describe patterns of genetic diversity and the abiotic environment: through installation of vast numbers of dataloggers and remote sensing, improvements in analytical frameworks, and the advent of affordable reference genome-enabled multi-species population genomics. This creates an opportunity to take up the challenge vacated by “chaotic genetic patchiness” and embrace the complexities (i.e. to understand interactions between the distributions of neutral to non-neutral genetic diversity, physical biogeography, functional diversity, behavior, etc.) and their implications for community assembly and dynamics. Exploring the complexity, rather than focusing on the unpredictability, is essential to better understand transient heterogeneity as a source of adaptive variation in dynamic environments such as the seas.

The influences of soil on plant communities on six Lower Mississippi River islands

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Mississippi River islands are fascinating botanically because they have periods of flooding that influence plant species dispersal and persistence. Flood duration varies with elevation on islands, but the effects of flood duration on plant communities and soils remain understudied. Increases in inundation are known to have positive effects on soil nutrient cycling in alluvial soils. Our objectives were to investigate soil abiotic properties at different elevations of six Lower Mississippi River islands to determine whether river hydrology is related to soil properties of these islands. We hypothesized that soil texture and nutrients are related to elevation (a proxy for inundation or flood period) and variation in plant species richness and compositional similarity on Mississippi River islands. Specifically, we predicted that soils vary in their physical and chemical make-up among different elevations, and this influences species richness and abundance because of varying water holding capacity and nutrient levels. Fifty-nine 100m2 plots were sampled for plant species richness and abundance and soils across six Mississippi River islands at three elevation classes. A composite soil sample was taken within each plot and was analyzed for nutrients, percent moisture, and texture. The average nutrients, organic matter, percent moisture, and cation exchange capacity increase from high to low elevation classes. Most plots had alkaline soils due to an abundance of Calcium. The ranking of macronutrients was consistent across samples from most abundant to least (in ppm): Ca, Mg, K, P, Na, and S; micronutrients were ranked as follows: Fe, Mn, Zn, Cu, and B.

The persistent cross-shelf bioregionalization of coastal oceans

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Coastal oceans are characterized by steep cross-shelf gradients and are frequently geomorphologically complex and oceanographically dynamic habitats. The biogeographic partitioning of coastal oceans is important to understanding how the resulting complex oceanographic processes affect ecosystem functioning and response to change. In this study, we investigate zooplankton communities to identify regional differences in species composition in the British Columbia, Canada, coastal ocean. We conducted a data-driven biogeographic regionalization of zooplankton abundance using net observation data collected between April and October from 1995–2014. The dataset included 3,773 samples and 155 zooplankton species. A k-means cluster analysis of the log-chord transformed zooplankton abundance was used to identify the bioregions. Four distinct bioregions emerged from the analysis representing the Offshore, Deep Shelf, Nearshore, and Deep Fjord bioregions. The cross-shelf regionalization of the zooplankton community was persistent across 20-years of observations. We then present a framework of the various oceanographic processes that may dominate in structuring the observed zooplankton communities in each bioregion and propose how this may compare to other coastal oceans globally.

Vegetation change on the Atlantic′s highest oceanic volcano inferred from the raw data underlying Humboldt′s Tableau Physique des Iles Canaries

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The Canary Islands are the World's second-largest oceanic volcanic archipelago and have played a unique role in the development of volcanology and biogeography. Their modern scientific exploration is tightly linked to the visit of Alexander von Humboldt, who climbed the Teide's 3715 m on 21 June 1799, but made few collections. For his Tableau physique des Iles Canaries (1817), a diagram of the vegetation zones on Mt. Teide, Humboldt therefore relied on the observations of the geologist Leopold von Buch and the botanist Christen Smith, who visited the Canary Is. from 6 May to 27 Oct. 1815 and climbed the Teide twice, taking different routes that we matched to modern maps. We have studied their collections, letters, and publications to infer floristic change on the Teide since 1815. Fifteen of 16 species for which Von Buch provides precise altitudes, have expanded upwards btw. 1.1 and 6.8 m/year; one species has barely changed its alt. range. In addition, several conspicuous species have newly arrived or disappeared since 1815. The vegetation change documented by these data is among the most extreme for any comparable island system and can be related to climate change, goat exclusion, and the expansion or control of other herbivores.

