INTERNATIONAL BIOGEOGRAPHY SOCIETY
EARLY CAREER BIOGEOGRAPHERS CONFERENCE
OCTOBER 22–24, 2021

ABSTRACT BOOK

ECBC VIRTUAL 2021
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EARLY CAREER BIOGEOGRAPHERS CONFERENCE
OCTOBER 22-24, 2021

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PLENARY TALKS

Whittaker, Robert (Presenter)

Session: Plenary Session 1

Title: Recent advances in the biogeography and macroecology of islands

Robert J. Whittaker (robert.whittaker@ouce.ox.ac.uk), University of Oxford

Abstract:

Remote islands provide excellent model systems for developing and testing general models in biogeography and macroecology. I will review recent work focused on explaining patterns of diversity variation among and between island systems, exploring how the sometimes the same systems can reveal signal from processes operating over different temporal scales. In particular, I will present updated analyses and interpretation of the co-dependence of the slope and intercept of the ISAR (the island species–area relationship) on archipelagic diversity.

Willis, Kathy (Presenter)

Session: Plenary Session 2

Title: Biogeography and its critical role in determining natural capital at local, regional, and global scales

Kathy Willis (kathy.willis@zoo.ox.ac.uk), University of Oxford

Abstract:

Policies to manage, conserve and enhance biodiversity have seen a dramatic shift in their framing over the past decade. Terms such as "natural capital" and "nature's contribution to people" are now commonly used. The focus of this framing is upon determining those aspects of nature (biotic and abiotic) that underpin important societal benefits. These range from determining aspects of nature that are important for carbon sequestration, to those that reduce flood risk, soil erosion, and provide important habitats for biodiversity. Aspects of nature that are important for health and wellbeing, including recreational areas, also come under this natural capital framing. Many countries are now developing 'Natural Capital' assessments to understand where their most important natural capital assets are located at national, regional and local scales. They are also devising payment mechanisms to ensure that those aspects of nature that are important in this respect, receive funding for maintenance and enhancement, and to limit degradation. Whilst the steps to undertaking these assessments appears relatively straightforward, in practice it is quickly becoming realised that one of the greatest obstacles to enabling a natural capital approach to become operational, is a paucity of datasets and models that can understand the dynamics of ecosystems in space and time. There is also almost no understanding of the impact of current and future climate change upon natural capital assets and their flows. This talk will illustrate the huge

potential of the discipline of biogeography to fill these knowledge gaps, discussing a number of excellent studies that have recently been published that demonstrate the importance of the discipline in providing the data and models, in terrestrial and marine environments, to understand different facets of natural capital at local, regional and global scales and how it varies in both time and space.

Smith, Felisa (Presenter)

Session: Plenary Session 3

Title: The missing piece: late Pleistocene changes in the ecological function of mammal communities in North America

Felisa A. Smith (fasmith@unm.edu), University of New Mexico

Abstract:

By the late Pleistocene, the genus Homo increased exploitation of other mammals for food and resources. As hominins, particularly archaic and modern humans, became increasingly abundant and dispersed across the globe, a temporally and spatially transgressive extinction of large-bodied mammals followed; the degree of selectivity was unprecedented in the Cenozoic fossil record. The rate of extinction has increased over time; today, the conservation status of the largest mammals is precarious owing to a disastrous combination of continued hunting, habitat loss /alterations, and conflict withhumans. Recent work suggests that large-bodied species perform many essential ecosystem services, which are not fully characterized. Because biodiversity threats are ongoing, conservation biologists cannot wait for the results of long-term studies before proposing potential mitigation strategies. Yet, understanding the functional role of large-bodied mammals is essential for effective management of the remaining wild areas on Earth. Thus, a paleoperspective can provide powerful insights; by studying the consequences of the catastrophic biodiversity loss at the terminal Pleistocene, we can elucidate the long-term ecological effects of the loss of large-bodied animals on the rest of the mammal community. Here, I review work at different temporal and spatial scales that use the late Quaternary as a proxy for modern biodiversity loss. A common theme is that the loss of biodiversity led to differences in community structure, species occurrence patterns, the diet and body size of survivors, and the connectivity and resilience of mammal communities. These results suggest that without major conservation efforts, the ongoing loss of megafauna will lead to further ‘missing pieces’ within mammal communities.

Ramakrishnan, Uma (Presenter)

Session: Plenary Session 4

Title: Biogeography and the future of biodiversity in the Indian subcontinent

Uma Ramakrishnan (uramakri@ncbs.res.in), National Centre for Biological Sciences

Abstract:

Biogeography helps us understand why species are found where they are. Over the last fifteen years, I have worked to understand the distribution of birds and mammals in the Indian subcontinent from a biogeographic, phylogeographic and population genetic perspective. Early work helped understand how mountain topography affects species. Integral to such investigation is the realisation that humans are significantly impacting biodiversity, connectivity between populations, and affecting species' communities. I will discuss work we have done on multi-species connectivity and impacts of land-use change on community composition. Finally, such change can result in zoonotic spillover. I will discuss how studying biogeography and community ecology can inform such research. This will be a broad talk, also discussing my research trajectory as a scientist who cares about biodiversity in the global south.

Bush, Mark (Presenter)

Session: Plenary Session 5

Title: Recent advances in understanding pre-Columbian impacts on South American ecosystems

Mark Bush (mbush@fit.edu), Florida Institute of Technology

Abstract:

Recent advances in understanding pre-Columbian impacts on South American ecosystems Abstract: Species distributions and diversity, the structure of forests or the amount of carbon sequestered in forest or soils, can all be strongly influenced by human disturbance. While these impacts are immediately apparent in systems undergoing modern disturbance, the extent to which Amazonian rainforests are still impacted by the actions of people from hundreds of years ago is actively debated. Known as 'legacy effects', historical ecologists suggest that past cultivation of trees could result in forests enriched with useful species. Similarly, harvesting for timber or other one-time use of species could lead to depletions. If those population changes persist to the present, they form a legacy effect. As a result of such legacies, it has been argued that no forest within Amazonia offers a natural baseline of species abundances. Such assertions should be tested. Paleoecology can address critical spatial and temporal questions such as: When and where did disturbance last occur? How were forests altered, and how long do signatures of disturbance last? Fossil pollen, phytolith and charcoal analyses of Amazonian lake sediments and forest soils are building a body of data that provides some important insights. 1) Indigenous communities often cleared land and cultivated species. 2) Most of those impacts disappeared very rapidly following site abandonment. 3) The initial concept of legacy effects needs to be revised to include indirect

effects, which can be long-lasting. 4) Assumptions that European arrival provided a well-defined watershed in Amazonian ecology are poorly founded.

Sax, Dov (Presenter)

Session: Plenary Session 6

Title: Advances in the application of niche concepts to forecast risks from climate change and evaluate controversial conservation strategies

Dov Sax (dov.sax@gmail.com), Brown University

Abstract:

Species Distribution Models (SDMs), a.k.a., climate envelope or climate niche models, are a mainstay of current efforts to forecast extinction risk from climate change. The application of these models to ecological forecasts depends upon a number of underlying assumptions; the greater the degree to which these assumptions are invalid, the greater the likelihood that forecasts will be misleading. One of the most important of these assumptions is that the climate conditions occupied by a species within its native, historic range are the only ones in which a species can thrive. Recent work exploring: 1) in situ survival following recent climate change, 2) occupation of different conditions identified with paleoecological data, and 3) occupation of different conditions in species non-native ranges, all indicate that many, if not most, species can thrive in conditions beyond those found within their historic, native ranges. Exploring these types of evidence indicates that those species with very small native ranges, which with traditional approaches would be the ones forecast to be most vulnerable to climate change, actually have more tolerance for climate change than would otherwise be expected. Likewise, these small-ranged species may have the broadest variety of alternative conservation management actions available to them. The Implications of these findings relative to extinction forecasts, future conservation actions and biogeographic theory are considered.

Nogué, Sandra (Presenter)

Session: Plenary Session 7

Title: The human dimension of biodiversity changes on islands

Sandra Nogué (sandranogue@gmail.com), University of Southampton

Abstract:

In this talk Sandra will present the latest findings from collaborative projects on the impact of humans on island's biodiversity. The findings suggest that the rate of change on plant biodiversity increases significantly during the years following human settlement, with the most dramatic changes occurring in islands settled in the last 1500 years. She also will discuss how their results may help to inform trajectories of change and targeted restoration efforts and provide greater understanding into plant biodiversity change.

Matias, Miguel（Presenter）

Session：Plenary Session 8

Title：mail.miguelmatias@gmail.com

Miguel Matias（mail.miguelmatias@gmail.com）, Museo Nacional de Ciencias Naturales

Abstract：

Abstract coming soon

ORAL PRESENTATIONS

Addae-Wireko, Louis (Presenter)

Session: CS10 – Climate Change Biogeography

Title: Ecoregions with the fewest species experience the greatest turnover

Louis Addae-Wireko (laweko@gmail.com), Kwame Nkrumah University of Science & Technology, Kumasi
A. Michelle Lawing, Texas A&M University

Abstract:

Climate changes affect ecosystems and the species they contain. Species have had dynamic geographic ranges and many track suitable climate more easily than adapting to new conditions. However, we don't know exactly where changing community compositions have been the most dynamic. Establishing where gains and losses of species are anticipated to occur within ecoregions will help elucidate consistency of community across space. In this study, we investigate temporal beta diversity from stacked ecological niche model projections of 59 species within the Agave genus in North America to evaluate shifts in modeled community composition manifested as gains / losses through time. We calculated temporal beta diversity for multiple variations of stacked Maxent models and summarized temporal change by ecoregion type. Temporal beta diversity showed little turnover for most ecoregion types, but there were significant diversity differences ($p < 0.01$) for Northern Forests in all future projections. There were relevant differences from the LGM and the Mid Holocene for Marine West Coast Forest ($p < 0.01$) and from the LGM for Eastern Temperate Forests and the Great Plains ($p < 0.01$). Importantly, we found that the ecoregions with the fewest species have the greatest change in temporal beta diversity. Knowledge of these shifts offer an avenue to direct monitoring of Agave species for conservation management and to explore gains anticipated for species and intervene in those that may not be able to track their climates due to habitat connectivity disruptions based on current land use practices.

Adeleye, Matthew (Presenter)

Session: CS12 – Paleobiogeography

Title: Biotic exchange and associated environmental conditions on an Australian ancient land bridge during the last glacial

Matthew Adesanya Adeleye (Matthew.adeleye@anu.edu.au), The Australian National University
Simon Haberle, The Australian National University
David McWethy, Montana State University
Simon Connor, The Australian National University
Janelle Stevenson, The Australian National University

Abstract:

Ancient land-bridge environments are generally understudied globally, with only a few detailed studies (e.g., Bering landbridge) despite their roles as biogeographic corridors for species distribution and diversification, as well as human migrations in the past. The Bassian Land Bridge (BLB) in southeast Australia is no exception. The BLB allowed one of the earliest movements of people into high southern latitudes on the globe between ~40 and 36 ka. While phylogenetic studies have shown that the BLB supported plant dispersal between mainland Australia and Tasmania during the Last Glacial Maximum (LGM), environmental conditions associated with biotic exchange and human migration across the land bridge is less well understood. We use a multiproxy palaeoecological approach to understand past environmental conditions on the BLB, which today is a submerged continental strait, by reconstructing vegetation, fire, and lake histories of one of the larger Bass Strait islands. We then compared this record to existing studies from the area in order to develop a broader understanding of the ancient land bridge environment. Results suggest people (and fauna) would have migrated through a wet-wooded, partially exposed BLB, with frequent fire usage when they first arrived in Tasmania before the LGM. Eucalyptus dispersed effectively between mainland Australia and northeast Tasmania at this time. Later biotic movements (including humans) during the LGM would have occurred on a drier and grassy fully-exposed BLB. Lake levels dropped markedly at this time, fire activity also decreased or became spatially variable, and dispersal routes increased. Dryland herbaceous taxa were mainly dispersed between adjacent mainland Australia and Tasmania during this period.

Albaladejo-Robles, Gonzalo (Presenter)

Session: CS15 – Gradients, range-limits & diversity

Title: Vertebrate Fast and Slow species response to spatial heterogeneity

Gonzalo Albaladejo-Robles (ucbtga1@ucl.ac.uk), University College London (UCL)

Abstract:

Historically, life history strategies have been a key concept in ecology and a major subject of study. According to life-history theory, species with different life strategies respond differently to environmental challenges. However, little is known about the real implications of these strategies for the distribution and response of species to spatial heterogeneity. Following this principle, we tested whether terrestrial vertebrate species respond differently to spatial heterogeneity due to land use. To do so, we collected life-history trait information of more than 2.000 species distributed across the globe. With this information, species were classified as fast or slow species according to their positions into two different life-history classification schemes, the fast-slow and the body-size continuums. Once species were classified, we combined the values of the fast-slow and body mass continuums with the available spatial information for the different species to test whether there was any relationship between them and the spatially explicit land-use information. We expected Slow species, those with slow growth rates and a lower number of offspring, to be more likely to occur in homogeneous ecosystems. Conversely, fast species, those with short development cycles and high reproductive outcomes, are expected to present a higher presence in more fluctuating or heterogeneous environments. Results from these observations could provide a step forward into the understanding of how biodiversity responds to environmental changes from a more functional point of view.

Anaya-Valenzuela, Luisa (Presenter)

Session：CS23 – Conservation & Invasion Biogeography

Title：The fate of Amazonian threatened species if mining was allowed in protected areas

Luisa Fernanda Anaya-Valenzuela (luisafer.anaya@gmail.com), Universidad Alcalá de Henares
Sara Villén-Pérez, Universidad de Alcalá (UAH)
Paulo De Marco, Universidade Federal de Goias

Abstract：

The Amazon biome sustains about 10% of the world's known biodiversity, including hundreds of vertebrates threatened by habitat loss and degradation. The basin also contains one of the largest unexplored reserves of mineral in the world. Brazil mining leases have increased rapidly in the last decades, and mining exploration is planned to further affect ca. 7000 kha in the next years. Protected areas represent an important barrier to mining expansion, though a number of bills have been recently proposed to allow mining in different categories of protected areas where it is currently forbidden. We quantified the direct impact of mining on the distribution of 125 threatened Amazonian terrestrial vertebrates to date and in the near future, considering four legislative scenarios of mining restriction in protected areas. Current mining projects impact an average of 0.31% of the distribution of each threatened vertebrate. In the near future this may increase to 2.3% if the law does not change, to 3.7% if mining was allowed in all sustainable use protected areas (currently it is allowed only in some of them), to 2,4% if mining was allowed in 10% of strictly protected areas, and to 2.5% if mining was allowed in indigenous lands. Even though mining projects occupy a relatively small area, the impact may multiply when considering indirect deforestation and pollution. Moreover, the most impacted species have small distributions, which itself increases their extinction risk. Downgrading Amazonian protected areas may trigger mining requirements and further reduce the distribution area of threatened species.

Araújo, Magno (Presenter)

Session：CS08 – Biogeography of the Anthropocene

Title：Does the species-habitat area relationship differs between plant life forms?

Magno Oliveira Gonçalves Araújo (magno__mm2006@yahoo.com.br), Federal University of Ceará /University of Tartu
Carlos Carvalho, Universidade Federal do Ceará
Pedro Aurélio Pequeno, Instituto Nacional de Pesquisas da Amazônia
William Magnusson, Universidade Federal do Ceará
Julia Sfair, Universidade Federal do Ceará

Abstract：

For more than forty years, conservation ecology has debated the best vegetation configuration for maintaining species diversity in fragmented landscapes: a single large fragment (SL: "single large") or several small fragments of vegetation (SS: " several small ") of the same total area, known as SLOSS. However, most of those studies were conducted on scales appropriate for academic studies, and not at the scales appropriate for conservation reserves. This study aims to understand whether many landscape units with small areas of suitable habitat are more effective than a smaller number of landscape units on species densities. For this, we used vegetation data collected for the Brazilian Caatinga drylands, to investigate the effect of different proportions of suitable habitat on various plant lifeforms in landscape units at a variety of scales. The smallest units, corresponded to squares of 200m by 200m, which is probably closest to the scales of most academic studies of fragment size. The other scales represented realistic areas for small (1km2), medium (25 km2) and large (100 km2) reserves in the southern regions of Brazil. When we investigated the effect of the proportion of habitat in landscape units, we found that the relationship between species density and reserve size varied greatly among plant life forms. Higher species densities of small plants (herbs, subshrubs) are found in combinations of landscapes with low proportional cover of forest than in combinations of landscapes with the same proportion of suitable habitat, but the conservation implications of this need to be investigated.