When the genus seems to be “extinct” – the problem in the biogeographical distribution of marine species.

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Family Melithaeidae (Cnidaria, Anthozoa) is a sessile colonial branching octocoral on the hard rocky bottom. The distribution is mainly restricted in the Pacific Ocean, excluding a few invaded species, from the tidal zone to the deep bathyal depth. WoRMs (World Register of Marine Species) counts only two genera in 2022. Previously there was a total of 12 genera in the world, and four genera (Acabaria Gray, 1859, Melithaea Milne Edwards, 1857, Mopsella Gray, 1858, Wrightella Gray, 1870) have been reported from Japanese and adjacent waters, North West Pacific (Iwase 1992, Nutting 1912, Matsumoto et al. 2007). Total n=153 specimen has been examined, including 43 type specimens. After revising Japanese Melithaeidae corals (Matsumoto & Ofwegen 2015), one genus disappeared from the distribution map (Acabaria). According to the synonymise, four common shallow (tidal – littoral) species in Japanese water disappeared. An old rarely recorded species (only two sites record) suddenly expanded the range of distribution with the revision. Many biogeographical research focuses on terrestrial animals/plants; in contrast, marine biogeographical studies are few and primitive. Here, we show the example of one of the most significant problems treating marine species for the biogeographical study, mainly when we focus on the organisms which have not been revised for a long time (>100 yrs.). The before-after revision of the Melithaeidae coral distribution map is shown.

Poster (Models & Methods in Biogeography)

A Bayesian methodology to estimate local extinction events using spatial information

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Quantifying species extinction is essential for understanding the magnitude of biodiversity loss. However, the occurrence and timing of extinction events are rarely observed and are very difficult to confirm. Several mathematical methods have been developed for inferring extinction using proxy information known as "sightings" (times at which a species has been recorded as present). Yet, spatial information has been mostly overlooked in these calculations. There is a growing interest, both ecological and political, in reliably detecting global and local extinctions, and to distinguish true extinctions from the failure to sample a species even when it is present. Extinction events occur more commonly at the local scale than at the global scale and therefore documenting their occurrence would help us to better understand the processes that lead to global extinction. Here, we present a Bayesian methodology to estimate the extinction probability of species at a different spatial scales using standard occurrence data. We have modified the Solow & Beet (2014) extinction date estimator model to incorporate the spatial heterogeneity in the environment and spatial autocorrelation of presence data. The spatial information is added as a prior using the posterior distribution of a point process model that generates the probability of sighting rates for each site, instead of using the same prior for all the sites. We compare the performance of our model using simulated data. The use of spatial information, i) improves the precision of the estimates, ii) reduces the biases and iii) allows the study of the spatial structure of local extinctions.

Deriving Accurate Water Thermal Maps From UAV-Mounted Thermal Camera.

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UAV-integrated thermal sensors have a wide range of applications in aquatic thermal ecology, but their ability to accurately determine the absolute temperature of water (Tk) remains open to question. Radiometric cameras capture relative thermal values within images, but due to their cost-effectiveness, is a strong appetite to derive absolute Tk from the calibration of radiometric thermal intensity recorded by these sensors. However, literature reports of errors in water Tk estimation after calibration remain up to 8°C, making these data hardly usable for ecological application where accurate Tk is needed. Additionally, for use in complex water bodies such as rivers, the extraction of the wetted area (i.e., the river water itself) can be a complex operation, especially due to the presence of emergent stones, vegetation, etc. We present here a method to efficiently extract the wetted area of a complex river confluence, and obtain Tk values with high accuracy (<1ºC error) from a UAV-mounted radiometric camera. All the parameters needed to convert thermal radiation intensity into Tk are recorded in field with no need of a-posterior correction. The wetted area extraction is based on reflectance value in the Red and Near Infrared wavelength of the object of the scene collected with a multispectral camera. These methods allow to obtain accurate Tk data (Average Mean Absolute Error <0.5 °C) and precisely remove all the non-wetted pixel from the original raster, to be used to answer ecologically relevant questions.