Arranz, Ignasi (Presenter)

Session: CS13 – Biogeography of the Anthropocene

Title: The disassembly of community size structure examined using size-spectra theory

Ignasi Arranz (ignasi.arranz-urgell@univ-tlse3.fr), Laboratoire Evolution et DiversitÈ Biologique, UniversitÈ Toulouse III Paul Sabatier, Toulouse, Fran
Julien Cucherousset, Laboratoire Evolution et Diversite Biologique, Universite Toulouse III Paul Sabatier, Toulouse
Gaël Grenouillet, Université Paul Sabatier

Abstract:

A key question in ecology is to understand if general assembly rules still apply in communities exposed to anthropogenic disturbances. Community disassembling acts at the individual level because the first response to a changing environment is through alterations of individuals' behavior and metabolism. Body size is a key individual trait linking metabolic theory and bioenergetics. Therefore, approaches based on community size structure (i.e. distribution of individual body sizes in communities independently of species identity; CSS) may provide further insights into our understanding of disassembly and natural processes shaping CSS because individual-level processes (e.g. metabolism) may respond more strongly than processes occurring at the species level (e.g. colonization or extinction rates). Using > 1,000 stream fish communities sampled across France, we estimated CSS using size spectrum theory, an approach widely used as a marine bioindicator and energy-flux model, that allows quantifying three facets of CSS: biomass conservation, carrying capacity, and stability. We then tested (i) the capacity of natural and anthropogenic environmental predictors to explain variation in each size-spectrum facet and (ii) if anthropogenic disturbances modified natural processes. First, we found that carrying capacity was positively affected by altitude and biomass conservation negatively by temperature, two key natural predictors of community assembly. Second, we found that the effects of natural processes on community stability were mediated by anthropogenic disturbances. Together, these findings indicate that community disassembly induced by anthropogenic disturbances may reflect changes in community stability and the size-based energy-fluxes within ecological communities.

Arruda, Thalita (Presenter)

Session: CS06 – Phylogeography

Title: What drives multifaceted diversity in a highly dynamic island system?

Thalita Ferreira Arruda (thalita.ferreira-arruda@uni-goettingen.de), University of Goettingen

Abstract:

Several studies have shown the importance of environmental and physical processes as drivers of insular biodiversity. Those studies usually focus on taxonomic diversity only and treat species as ecologically equivalent. Yet, it is unclear if the importance of environmental and physical processes as predictors of vascular plant diversity holds when accounting for evolutionary history and trait variation. To address this question, we assess the extent to which environmental and physical processes drive multifaceted diversity (taxonomical, phylogenetic and functional diversity) on the Frisian Islands. The Frisian Islands are a highly dynamic barrier island system in the Wadden Sea and are especially susceptible to the physical processes of sedimentation and erosion. These processes give rise to a constant and often rapid changes in area and the distribution of habitats. We investigate the role of island area, habitat heterogeneity and geomorphological dynamics as drivers not only taxonomical diversity but also, of phylogenetic and functional diversity. Across multiple diversity facets, we find area to be the most efficient predictor. However, there is evidence for an area-heterogeneity trade off affecting functional diversity. Our study highlights the importance of going beyond species identity when investigating diversity drivers, since abiotic and environmental processes influence may vary for different diversity facets.

Bach, Wilhelmine (Presenter)

Session: CS24 – Biodiversity patterns, distribution & maintenance

Title: Dimensions of diversity metrics in terrestrial vertebrates

Wilhelmine Bach (wilhelmine.bach@usys.ethz.ch), Landscape Ecology, Institute of Terrestrial Ecosystems, ETH Zürich
Alex Skeels, Landscape Ecology, Institute of Terrestrial Ecosystems, ETH Zürich & WSL, Birmensdorf, Zürich

Abstract:

Understanding large-scale biodiversity distribution in macroecology and biogeography has been limited by our understanding of the spatial co-variation of distribution patterns. For instance, ubiquitous patterns like the latitudinal diversity gradient present very differently across dimensions of diversity e.g. taxonomic, phylogenetic, functional as well as alpha and beta diversity. At the same time, the distribution of diversity dimensions varies among clades, with no concise answer as to how taxa differ and whether ecologically similar clades show similar distribution patterns. We lack a synthetic understanding of the variation of diversity across

dimensions, which is needed to discover how biodiversity patterns have emerged over geological time spans. In particular, there is an ongoing debate, to which degree diversity patterns in terrestrial vertebrates, a clade with unique ecological radiations during the Cenozoic and Mesozoic, are driven by historical or geographic contingencies or by ecological differences between lineages. Here we will go into some of the ways we can use spatial simulation models to explore the spatial distribution of different facets of diversity metrics, spatially and among clades. We can implement variations of mechanisms through four core processes in the model and compare the metrics produced to empirical patterns, which allows us to discriminate between mechanisms. We will explore how we can reduce dimensionality in the covariation, identify distinct axes with representative core metrics and use these to illuminate the variation of diversity dimensions between tetrapod clades. Reconciling multidimensional patterns in empirical data with the underlying eco-evolutionary processes can ultimately help us answer questions about present large-scale biodiversity distribution and the formation of biodiversity itself.

Bansal, Mahi (Presenter)

Session: CS12 – Paleobiogeography

Title: Cretaceous origin of plant family Linaceae and its palaeobiogeography

Mahi Bansal (mahibansal6@gmail.com), Birbal Sahni Institute of Palaeosciences
Shivaprakash Nagaraju, The Nature Conservancy Centre, India
Vandana Prasad, Birbal Sahni Institute of Palaeosciences

Abstract:

Linaceae is a cosmopolitan family comprising a “family pair” of Hugonioideae embracing 6 genera distributed in tropical regions and Linoideae embracing 8 genera distributed in temperate to cosmopolitan regions. The current study witnesses presence of the oldest fossil pollen of Linaceae showing affinities with extant genera Linum and Reinwardtia (Reinwardtia indica) in the Late Cretaceous infratrappean sequences of Maharashtra, India. We performed phylogenetic analyses combining both pollen morphological characters and molecular sequences of extant as well as fossil Linaceae members to resolve the so far unsettled phylogenetic relationship of the family and estimate its divergence and palaeobiogeographic history. We suggest the Gondwanan origin of the family Linaceae during the Late Cretaceous. The subfamily Linoideae radiated on Africa-India block in Maastrichtian whereas, the subfamily Hugonioideae stemmed from its ancestral lineage in South America during Oligocene. The study postulates the origin of the largest cosmopolitan genus of the family, Linum, on Indian subcontinent (possibly in the aseasonal climate of Kohistan Ladakh Arc) in the latest Maastrichtian. However, the genus adapted to seasonal climate in time and expanded in the Euroafrican region around 63.8 Ma. Another lineage of Linum got dispersed to Southeast Asia from Indian subcontinent after India-Asia collision during mid to late Eocene. The study supports the subsequent diversification of the family in other regions followed by several events of long-distance dispersion. The study also propounds high speciation rate in the New World and African lineages of Linoideae.

Barrasso, Caterina (Presenter)

Session: CS16 – Models & Methods in Biogeography

Title: A global assessment of data uncertainties in available land-use and land-cover time-series

caterina barrasso (caterina.barrasso@idiv.de), German Centre of Integrative Biodiversity Research
Carsten Meyer, German Centre for Integrative Biodiversity Research (iDiv)
Ruben Remelgado, German Centre for Integrative Biodiversity Research (iDiv)

Abstract:

Land-use and land-cover (LULC) changes are likely the main cause of global biodiversity change. Time-series of accurate LULC information are therefore vital to understand the factors shaping biogeographical patterns and their changes in the Anthropocene. Although the number and quality of open-access remotely sensed LULC products is increasing, they have uncertainties due to widespread classification errors. The relative magnitude of uncertainties among exiting LULC products, however, is largely unknown, which hampers their confident selection and robust use by biogeographers and global change ecologists. To close this gap, we quantified region-, time-period-, and LULC class-specific data uncertainties for the most widely used global LULC time-series products. To validate the LULC products we developed a novel multi-scale framework accounting for differences in mapping resolutions and scale mismatches between grid cells and ground-truth reference samples. To control for the effect of landscape heterogeneity in LULC class-wise accuracies, we support the validation assessment with Landsat-based measures of cross-scale spectral similarity computed through Google Earth Engine. We base our accuracy assessment on several 100,000 global LULC ground-truth reference samples integrated through an extensive data collection effort from both field and crowdsourcing campaigns. Here, we present an overview of our preliminary results, providing insights on global and regional patterns of LULC data uncertainties and recommendations on the selection of fit-for-purpose LULC products.