Ecological Niche Modeling for Conservation of Native Species (Diospyros rhodocalyx) in Rajamangala Universiy of Technology Isan, Nakhonratchasima, Thailand

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Diospyros rhodocalyx is an important native species and identity for Rajamangala University of Technology Isan (RMUTI). Moreover, one critical mission of RMUTI-green university is conservation of native plant species. Therefore, this study requires Ecological Niche Modeling (ENM) for conservation of Diospyros rhodocalyx in various five-green space types of RMUTI (such as 1) recreation and land scape outlook, 2) multiple-use, 3) environmental preservation, 4) narrow stipes along traffic ways and 5) abandoned spaces). ENM was analyzed by integration of Ecological Niche Factor Analysis (ENFA) in Biomapper and ArcMap using GIS layers: tree-point layer and environmental layers (such as bio-climate, topography and soil). ENFA model is evaluated by Absolute Validation Index (AVI) and Contrast Validation Index (CVI).
The results were explored by five ENFA models of Diospyros rhodocalyx in each RMUTI green space above. The top three green spaces are tending to marginality (represents the deviation of the niche space of a species widely distributional in the study area. At the same time, the last two green spaces are tending to specialization (represent the tolerance of the niche space of a species in study area). For evaluation of five-ENFA model, the highest value of AVI and CVI was seen in the ENFA model in the fourth green space type (AVI=1 and CVI=0.72). This study will be not only for preserving in level of universitybut also there is benefit and knowledge for conserving in level of City Municipality.

Effects of eigenfunction-based spatial variables on the prediction of species distribution model.

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Effect of Eigenfunction based spatial variable on MaxEnt based species distribution model was evaluated under random and spatial block cross-validation. It turns out that spatial variable was effective to increase discriminative indices such AUC and TSS but decrease in Boyce index. This result is caused from different distance matrix structure for presence and background points. Model prediction performance was not related with spatial transferability from spatial block cross validation. It is recommended for a additional effort to account spatial autocorrelation in presence only species distribution model such as MaxEnt.

Fingerprints of recent climate change in ecological niche models: the case of the Mexican small-eared shrew

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Ecological niche models (ENMs) are commonly used to estimate shifts in the geographic distribution of species in response to climate change. Typically, ENMs are built using long-term, historical climate information, which can hide recent trends in temperature and precipitation. This practice makes it challenging to track shorter-term range shifts at the limits of the distribution (range edge). Many range shifts, both pole-ward and upslope, are being detected for species around the globe in response to global warming. This study aims to detect habitat

suitability trends for a cloud-forest montane species in the recent past (~ 40 years), which could predict current range shifts. An ENM for the Mexican small-eared shrew (Cryptotis mexicanus), a species whose distribution is constrained by humidity and temperature, was built with Maxent using a single twenty-year CHELSA climatic baseline. After tuning key settings, the optimal model was transferred to several twenty-year periods based on monthly data between February 1979 and January 2016 (n = 205; 240 consecutive months each). Cells considered as range edge were defined if the suitable/unsuitable prediction differed among any transfers. Increasing or decreasing trends in habitat suitability were detected in edge cells using a Mann-Kendall test. The location and direction of suitability trends are not as simple as pole-ward or upslope shifts expected under global warming. Instead, suitability trends follow precipitation patterns at a regional scale. Combining ENMs with recent climatic data can give us insights into multifaceted species responses to ongoing climate change.

Incorporating Genotypic Variability of Plant Populations in Continental-Scale Phenological Models

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Phenological changes of plant species are a sensitive indicator of climate change impact on the biosphere. While most studies along this line have focused on timing shifts of phenological events at various locations as influenced by changing atmospheric conditions, the underlying spatial drivers of phenology, especially genotypic heterogeneity shaped by historical climatic conditions are often overlooked. Also, to extend predictions to broad geographic regions, existing phenological models must assume spatial uniformity of plant responses. Therefore, it is imperative to incorporate genotypic variability of plant species in broad-scale plant phenological models if we intend to track phenoclimatic interactions more accurately over space. Built upon previous work, this study is focused on calibrating a cloned-plant-based Spring Index (SI)-First Leaf (FL) model in the temperate Eastern U.S. using data from the Nature's Notebook program, USA-National Phenology Network. The algorithm of calibration assumes that the geographic variation of the temperature requirement of different populations of a species for leaf out mirrors that of the historical temperature gradient across the species' distribution range due mainly to local adaptation. Apart from the calibration, a uniform model at the continental-scale overestimates FL dates in colder regions and underestimates those in warmer regions. Climate-calibrated SI-FL models remove such geographic discrepancy and allow more accurate predictions to be made for geographically different plant populations and communities. The climate-calibrated phenological models enhance our ability to predict geographically varied biospheric responses to climate change.

Mapping Climate-Associated Risk for Cholera in Bangladesh

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Several studies have investigated how Vibrio cholerae infection risk changes with increased rainfall, temperature, and water pH levels for coastal Bangladesh, which experiences seasonal surges in cholera infections associated with heavy rainfall events. While coastal environmental conditions are understood to influence V. cholerae propagation within brackish waters and transmission to and within human populations, it remains unknown how changing climate regimes impact the risk for cholera infection throughout Bangladesh. To address this, we developed a random forest species distribution model to predict the occurrence probability of cholera incidence within Bangladesh for 2015 and 2050. Using R, our random forest model was trained on cholera incidence data and spatial environmental raster data at a resolution of 250 meters. This model was then predicted to environmental data for the training data year (2015) and for 2050. We interfaced R with ArcGIS to develop risk maps for cholera infection for the years 2015 and 2050, proxying infection risk with cholera occurrence probability predicted by the model. The best-fitting model predicted cholera occurrence given population density and elevation but not temperature. Several districts in Bangladesh see reduced infection risk in 2050, despite increases in population density nationwide. Regions with low elevation (<75 meters) and less than 10,000 persons/sqkm were associated with infection risks of 0.50 and higher. Mapping the geographic distribution of cholera infections given projected environmental conditions provides a valuable tool for guiding proactive public health policy tailored to areas most at risk of future disease outbreaks.

Towards a standardization and unification of global terrestrial biome classifications

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Global terrestrial biome classifications function as basic units in large-scale biogeographic and ecological research. Although there is an implicit agreement about general global patterns, there is a great variety of such concepts with significant deviations in numbers of categorial classes and their spatial extent. These differences result from variant methodological approaches (e.g., expert-based, remote sensing, modelling) and distinct underlying criteria. Although frequently used as a reference, the decision for a specific biome classification is often uninformed or based on the assumption of general consensus. However, the spectrum of biome classifications ranging from expert-based delineations only available as paper prints to high-resolution global maps derived from Earth observation exhibit great variability. Class numbers differ immensely between different concepts and spatial agreement is low. Here, we aim at providing a standardized catalogue of global terrestrial biome and land-cover classifications. Comparison between concepts reveals the degree of spatial congruency and overall similarity to ease informed selection and to avoid discrepancies with more consistent approaches. We propose an optimized product that is condensed from the characteristics of commonly used classifications. 31 published biome classifications were standardized to equal resolution and projection. Hierarchical clustering was used to provide a congruent biome map and to produce a disagreement map of the reviewed concepts. The standardized final biome catalogue enables easy application of individual classifications by setting up a context of common standards. We encourage refined considerations in the selection of global terrestrial biome classifications in biogeographic and ecological research. Therefore, we present a standardized inventory, the biome catalogue, and a novel map combining the expertise of present concepts.

Using Planning Green Space Network for Forest Restoration

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The forest ecosystem can provide many ecological services and benefits to communities including energy conservation, contributing to global biodiversity, and maintaining hydrologic and nutrient cycles. This paper purposes a theoretical and methodological approach to plan green space network for forest restoration that accounts for regional biodiversity and systematizes the selection of greenway links. The method uses in this paper is based on the premise that a GIS-based network analysis of various forest areas-based land use data of Land Development Department (LDD) should serve as the skeletal framework of a comprehensive greenway system. The paper draws from the knowledge bases of landscape ecology, conservation biology, network theory, and landscape planning. A case study is presented to demonstrate the approach using a forest area of Nakhon Ratchasima province, Thailand.