Bastidas Urrutia, Ana Maria (Presenter)

Session: CS05 – Island Biogeography

Title: An analysis of global trait spaces of birds on islands

Ana Maria Bastidas Urrutia (anamaria.bastidas-urrutia@tum.de), Technische Universität München
Christian Hof, Technical University Munich

Abstract:

The equilibrium theory of island biogeography (ETIB) predicts island species richness patterns based on immigration and extinction processes, which are influenced by island characteristics (e.g., isolation and area). Recently, the rise of trait-based approaches has been influencing the field of biogeography, including the ETIB. For example, trophic characteristics and dispersal traits should influence the likelihood of species to colonize islands, i.e., whether they can get to the island and maintain a population. Here, we present an analytical framework that integrates various traits in a multi-dimensional trait space and links them to the predictions of the ETIB and its trait-based extensions. Using the bird communities of the world's islands as a study system, we used eco-morphological traits as surrogates for resource acquisition and dispersal characteristics. Trait information was compiled from museum specimens, public databases, and the literature. Information on species distributions and geophysical island characteristics were also compiled from published databases. Globally, 6.193 species of birds are occurring on 18.428 islands larger than 1km^2. Our preliminary results show that dispersal ability (as indicated by the particular morphological traits) increases with increasing isolation. Furthermore, the average trophic level increases with island size and decreases with island isolation, suggesting that the occurrence of species on small islands is mainly limited to species from lower trophic levels. Overall, these and other results provide general insights into the determinants of the variation of trait spaces among different island bird communities and increase our understanding of the variation of functional diversity on islands in general.

Bellard, Céline (Presenter)

Session: CS23 - Conservation & Invasion Biogeography

Title: Looming extinctions due to invasive species: Irreversible loss of ecological strategy and evolutionary history

Céline Bellard (celine.bellard@universite-paris-saclay.fr), Univ. Paris Saclay

Camille Bernery, Universite Paris Saclay
Camille Leclerc, INRAE

Abstract:

Biological invasions are one of the main drivers of biodiversity decline worldwide. However, many associated extinctions are yet to occur, meaning that the ecological debt caused by invasive species could be considerable for biodiversity. We explore extinction scenarios due to invasive species and investigate whether paying off the current extinction debt will shift the global composition of mammals and birds in terms of ecological strategy and evolutionary history. Current studies mostly focus on the number of species potentially at risk due to invasions without taking into account species characteristics in terms of ecological or phylogenetic properties. We found that 11% of phylogenetic diversity worldwide is represented by invasive-threatened species. Further, 14% of worldwide trait diversity is hosted by invasive-threatened mammals and 40% by invasive-threatened birds, with Neotropical and Oceanian realms being primary risk hotspots. Projected extinctions of invasive-threatened species result in a smaller reduction in ecological strategy space and evolutionary history than expected under randomized extinction scenarios. This can be explained by the strong pattern in the clustering of ecological profiles and families impacted by invasive alien species (IAS). However, our results confirm that IAS are likely to cause the selective loss of species with unique evolutionary and ecological profiles. Our results also suggest a global shift in species composition away from those with large body mass, which mostly feed in the lower foraging strata and have a herbivorous diet (mammals). Our findings demonstrate the potential impact of biological invasions on phylogenetic and trait dimensions of diversity, especially in the

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Bello-Rodríguez, Víctor (Presenter)

Session：CS21 – Climate Change Biogeography

Title：Biotic velocity in response to climate change in the alpine ecosystem of the Canary islands

Víctor Bello-Rodríguez (vbellorod@gmail.com), Universidad de La Laguna / Fundación General Universidad de La Laguna
Andreas Hamann, University of Alberta
Jose L. Martín, Teide National Park
Jonay Cubas, Universidad de La Laguna
Marcelino J. Del Arco, Universidad de La Laguna
Juana María González-Mancebo, Universidad de La Laguna

Abstract：

Climate change is shifting species habitat pole ward and towards higher elevation. These habitat shifts are especially worrying in oceanic islands, due to their high number of endemic threatened species, and speciphycally on alpine habitats, that represent "ecological islands whithin geographical islands". The Canary Islands, one of the archipelagos with highest endemicity rate worlwide includes two ecological islands with a fragile and limited alpine ecosystem above 2000m. This ecosystem is present in La Palma with its maximum peak at 2426 m and Tenerife with 3715 m. Here we present habitat shifts under observed climate change (1970s to 2000s) for 41 as well as for future projections (2050s and 2080s). We analysed the potential habitat area variations at different scenarios, but also the biotic velocity of climate change for these species as a metric for migration requirements. Our results show at what time frames the main peaks of La Palma and Tenerife are expected to become first as biodiversity refugia and after that as biodiversity sinks. We identified an area of particular conservation concern, the Cumbre Vieja Natural Park of La Palma, where species lose climatic habitat under observed climate trends. In Tenerife, where mountain ranges reach higher altitudes, the studied species can find future habitat in El Teide volcano and other surrounding elevated areas, but migration paths towards these refugiums are complex, increasing the values of biotic velocity. We conclude by discussing the value of specific management interventions, such as population reinforcements, translocations or installation of herbivores exclusion fences, guided by species-specific habitat projections.

Bernery, Camille (Presenter)

Session：CS18 – Invasion /Conservation /Climate Change

Title：Important characteristics to become a successful freshwater fish invader

Camille Bernery (camille.bernery@universite-paris-saclay.fr), Universite Paris Saclay
Céline Bellard, Univ. Paris Saclay
Franck Courchamp, CNRS
Sébastien Brosse, MUSÉUM NATIONAL D’HISTOIRE NATURELLE
Boris Leroy, MUSÉUM NATIONAL D’HISTOIRE NATURELLE

Abstract：

Freshwater fish species are among the main introduced taxa and occur in all the biogeographic realms. These introduced fish species can cause several impacts if they become invasive. Invasions of freshwater fishes are known to be influenced by a variety of factors from the introduction pathway and the characteristics of the introduced species until the properties of the receiving ecosystems. However, for freshwater fishes, these characteristics are studied only at local scale, or regarding only one type of characteristics or step of the invasion. For the first time, we investigated the relative importance of intrinsic and extrinsic drivers of freshwater fishes to succeed in invasions. Our worldwide scale analysis focused on 840 freshwater fish species, 14 variables and three steps on the invasion: the introduction, the establishment and the impact step. Specifically, we studied a variety of variables pertaining to species and ecological characteristics, as well as socio-economic drivers such as introduction pathways. Our findings revealed that the number of introduction pathways and diet, as well as a high level of parental care appeared to be the most important characteristics explaining the introduction and establishment success. We also considered species separately following their pathway of introduction, and highlighted driver importance differences, confirming the importance of the pathway of introduction in invasion success. Finally, a high parental care and the type of introduction pathway are important driver explaining the success of the impact step. Our results provide important insights into the main drivers of freshwater fish invasions at a worldwide scale.

Biber, Matthias (Presenter)

Session: CS07 – Conservation Biogeography

Title: Representation of the world's biophysical conditions by the global protected area network

Matthias F. Biber (matthias.biber@tum.de), Technical University of Munich

Alke Voskamp, Senckenberg Biodiversity and Climate Research Centre
Christian Hof, Technical University Munich

Abstract:

Protected areas (PAs) are often implemented without considering already existing PAs, which is likely to cause an over-representation of certain biophysical conditions. We assessed the representativeness of the current PA network with regard to the world's biophysical conditions to highlight which conditions are under-protected and where these are located. We overlaid terrestrial and marine PAs with information on biophysical conditions and then quantified the percentage of area covered. Considering one variable at a time, for the terrestrial realm high temperature, low precipitation, and medium and very high elevation were underrepresented, while for the marine realm, low and medium sea surface temperature (SST), medium and high sea surface salinity (SSS), and the deep sea were underrepresented. Overall, protection was evenly distributed for elevation across the terrestrial realm and SST across the marine realm. Looking at the pairwise interaction of variables, cold and very dry terrestrial environments had mostly low protection, which was also the case for low SST and low and medium SSS across most depths for marine environments. Low protection occurred mostly in the Sahara and the Arabian Peninsula for the terrestrial realm and along the Tropic of Capricorn and toward the poles for the marine realm. Although biodiversity measures are of prime importance for the selection of new PAs, biophysical gaps in current PAs may weaken their potential to conserve biodiversity. Highlighting these gaps adds a frequently overlooked

perspective, but may provide useful insights for researchers, practitioners, and policy makers to establish a more comprehensive global PA network.