Poster (Paleoecology & Paleobiogeography)

Tropical paleoecology data mobilization in Neotoma to study ecoclimatic sensitivity of tropical ecosystems to glacial-interglacial climate change

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The sensitivity of tropical ecosystems to global climate change is a pressing question, because of their high biodiversity, high carbon storage in rainforests, and positive carbon and water feedbacks. By studying ecosystem responses to past climatic forcings, we can identify common climate-related ecosystem responses across continents and time periods with more regional trends, enabling better ecosystem response predictions to anthropogenic climate change. Pollen data in the Neotoma Paleoecology Database, a community-curated paleoecology resource, historically were weighted towards temperate and high-latitude ecosystems in North America and Europe. However, current data mobilization campaigns across the tropics now enable macro-scale analysis of tropical ecosystems' climate sensitivity since the Last Glacial Maximum (LGM). Recently, an international group of researchers worked together to upload pollen records from the Indo-Pacific Pollen Database. We compiled existing data from Excel spreadsheets, added information from primary literature, and created new age-depth Bayesian models before uploading records to Neotoma. Using Neotoma APIs, we downloaded 300 Neotoma pollen records between 30˚N and 30˚S from 23ka BP to present. Of these, 280 sequences had two or more chronology control points, for which we recalibrated age models for >90 using bchron. We obtained the latest reconstructions of full-glacial global surface air temperature (SAT) data at 5°×5° resolution and bilinearly interpolated to site locations. There are 44 records between 23-19ka BP and 279 sequences between 3ka BP-present. Our current work focuses on estimating climate sensitivity via various metrics of community turnover and analyzing the spatiotemporal patterns through mixed-effects models with elevational and temperature predictors.

Poster (Species Distributions)

A neighborhood approach for using remotely sensed data to post-process species distribution models: results for a threatened Mexican mammal (Handleyomys chapmani)

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Species distribution models can be used to predict environmental suitability, quantify changes in species' geographic ranges, and support conservation assessments. Masking suitability maps to remove areas currently lacking appropriate vegetation can refine predictions and aid conservation applications. However, even for recent records, often the uncertainty around georeferences exceeds the resolution of remotely sensed vegetation data. Here, we present a novel methodological approach to resolve these discrepancies and implement it for Handleyomys chapmani, a montane rodent endemic to Mexico considered threatened by the IUCN. We defined deforestation tolerance thresholds (the lowest value of forest cover where the species has been observed) using two approaches: 1) extracting the exact pixel value where an occurrence record fell; and 2) using an aggregate measure of that and surrounding pixels (the "neighborhood" likely within the radius of actual sampling). We applied these thresholds to the respective annual forest data (raw and neighborhood-processed) to mask the suitability prediction for H. chapmani, identifying areas of habitat loss due to insufficient forest cover. Habitat loss was especially prevalent along the western slopes of the Sierra Madre Oriental mountain chain. The neighborhood approach indicated less tolerance to deforestation, leading to a smaller area indicated as suitable and still containing sufficient habitat. This approach of processing vegetation data for habitat masking may prove useful for many species, particularly those having occurrence records with high coordinate uncertainty. This research also highlights the importance of obtaining accurate georeferences (corresponding precisely to the habitat sampled) when collecting field data.

A Sky Island Perspective: New England, USA Alpine Plant Community Change Through Space and Time

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New England alpine plant populations exist as scattered mountaintop islands separated by a matrix of northern hardwood forest. After deglaciation, the region was initially dominated by tundra plant species found largely in the Arctic today. As climate changed, these species were limited to high elevation sites, where high winds and freezing temperatures limit tree growth. New England's alpine ecosystems are thought to be climatic refugia for these tundra relic species. Understanding their history and present-day assembly could then provide insight into their future vulnerability to climate change. Because these rare mountaintop communities are often managed by separate agencies, plant distribution surveys have taken place sporadically over the last century, and standardization is lacking. Therefore, it is not entirely clear how interconnected these communities are, or how they may have changed through time. To address this, in summer 2021 we conducted vegetation transect surveys on 8 peaks to assess whether the size and isolation of each "sky island" affects species presence, richness, and diversity. Mountaintop locations were chosen to incorporate various sizes, levels of isolation from other peaks, and the presence of historic surveys. We found that levels of isolation may be more important for species richness and diversity than the size of each alpine island. We also present a new technique for virtual permanent plots using photogrammetry to standardize re-surveys in the future. As climate continues to change, it becomes increasingly important to monitor these fragile communities without disruption and track changes through time.