Bland, Wallis (Presenter)

Session: CS01 – Models & Methods in Biogeography

Title: State-dependent Speciation-Extinction (SSE) biogeography models with the programming language Julia

Wallis Bland (wallisbland@gmail.com), University of Auckland

Nick Matzke, University of Auckland

Abstract:

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 lineage extinction, and continuous change in distances and/or area sizes over geological time. SSE models require calculating numerical solutions to systems of Ordinary Differential Equations (ODEs), specifically 2 equations for each possible geographic range. Because the number of possible geographic ranges grows at 2^(number of areas), a routine 10-area problem will have 2^10=1024 possible geographic ranges (combinations of presence/absence across the 10 areas), and require the solution of 2048 ODEs. Typical ODE solvers become prohibitively slow for these problems. However, the programming language Julia contains dozens of ODE solvers specialized for very large problems, as well as other useful features, such as allowing continuously changing inputs into the equations. We compare the speed and capability of Julia solvers for large SSE problems. We also explore the potential for integration with the GPlates plate-tectonics software to allow the inclusion of paleodistances into our SSE models, as a factor in determining changing dispersal, speciation and extinction rates. The use of Julia creates a more fast paced environment for the development and deployment of SSE models for biogeography.

Bodin, Stéphanie (Presenter)

Session: CS12 – Paleobiogeography

Title: Anthracology as a tool to assess the impact of pre-Columbian activities on the tropical forests of French Guiana

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Jean-François Molino, AMAP
Guillaume Odonne, LEEISA
Laurent Bremond

Abstract:

In Amazonia, past human impacts on the forests are now increasingly documented. The Guiana Shield is much less studied, although past human occupations have also been reported in this region. Therefore, the impact of pre-Columbian societies on Guianan forests is still poorly known. We aimed to define this impact thanks to an anthracological approach, based on the anatomical identification of charcoal remains. We searched for charcoal in 12 sites of the Nouragues Reserve, French Guiana, hosting different types of vegetation such as Lasiacis thickets, liana forests or high canopy forests, either apparently non-anthropogenic or clearly anthropogenic. Charcoals were ^{14}C-dated and identified to infer the kind of vegetation that was present and burnt near the occupied sites. ^{14}C-dating points a first period of occupation between 1,300 and 1,000 cal BP and a second one between 600 and 400 cal BP. The anthracological assemblages of the most recent period contained secondary vegetation taxa and useful taxa in several sites, reflecting an opening of the vegetation and a wood selection for domestic purposes. A comparison with the present day vegetation suggests that this wood selection may have been adapted locally to the vegetation composition. Charcoal identification reveals that all the sites containing charcoal were under forest cover during the occupation, including those now covered by lianas and Lasiacis. We therefore suggest that the type of human activity may have had different impacts on the structure and composition of subsequent vegetation resulting either in anthropogenic forests or liana and Lasiacis patches after land abandonment.

Böhnert, Tim (Presenter)

Session: CS03 – Biodiversity patterns, distribution & maintenance

Title: Historical Biogeography and Evolution of the Atacama Desert Flora

Tim Böhnert (tboehnert@uni-bonn.de), Nees Institute for Biodiversity of Plants, University of Bonn
Federico Luebert, Universidad de Chile
Dietmar Quandt, University of Bonn
Felix Merklinger, University of Bonn
Maximilian Weigend, University of Bonn

Abstract:

The Atacama Desert in northwestern Chile is surprisingly biodiverse and harbors a range of endemic species adapted to hyperarid conditions. Vegetation is largely restricted to the coastal fog oases and the Andean foothills,

respectively, and separated by a hyperarid desert core. Understanding the distribution and dispersal patterns of the Atacama Desert is fundamental to understanding the origins and diversification of the Atacama Desert flora. Atacama diversifications, have been shown to be surprisingly recent, which is at odds with the high age assumed for this desert. In the framework of a large-scale project on landscape and biotic evolution of hyperarid environments, we aim at investigating the biogeographic history of plants in the Atacama Desert and the underlaying macro- and microevolutionary processes. Here, we present results from a variety of methodological approaches on several plant groups (Amaranthaceae, Malvaceae & Zygophyllaceae) as well as plant communities. Species diversity of Atriplex is the result of multiple colonization events rather than the result of in-situ diversification as it is the case, e.g., in Cristaria. A limited carrying capacity driven by the prevailing climatic conditions seems responsible for limited diversification processes in shrubby taxa in the Atacama Desert. However, metapopulation dynamics and quaternary climate variability lead to increased diversification in other groups. A genetic link to south-western Peru is demonstrated for at least two of the groups investigated. This floristic connection via the Andean foothills (but not the coast) is corroborated by data on the floristic affinity the Andean desert of northern Chile and southwestern Peru.

Borissov, Simeon (Presenter)

Session: CS11 - Phylogeography

Title: Phylogeography of the Eurasian bush-cricket genus Poecilimon Fischer, 1853

Simeon Borissov (borissovsb@gmail.com), Bulgarian Academy of Sciences, Institute of Biodiversity and Ecosystem Research
Dragan Chobanov, Bulgarian Academy of Sciences, Institute of Biodiversity and Ecosystem Research
Georgi Hristov, Bulgarian Academy of Sciences, Institute of Biodiversity and Ecosystem Research
Aneliya Bobeva

Abstract:

The Eurasian tribus Barbitistini (Insecta: Orthoptera) unites exclusively flightless bush-crickets with complex bi-directional bio-acoustic communication. They provide suitable model groups for biogeographic studies due to their poor mobility, high levels of endemism and diversity. Genus Poecilimon includes more than 140 species ranging from Central Europe and Italy to China although most species are found in the Balkans, Anatolia and the Caucasus. Previous studies, concentrated on separate species groups, have linked the diversification of Poecilimon with the geological history of the Eastern Mediterranean and the Pleistocene climatic oscillations. Our aim is to study the origin of Poecilimon and provide a time frame for the deep splits within the genus, thus highlighting the main factors and mechanisms that explain its incredible diversity and contemporary distribution. A strongly supported phylogeny of Poecilimon is provided, based on mitochondrial and nuclear molecular markers. Characteristics of the calling songs are studied and correlated to the phylogenetic splits. Divergence times are estimated with geotectonic calibration. The obtained ages are related to known geological and climatic events in the Eastern Mediterranean, such as the formation of the Mid-Aegean Trench, the Messinian salinity crisis and the Pleistocene climatic oscillations. Ancestral areas of the major species groups are inferred and discussed in the context of paleoclimate and vegetation maps. Based on all data we compare alternative biogeographic scenarios and outline possible routes and barriers to dispersal in the Eastern Mediterranean during the Neogene.

Boschman, Lydian (Presenter)

Session: CS12 – Paleobiogeography

Title: Mountain radiations are not only rapid and recent: Ancient diversification of South American frog and lizard families related to Paleogene Andean orogeny and Cenozoic climate variations

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Fabien Condamine, CNRS, UMR 5554 Institut des Sciences de l'Evolution de Montpellier, (Université de Montpellier), Pla

Abstract:

Mountainous areas host a disproportionately large fraction of Earth's biodiversity, suggesting a causal relationship between mountain building and biological diversification. Mountain clade radiations are generally associated with changes in environment, climate, and the increase in heterogeneity therein during mountain building. However, examining the causal relationship between mountain building and diversification is a complex challenge, because isolating the effects of surface uplift from other abiotic (climate) or biotic variables is not straightforward. In this study, we investigate the relative contributions of abiotic climate-driven (temperature) and geology-driven (elevation) drivers on evolutionary rates of ancient groups of organisms in the South American Andes. We present regional curves of Andean elevation based on a recent compilation of paleo-elevational data back to the Late Cretaceous, and analyse the diversification history of six Andean frog and lizard families that originated equally far back in time. For two clades (Aromobatidae and Leptodactylidae), we find that they diversified most rapidly during the early phase of mountain building (Late Cretaceous - Paleogene), when the first high-elevation habitats emerged in South America. The diversification of one clade (Centrolenidae) is correlated with Cenozoic temperature variations, with higher speciation rates during warm periods. The last three clades (Dendrobatidae, Hemiphractidae and Liolaemidae) are best explained by environment-independent diversification, although for Liolaemidae, an almost equally strong positive correlation was found between speciation and Andean elevation since the late Eocene. Our findings imply that throughout the long-lived history of surface uplift in the Andes, mountain building drove the diversification of different clades at different times, while not directly affecting other clades. Our study illustrates the importance of paleogeographic reconstructions that capture the complexity and heterogeneity of mountain building in our understanding of the effects that a changing environment plays in shaping biodiversity patterns observed today.