Assessing species distribution models′ abilities to locate unknown populations of rare sedges in eastern Arkansas

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Documenting and monitoring extant populations of rare species is vital for planning and prioritizing conservation activities. However, our knowledge of rare species’ population locations is often incomplete, inhibiting our ability to develop informed conservation strategies. Species distribution models (SDMs) can direct efficient surveys for previously unknown populations of rare species and increase our knowledge of species’ geographic ranges and vulnerability statuses. The first goal of our project is to locate unknown populations of rare sedges (genus Carex, Cyperaceae) in eastern Arkansas through field surveys guided by SDMs. Carex is a highly diverse group in North America, and many species in the genus can be difficult to identify or may be overlooked, which is common among graminoids. The second goal is to identify parts of the modelling process that have the greatest effect on the success rate of surveys. These goals will be accomplished by (1) training species distribution models based on known occurrences of rare Carex spp. in Arkansas and associated environmental and biotic factors, (2) testing various models’ abilities to locate new populations of sedges through ground-truthing field surveys directed by these models, and (3) assessing which aspects of SDMs (e.g., type and parameter settings) and available data sources (e.g., number of known occurrences of a species) are most important when attempting to locate new populations of rare species. Ultimately, this project will develop improved methods for locating, monitoring, and conserving rare species with few known occurrences in highly modified landscapes.

Biodiversity Distribution Index: Tracking spatial and temporal trends in species ranges

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Biodiversity indicators have been intensively developed in the past few years to address the need for measuring progress towards biodiversity conservation targets such as the Aichi 2020 Targets. These indicators measure, among other things, changes in species habitat sizes, population size trends and protected area covers. However, none of these indicators measures changes in species ranges. Such an indicator would be relevant, since climate change-induced range shifts is one of the most widely anticipated biodiversity changes. Here, we propose a biodiversity indicator that uses species distribution models to measure temporal and spatial trends in species ranges. We build the models considering only spatio-temporal autocorrelation to describe the species distribution. Using a similar approach to Living Planet Index, we calculate the mean aggregate change in species ranges for a given year and region. One advantage of using species distribution models is that the indicator can be spatialized, which allows changes to be mapped on the entire studied region. It is also possible to decompose the net change showed by the indicator into gross changes resulting from local colonizations and extinctions that produced species ranges shifts. By measuring gross changes, the proposed indicator would allow i) linking local colonizations and extinctions to land use and bioclimatic variables and ii) to project the value of the index into the future under different land use and climate change scenarios, which would be useful in a context where conservation actions must be planned to meet future biodiversity targets.

Current dung beetle distributions as indicators of abiotic and biotic changes in the African continent: a case study using Catharsius Hope, 1837 (Scarabaeidae, Scarabaeinae)

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Dung beetles are well documented to perform a range of ecosystem services such as dung removal, soil perturbation, and secondary seed dispersal, and so are amongst the most well-studied of invertebrate taxa. Such studies have shown dung beetles to be effective biodindicators and sensitive to environmental change, but are often geographically confined. Thus, it has not been possible to investigate these sensitivities at a larger scale, a task heavily dependent on reliable taxonomy, lacking for many dung beetle species at present. Using the largest revision of any group of dung beetles in the world for maximum entropy modelling, this study provides continent-wide evidence of habitat fidelity in the genus Catharsius, as well as uncovering the relative strength of environmental drivers behind these distributions such as soil type, ecoregion, and a number of climate variables. Preliminary results indicate soil type to be a significant driving force behind distribution, aligning with their strategy of burrowing beneath dung pats. In undertaking such analysis, this work not only builds on current evidence that dung beetles are excellent indicators of habitat on an unprecedented scale, but also underlines taxonomy's fundamental importance as the foundation to wider-scale studies of biogeography, despite the common misconception that it fulfils a merely supplemental role to the primary line of enquiry in biological studies. Recommendations for further research suggest exploration of whether the distributions of dung beetle species that do not burrow rely so heavily on soil type, and the opportunities afforded to biogeography by taxonomically revised natural history collections.

Molecular markers and ecological niche modeling uncover migration routes of the Carpathian endemic round leaved ox-eye daisy (Leucanthemum rotundifolium)

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Carpathian Mts are located in central Europe and are important as a biodiversity hotspot and as a link between mountain ranges in other parts of the continent. Their endemic flora consists of ca. 420 plant taxa. A small but interesting part of that number are subendemics (ca. 39 species) – taxa which typically occur in one to a few isolated populations outside the Carpathians. Here we study one of them, round-leaved oxeye daisy (Leucanthemum rotundifolium (Willd.) DC.) – a Carpathian subendemic plant linked to montane and subalpine climatic belts distributed throughout the whole Carpathian Mts and in one isolated stand in Dinaric Alps. Using a range-wide sample collection, we examine the phylogeographic patterns within this species to gain new information about its origin and evolutionary history. We are utilizing molecular methods (sequencing of cpDNA markers and genome-wide SNPs) and ecological niche modeling. We also examine links with other species through phylogeny and document a possible ongoing hybridization with sympatric alpine and lowland species (L. gaudinii Dalla Torre (2x) and L. ircutianum DC. (4x)). We hope that this study will also contribute data to analyze more general patterns in the Carpathian region.

Oh, the places they'll go!: Examining Contemporary Tree Range Shifts

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The geographic range of a species is a fundamental unit of ecology and biogeography. The rapidly growing availability of species occurrence data presents opportunities to readily estimate geographic ranges using diverse tools. To date, efforts to understand geographic ranges and how they shift through time and space have largely focused on forecasting future distributions using predictive models, mapping historic distributions using geologic data, or monitoring single sites and/or species. These descriptive approaches suggest widespread and multi-directional range shifts across taxa, which runs counter to predictions that species will migrate uniformly northward in latitude and upward in elevation as climate warms. Little effort has been made to systematically understand and summarize the variability in range shift dynamics and the processes that delimit range boundaries in a large-scale, multi-species context. Aiming to fill this gap, we evaluate the geographic ranges of all U.S. tree species partitioned into distinct life-history stages (seedling, sapling, adult) to assess range shifts in contemporary environments on generational timescales over which birth and death, the processes that set range limits, readily play out. Using occurrence data from the U.S. Forest Inventory and Analysis database we measure the distribution of each life-stage for each species as a convex hull polygon. We quantify changes in range size, position, and direction between life-stage polygons to evaluate within- and among-species variation. Considering where juveniles exist in relation to conspecific adults presents an opportunity to evaluate incipient range shifts, moving beyond predictive models and historical inferences to query real-time empirical data.

Phylogenetic Niche Modeling

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When studying how species will respond to climatic change, a common goal is to predict how species distributions change through time. Species distribution models (SDMs) are commonly used to estimate a species' environmental niche from observed patterns of occurrence and environmental predictors. However, species distributions are often shaped by non-environmental factors–--including biotic interactions and dispersal barriers—truncating niche estimates. Though a truncated niche estimate may accurately predict present-day species distribution within the sampled area, this accuracy decreases when predicting occurrence at different places and under different environmental conditions. Modeling niche in a phylogenetic framework leverages a clade's shared evolutionary history to pull species estimates closer towards phylogenetic conserved values and farther away from species specific biases. We propose a new Bayesian model of phylogenetic niche implemented in R. Under our model, species SDM parameters are transformed into biologically interpretable continuous parameters of environmental niche optimum, breadth, and tolerance evolving under multivariate Brownian motion random walk. Through simulation analyses, we demonstrated model accuracy and precision that improved as phylogeny size increased. We also demonstrated our model on a clade of eastern United States Plethodontid salamanders by accurately estimating species niche, even when no occurrence data is present. Our model demonstrates a novel framework where niche changes can be studied forwards and backwards through time to understand ancestral ranges, patterns of environmental specialization, and niche in data deficient species.