Boussange, Victor (Presenter)

Session: CS01 – Models & Methods in Biogeography

Title: Using graph-based metrics to assess the effect of landscape topography on diversification

Victor Boussange (boutor2@gmail.com), ETH Zürich

Abstract:

Biodiversity is unevenly distributed across the Earth, and empirical studies suggest that landscape features have a crucial role in shaping such patterns. Montane regions or riverine systems sustain high levels of species diversity, indicating that topography and habitat complexity are major drivers of biodiversity. Nonetheless, there exists a gap between theory and observations. The complexity of the eco-evolutionary processes that shape species' evolution blur our understanding on how exactly diversification mechanisms are influenced by landscapes. Recently, insights from an eco-evolutionary model where landscapes are represented as a graphs – that capture landscape topographical complexity – revealed that simple graph properties have a major influence on the diversification processes. In particular, the theory demonstrates how heterogeneity in degree, characteristic length and habitat assortativity differently affect neutral and adaptive diversification. In this talk, we propose a simple methodology to project real landscapes on graphs, and illustrate how to characterize large geographical areas by using graph-based topography metrics. Because they connect differentiation patterns to generating eco-evolutionary mechanisms and landscape features, such metrics could improve our understanding of the origin of spatial biodiversity gradients.

Buschke, Falko (Presenter)

Session: CS14 – Biodiversity patterns, distribution & maintenance

Title: The macroecology of Modern Coexistence Theory

Falko Buschke (falko.buschke@gmail.com), University of the Free State
Daryl Codron, University of the Free State

Abstract:

A persistent question in ecology is how diverse sets of species can coexist on a limited number of resources. Modern Coexistence Theory explains species coexistence as the balance between 'equalising' effects, which reduce the fitness differences between pairs of competing species; and 'stabilising' effects, which increase the strength of intraspecific competition relative to interspecific competition. Although modern coexistence theory is conceptually appealing, its empirical application has been limited to local communities with few competing species due to the difficulty of quantifying vital demographic parameters. Here we develop an approach to quantifying the pair-wise equalisation and stabilisation for large and long-lived species based on resource use. We demonstrate this approach using data on the coexistence of 16 large mammal herbivore species across nine protected areas in the grasslands of South Africa. By combining life-history traits and dietary information from carbon and nitrogen stable isotopes, we showed that there is generally an excess of stabilising effects across the study area, demonstrating that the degree of niche partitioning was stronger than was strictly necessary given the small fitness differences between species. We then examined geographic variation the degree of 'over-

stabilisation' and found that this was uniform across temperature (annual averages: 12.5° – 17.6°) and precipitation (annual averages: 430 mm – 866 mm) gradients. Therefore, the excess of stabilisation is a consistent macroecological pattern for mammal herbivores in South African grasslands, suggesting that niche partitioning, while not strictly necessary for coexistence, is a ubiquitous feature of community assembly.

Cabral, Andressa (Presenter)

Session: CS03 – Biodiversity patterns, distribution & maintenance

Title: Frugivores as the main drivers of the global variation of species richness in a typical tropical rainforest plant family (Annonaceae)

Andressa Cabral (acabral@outlook.com.br), German Centre for Integrative Biodiversity Research (iDiv)

Irene Bender, Instituto de Ecología Regional (CONICET-UNT)

Isabell Hensen, Martin Luther University Halle-Wittenberg

Ingolf Kühn, German Centre for Integrative Biodiversity Research (iDiv)

Renske Onstein, German Centre for Integrative Biodiversity Research (iDiv)

Abstract:

Plant species richness is not evenly distributed across the globe. Although the processes underlying species richness patterns are intensively debated, the role of mutualistic interactions in driving species diversity remains unclear. Here, we test the hypothesis that species richness of frugivores (i.e., fruit-eating and seed dispersing animals) is a major driver of species richness in a large (ca. 2400 species), vertebrate-dispersed, pantropical plant family (Annonaceae, Magnoliales). To this end, we applied a macroecological framework and gathered global distribution data for 2259 Annonaceae and 1138 frugivorous bird and 5249 mammal species from the World Checklist of Selected Plant Families (WCSP) and International Union for Conservation of Nature (IUCN) databases. To correct for abiotic effects on species richness, we also assembled environmental variables from the WorldClim database. Multiple linear regression indicated that frugivore diversity of both birds and terrestrial mammals had the strongest positive effect on species richness of Annonaceae, but altitude range, area size, latitude, and precipitation explained an additional variation of Annonaceae species richness. The total explained variation by all our variables combined was >70%. Interestingly, our results also evidenced that Annonaceae diversity is negatively correlated with altitude range, and is probably not dependent on temperature or primary productivity. We suggest that a strong and positive relationship between plant and frugivore species richness could result from co-evolutionary dynamics and reciprocal adaptations in morphological traits related to frugivory. These interactions have important consequences for long-distance seed dispersal and plant speciation, and can thus explain the extraordinary species richness of tropical systems.

Canteri, Elisabetta (Presenter)

Session: CS21 – Climate Change Biogeography

Title: Process-based models reveal 21,000 years of climate-driven range dynamics of muskox

Elisabetta Canteri (elisabetta.canteri@adelaide.edu.au), University of Adelaide
Damien Fordham, University of Adelaide
David Nogues Bravo, Center for Macroecology, Evolution and Climate
Stuart Brown, Aarhus University
Niels Schmidt, Aarhus University
Rasmus Heller, University of Copenhagen

Abstract:

Abrupt shifts in temperature and global warming, together with the spreading of Paleolithic humans, have been driving the range collapse and extinction of arctic megafauna during the Late Pleistocene through to the Holocene. However, the relative contribution of each driver, or a synergy of these impacts, still remains fiercely contested. We reconstruct the range dynamics of the muskox (Ovibos moschatus), over the last 21,000 years, to determine the global change threats and biological processes that drove its long-term population decline and range collapse, and to quantify the roles of climate and human hunting in the muskox extinction risk. We integrate modern occurrences and inferences of past demographic history from fossils and aDNA into process-explicit ecological models, combined with paleoclimate reconstructions and human expansion simulations. Model simulations are being validated against inferences of timing of extirpation from fossils and population decline from aDNA using pattern-oriented methods. Our models are able to reconstruct the extirpation pattern of muskox until industrialisation with fair-to-good accuracy. To accurately reconstruct early-stage population declines and range collapse of muskox, populations needed the ability to disperse in long distances, a small Allee effect, a rapid population growth, and climatic driven shifts of niche requirements. Our results indicate that the main driver of range contraction and extinction risk for the muskox was climate change and not human hunting. This modelling approach results not only in a more informed understanding of the historic range dynamics of the muskox, but also in information needed for the future conservation of this iconic species.

Carey, Mark (Presenter)

Session: CS01 – Models & Methods in Biogeography

Title: Generalised Logarithmic Species-Area Relationship resolves the Arrhenius-Gleason debate

Mark Douglas Carey (mark.carey79@gmail.com), University of South Australia
John Boland, University of South Australia
Gunnar Keppel, University of South Australia

Abstract:

The species-area relationship (SAR) is widely applied in ecology. It is mathematically usually expressed as either a semi-log or power-law relationship, with the former being introduced by Henry Gleason and the latter by Olof

Arrhenius. We here resolve the dispute about which form of the SAR to use by introducing a novel model that smoothly transforms between the Gleason semi-log (GSL) and Arrhenius power law (APL) forms of the SAR. This model takes the form of $\mathrm{lnq}(S) = a + z\,\mathrm{lnA}$, with lnq being a generalized logarithmic function which is a linear map ($y = x$) for $q = 0$ and a logarithmic map $y = \ln(x)$ for $q = 1$. In addition, q can take on other values between 0 and 1, producing intermediate maps. We applied this model to 100 datasets (mostly from islands) linking species richness to island area. The APL was the preferred model in 68% of head-to-head comparisons with the GSL and both models were supported in 40% of cases. However, in just under half (44\%) of the cases neither the GSL nor APL, but intermediate models, best explained the data. This demonstrates the utility of a simple intermediate SAR model. Visualizing the profile of the range of model fits for all q in [0, 1], which is possible with this model, allows us to gain extra insight into SARs not yielded by head-to-head comparisons of GSL and APL. In addition, the mathematics related to the generalized logarithmic function introduced here promises to have application to many other areas of mathematical ecology.

Cartereau, Manuel (Presenter)

Session: CS10 – Climate Change Biogeography

Title: The vulnerability of tree species to future climate change in warm drylands

Manuel Cartereau (manuel.cartereau@imbe.fr), Aix-Marseille University, IMBE

Alex Baumel, Aix-Marseille University, IMBE

Agathe Leriche, Aix-Marseille University, IMBE

Frédéric Médail

Abstract:

Our aim was to quantify climate change vulnerability of tree species in the warm drylands of the world and to address the role of biogeographic regions. Warm drylands cover roughly 19% of Earth's land mass and harbour more than a thousand tree species. Our first assessment of 829 IUCN evaluated tree species revealed that 21% are threatened with extinction and that 43% have declining population trends. According to general circulation models predictions, global climate is expected to become warmer and drier in the future, and drylands spatial extent is likely to increase. We chose to focus our work on warm and very dry (i.e., hyper-arid and arid) areas, as these regions may already be close to the upper thermal limits for some trees. Additionally, as climate change is spatially heterogeneous, and biogeographic history plays an important role in species' adaptations to climate, we integrated our study into a biogeographic comparative framework using bioregionalization. First, we retrieved georeferenced occurrence records for more than 1,000 tree species from online databases and we produced a global bioregionalization of warm drylands. Secondly, using occurrence records and aridity index maps, we assessed the aridity niche of those species. Then we compared aridity niches to aridity conditions predicted in the future, allowing us to assess their vulnerability to future climate change, with a particular emphasize on aridity. Here, we present the climate change vulnerability assessment for c. 1,000 tree species inhabiting warm drylands throughout the world and discuss the effect of the bioregions they belong to.

Castilla-Beltrán, Alvaro (Presenter)

Session: CS12 – Paleobiogeography

Title: Integrating long-term records of ecological change across the islands of Cabo Verde

Alvaro Castilla-Beltrán (a.castilla-beltran@soton.ac.uk), University of Southampton
Lea de Nascimento, Universidad de La Laguna
José María Fernández-Palacios, Universidad de La Laguna
Mary Edwards, University of Southampton
Sandra Nogué, University of Southampton

Abstract:

Cabo Verde is a dry tropical Atlantic archipelago that currently faces severe threats related to land-use, Climate Change, and volcanism. Long-term records of ecological change based on multiple palaeoecological analyses of highland volcanic calderas are yielding data about culture-environment interactions and biodiversity change. In our study, we carry comparative analyses of palaeoecological datasets from Northern (Santo Antão, São Nicolau) and Southern (Fogo, Brava) islands of Cabo Verde, and compare them to long-term ecological data from Macaronesia. Our analyses show that vegetation, ferns and fungal assemblages experienced different trajectories of change after the evidence of land-use by Portuguese settlers, yet there is an overall trend towards biotic homogenization. Erosion, grazing, volcanism and fire occurrence were major drivers of landscape change, and introduced species differ depending on local economic strategies. We discuss the prospects and caveats of integrating long /term ecological datasets in the archipelago, reflecting on their potential to guide conservation and restoration initiatives.

Chakravarty, Rohit (Presenter)

Session: CS04 – Functional Biogeography

Title: Functional diversity of Himalayan bat communities declines without the loss of phylogenetic diversity at high elevation

Rohit Chakravarty (rohit.chakravarty77@gmail.com), Leibniz Institute for Zoo and Wildlife Research
Ram Mohan, Indian Institute of Science, Education and Research Pune
Christian Voigt, Leibniz Institute for Zoo and Wildlife Research
Anand Krishnan, Leibniz Institute for Zoo and Wildlife Research
Viktoriia Radchuk, Leibniz Institute for Zoo and Wildlife Research

Abstract:

Species richness exhibits well-known patterns across elevational gradients in various taxa. However, species richness represents only one aspect of quantifying biodiversity patterns. Functional and phylogenetic diversity, although they provide mechanistic insights into the structuring of communities, have received much less attention, particularly for vertebrate taxa. There is still a limited understanding of how functional, phylogenetic and taxonomic diversity change in concert across large gradients of elevation. Here, we focused on the

Himalaya—representing the largest elevational gradients in the world—to investigate the patterns of taxonomic, functional, and phylogenetic diversity in a bat assemblage. Combining field data on species occurrence and functional traits with measures of phylogenetic diversity, we found that bat species richness and functional diversity declined at high elevation but phylogenetic diversity remained unchanged. At the lowest elevation, we observed low functional dispersion despite high species and functional richness, suggesting a niche packing mechanism. The decline in functional richness, dispersion, and divergence at the highest elevation is consistent with patterns observed due to environmental filtering. These patterns are driven by the absence of rhinolophid bats, four congeners with extreme trait values, at high elevations. Our functional trait data, some of the first on mammals from the Himalayan region, suggest that bat assemblages with relatively high species diversity may be functionally and phylogenetically redundant.

Chen, Chuanwu (Presenter)

Session: CS05 – Island Biogeography

Title: The roles of habitat diversity and species traits in generating the small-island effect

Chuanwu Chen (ccw90415@gmail.com), Nanjing Normal University
Yanping Wang, Nanjing Normal University

Abstract:

The less dependent of species richness on area on small islands (the small-island effect; SIE) is a common phenomenon of small-island systems worldwide. However, previous studies often use area for the detection of the SIE, while habitat diversity and species traits are rarely considered. To explore the role of habitat diversity in generating SIEs, we compiled global datasets that included habitat diversity, area, and species richness. The path analysis showed that habitat diversity was influential to the detection of SIEs in 32 cases (52.5%). The logistic regression analyses also showed that Number of sites, Habitat range, and Species range were key variables that determined the importance of habitat diversity. This study thus demonstrates that the effect of habitat diversity on generating SIEs is quite prevalent. To explore the role of species traits, we sampled butterfly diversity on 42 islands of a large archipelago in China. We also collected ecological traits of wingspan, wing loading, and body weight, and split islands into small and large islands based on the area threshold. We found that for small islands, small area and large isolation were positively correlated with species with large wing loading and body weight. For large islands, perimeter to area ratio was significantly and positively related to wing loading. Obviously, the trait-environment analyses can further provide novel and mechanistic insights into processes generating the area threshold. Overall, we suggest that for a better understanding of the causes of SIEs, habitat diversity and species traits should be included in future studies.

Chen, Zheng（Presenter）

Session：CS09 – Biodiversity patterns, distribution & maintenance

Title：Rethinking elevational zonation of avian communities：How do vegetation structure and geometric constraints influence the community composition?

Zheng Chen（chen.zheng24@foxmail.com）, Center for Macroecology, Evolution and Climate, University of Copenhagen
Michael Borregaard, Center for Macroecology, Evolution and Climate, GLOBE Institute, University of Copenhagen
Sebastian Rojas, Department of Geosciences and Natural Resource Management, University of Copenhagen
Carsten Rahbek

Abstract：

Traditionally, the richness and composition of forest bird communities have been hypothesized to be shaped by the physical vegetation structure of the habitat. Thus, bird community zonation along gradients should be predicted by clear changes in vegetation structure. Surprisingly, an earlier study revealed distinct elevational zonation of bird communities along a seemingly completely homogenous forest gradient in the Udzungwa Mountains. Here, we revisited the same elevational gradient and re-surveyed the bird community. Meanwhile, the homogeneity of the vegetation was re-assessed using a modern handheld LiDAR scanner that allows quantitative characterisation of vegetation structure. The elevationally structured communities were re-examined and compared with a simple model incorporating the effect of geometric constraints（the so-called "mid-domain effect"）. The novel quantitative characterisation revealed substantial local variation in vegetation complexity but no discontinuities in the forest structure, thus supporting the homogeneity along the elevational gradient. The re-survey of the bird community, on the other hand, revealed no significant compositional discontinuity along the gradient, as the community designated as montane species in the earlier study had shifted their lower range limits downwards in the current survey, potentially blurring the previously observed zonation boundary at mid-elevations. There was also little evidence to support that vegetation complexity should determine bird species richness. Instead, species richness and community zonation in the historical survey appeared to be largely explained by the mid-domain effect. Taken together, the substantial local variation in vegetation complexity and the lack of temporal consistency in the structure of the bird community composition suggest the spatiotemporal dynamic characteristic of bird community structure, which are possibly explained by local factors. These findings indicate that environmental changes within elevations would be critical to identify the specific mechanisms underlying the zonation of Afromontane bird communities.

Coutinho Soares, Filipa (Presenter)

Session: CS13 – Biogeography of the Anthropocene

Title: Niche differences may reduce susceptibility to competition between native and non-native birds in oceanic islands

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Abstract:

Few bird extinctions on oceanic island have been attributed to competition with non-native species, even though it might be an overlooked driver of biodiversity loss. We evaluate the potential competition between native and non-native island bird species in seventy-three (>100km2) oceanic islands worldwide, identifying species and island characteristics that enhance it and may promote future extinctions. We compiled a species list for each island and used single-trait meta-analyses to assess differences between native and non-native species. Then, we used single-trait beta regression models to identify species traits linked to potential competition. Finally, we used a trait-based approach to calculate the potential competition between native and non-native species on each island and identify island characteristics linked to potential competition. Native bird species tended to be smaller forest dwellers, that were either carnivore, frugivore or insectivore, and that foraged in flight, in the canopy or at mid-height. In contrast, non-native birds tended to be open habitat granivores, that were either ground or unspecialized foragers. Potential competition tended to be higher for native species with typical non-native traits and forest-dwelling unspecialized non-native species. Potential competition between native and non-native birds was consistently higher in islands that were larger, had more non-native birds or were drier. Niche differentiation of native and non-native species may explain the scarcity of reported competition-driven extinctions since non-natives clearly tend to favour and are better adapted to anthropogenic environments. However, the few non-native birds that occur in native ecosystems may be problematic. The loss of native ecosystems coupled with the introduction of species that might outcompete native species may enhance the relevance of competition in future island extinctions.