Potential decline in the distribution and food provisioning services of the mopane worm (Gonimbrasia belina) in southern Africa

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The mopane worm (Gonimbraisa belina) is an edible insect found across southern Africa which provides nutrition, and contributes to social and economic wellbeing for rural communities. However, the mopane worm's future distribution and abundance is likely to be impacted by climate change, with a consequential decline in its reliability as a food source. We modelled the potential future species distribution of the mopane worm by considering both abiotic drivers and biotic interactions, including food trees and predator species. Our predictions point to as much as 70% decline in mopane worm habitat by the 2080s. Such a decline could mean mopane worms are unavailable as a source of food, causing households to lose the income provided by their harvest and deepening food insecurity and socio-economic inequalities. Our study highlights how biodiversity responses to climate change may cascade beyond species distribution decline, and most negatively impact rural communities dependent on natural resources.

Range-wide and regional distribution of the Western Tragopan (Tragopan melanocephalus) and effects of disturbance on local abundances

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The Western Tragopan, Tragopan melanocephalus, is endemic to the Western Himalayas and currently listed as ‘vulnerable’ by the IUCN who also emphasized a data deficiency regarding its distribution and population size. With this study we provide new data from the Palas Valley, northern Pakistan and deliver a range wide estimate of the species current, past and future potential distribution as derived from environmental niche models. In the Palas Valley, Western Tragopans occupied different summer (dense mixed coniferous-deciduous forests on north-facing slopes) and winter habitats (mixed oak forests on south-facing slopes). Based on call count surveys, population density in the Palas Valley was 30.4 individuals per km2. Niche models suggest that the species range between Himachal Pradesh and northwestern Pakistan might be less fragmented than currently considered with a major distribution gap only in the Kashmir Valley. During the Last Glacial Maximum (LGM) T. melanocephalus was probably restricted to small forest Refuges and expanded its range during the subsequent interglacial period to the present extent. Projections onto eleven future climate simulations were inconclusive with the majority suggesting that climatically suitable space for T. melanocephalus will likely expand in response to anthropogenic climate change. However, we recorded notably fewer birds in study sites with high levels of disturbance (livestock, plant collectors and hunters), particularly where disturbances occurred during the breeding season. Therefore, we recommend that future conservation measures should be planned with regard to the species’ sensitivity to anthropogenic disturbances.

Resolution in species distribution models shapes spatial patterns of plant multifaceted diversity

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Species distribution models (SDMs) are statistical tools that relate species observations to environmental conditions to retrieve ecological niches and predict species’ potential geographic distributions. The quality and robustness of SDMs clearly depends on good modelling practices including ascertaining the ecological relevance of predictors for the studied species and choosing an appropriate spatial resolution (or ‘grain size’). While past studies showed improved model performance with increasing resolution for sessile organisms, there is still no consensus regarding how inappropriate resolution of predictors can impede understanding and mapping of multiple facets of diversity. Here, we modelled the distribution of 1’180 plant species across the European Alps for two sets of predictors (climate and soil) at resolutions ranging from 100 m to 40 km. We assessed predictors’ importance for each resolution, calculated taxonomic (TD), relative phylogenetic (rPD) and functional diversity (rFD) accordingly, and compared the resulting diversities across space. In accordance with previous studies, we found the predictive performance to generally decrease with decreasing predictor resolution. However, a threshold of 10 km was found, above which performances reached a plateau. Overall, multifaceted diversity was found to be strongly affected by resolution, particularly rPD, as exhibited by weak to average linear relationships between 100 m and 1 km resolutions ($0.13 \leq R2 \leq 0.57$). Our results demonstrate the necessity of using highly-resolved predictors to explain and predict sessile species distributions, especially in mountain environments. Using coarser resolution predictors might cause multifaceted diversity to be strongly mispredicted, with important consequences for biodiversity management and conservation.

Wolf in the Central Europe - geographic and genetic crossroads

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The aim of the study is to present a dynamic situation regarding species distribution and population genetic structure of the grey wolf in Central Europe, a region considered as a frequent crossroad and contact zone of different phylogeographic lineages, in a biogeographic context. Genetic differentiation shows population isolation and recognized environmental clusters, suggesting ecotypic variation. The east–west split in the Western Carpathians likely represents the signature of range fragmentation during bottlenecks in the 20th century.