Craffey, Matthew (Presenter)

Session: CS20 – Paleobiogeography

Title: The structure of Ediacaran and Cambrian communities

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Simon Darroch, Vanderbilt University
Peter Wagner, University of Nebraska – Lincoln
David Watkins, University of Nebraska – Lincoln
Daizaburo Shizuka, University of Nebraska – Lincoln
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Abstract:

Despite the sudden onset of prominent metazoan phyla in the Cambrian, the Cambrian Explosion may represent a gradual development of ecological and morphological complexity with roots in the Ediacaran period. However, we do not fully understand how global community structure in the Ediacaran and Cambrian responded to combined ecological, biogeographic, and environmental shifts or how those potential responses relate to intervals of high diversification. We compared community structure using genus pairwise co-occurrence between Ediacaran assemblage zones (Avalon, White Sea, Nama) and Cambrian stages (Fortunian, Stage 2, Stage 3) from macrofossil occurrence data from the Paleobiology Database and primary literature. Genus pairs were identified as aggregated or segregated, and the distributions of co-occurrence strengths were compared across all time intervals. We found significant shifts in global co-occurrence structure at different points in the Ediacaran and Cambrian. The proportion of aggregated pairs declined significantly between each Ediacaran interval as the evolution of shallow water communities and metazoan bioturbators altered species association patterns. The proportion of aggregated pairs increased between the Nama and Fortunian, which may have been influenced by the loss of Ediacaran biota which tended to form segregated pairs with metazoans. The proportion of aggregated pairs significantly declined between Stage 2 and 3, which may be linked to a dramatic increase in biogeographic differentiation between communities and diversification. While this indicates a punctuated shift in global community structure at the Cambrian Explosion, community structure in the Fortunian and Stage 2 may have been influenced by shifts in late Ediacaran community structure.

Davison, Charlie (Presenter)

Session: CS24 – Biodiversity patterns, distribution & maintenance

Title: The effect of habitat structure on bird diversity across broad spatial extents

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Abstract:

Vertical habitat structure is important for mobile animals and is a strong driver of biodiversity patterns, particularly in forests, where increasing structural diversity correlates with an increase in available habitat niches. This hypothesis was first confirmed in 1961 by MacArthur and MacArthur, who laboriously assessed the fine-scale vertical distribution of leaves and correlated this to local patterns of bird diversity. Given the importance of vertical structure for biodiversity, airborne laser scanning systems, such as LiDAR, present a unique opportunity to measure fine-scale 3D habitat structure over broad geographical extents and assess the importance of animal-habitat relationships under contrasting scenarios.

Land-use change is the greatest driver of global biodiversity loss, however traditional measures of land-use and land-cover may fail to capture important changes in 3D habitat structure. Expansion of agricultural areas, intensive management of forests, and rapid urbanisation can all decrease vertical habitat complexity, with important implications for habitat niche availability and species diversity. Denmark is the EU country with the most intensive agricultural land-use, with large changes to the management and extent of different farming practices over the past 50 years. This study aims to contribute to our understanding of the habitat structure – species diversity relationship by combining unique access to datasets of fine-scale 3D habitat and biodiversity information covering all of Denmark (~ 43,000 km2). The results will shed light on how structural changes across different land-use practices affect the richness and composition of species assemblages and the implications of this for future conservation management.

de Manuel Martín, Berenice (Presenter)

Session: CS24 – Biodiversity patterns, distribution & maintenance

Title: Organization of bird and amphibian metacommunities in tropical temporary ponds of Costa Rica

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Ángel Gálvez, University of Valencia
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Fabian Bonilla, University of Valencia
Juan Monrós, University of Valencia
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Mahmood Sasa, Universidad de Costa Rica
Javier Armengol, University of Valencia
Francesc Mesquita-Joanes, University of Valencia

Abstract:

The study of the ecology of metacommunities has experienced a great development during the last decades. But the understanding of the factors that control their organization still constitutes a big challenge for this discipline. In our work, we try to quantify the relative contribution of spatial and environmental effects when explaining the structuring of metacommunities of birds and amphibians in tropical temporary ponds in Costa Rica. On top of that, variables with greater explanatory capacity within each group of factors were analyzed in depth and attempts were made to relate them to the distribution of amphibian and bird species. Our results determined that the structuring of metacommunities of birds depends fundamentally on environmental factors, probably related to their high dispersal capacity. However, in amphibian metacommunities, environmental and spatial factors contribute in the same proportion, perhaps due to their greater dispersal limitations. We conclude that vertebrate metacommunities in tropical ponds are affected by environmental constraints, and spatial effects depend on the dispersal abilities of the organisms under study.

De Novaes Nascimento, Majoi (Presenter)

Session: CS02 – Paleobiogeography

Title: The adoption of agropastoralism and increase in ENSO frequency in the Andes

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Mark Bush, Florida Institute of Technology
Nicole Mosblech, Florida Institute of Technology
Liviu Giosan, University of Amsterdam
Marco Raczka, University of Amsterdam

Abstract:

Humans first occupied the Andes about 13,000 years ago, existing as hunter-gatherers for millennia, but evidence of plant cultivation in the Andes only began at 7000 calibrated years before present (cal BP) during a time when

ENSO activity seemed to increase. Yet, the increase in ENSO activity was detected in only one lake and, as a result, the representativeness of that record of ENSO activity is questioned. Besides, the timing and effects of the development of agropastoralism in the wet mid-elevation section of this Andean setting are still unknown. Using titanium from loss-on-ignition (LOI) analysis, fossil pollen, Sporormiella, and charcoal, I present a high-resolution 12,000-yr paleoecological history of Lake Llaviucu, a mid-elevation, at the Ecuadorian Andes, known for its archaeological sites that date to pre-Incan and Incan times. We found the same patterns of increase in ENSO frequency in our record, confirming that the increase in ENSO activities happened at the landscape level. For the entire period of study humans were probably active in this landscape, with signs of agropastoralism being present since before c. 6000 cal BP. A trajectory of increasing use seems to have peaked in terms of maize production between c. 2900 and 800 cal BP, and thereafter pastoralism was of increased importance until European arrival disrupted the system. We contend that these are human-manufactured landscapes in that the balance of species has been continuously altered by human actions, but they are not novel communities in the sense of a wealth of introduced species.

Dove, Shawn (Presenter)

Session: CS14 – Biodiversity patterns, distribution & maintenance

Title: Measuring accuracy in population based global biodiversity indicators

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Abstract:

Our understanding of global biodiversity and its trends is limited by lack of data. Governments and organizations rely on global biodiversity indicators such as the Living Planet Index, which tracks vertebrate population trends, to make policy and conservation decisions. The Living Planet Index is geographically and taxonomically biased due to severe data limitations. Statistical techniques have been applied to reduce bias, yet no one knows how accurate the index is because there is no baseline for comparison. All global biodiversity indicators suffer from similar data limitations, yet indicator accuracy is a rarely mentioned and little-studied topic. I present a method to quantify expected accuracy by applying a population-based biodiversity indicator to synthetic data and comparing trends generated at different sample sizes to the full dataset. I also discuss the factors which affect accuracy at a given sample size.

Eibes, Pia (Presenter)

Session: CS14 – Biodiversity patterns, distribution & maintenance

Title: Habitat islands and their “ocean”: species diversity patterns across distinct habitat island boundaries

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Severin Irl, Institute of Physical Geography, Goethe-University Frankfurt
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Nicole Kühne, University of Hamburg
Ute Schmiedel, Institute for Plant Science and Microbiology, University of Hamburg

Abstract:

The area of an island is clearly defined by the boundary to a contrasting matrix, limiting the distribution of the respective island species. While true islands are surrounded by water, the adjacency of habitat islands can be of varying nature, and thus, of different permeability for some taxa. This leads to fascinating transition zones of different spatial and environmental scales between habitat island and matrix habitats, ranging from abrupt boundaries, through gradual shifts to broad zones of ecotonal character. In this study, we quantify patterns in plant species diversity across the boundaries between habitat islands and adjacent matrix habitats. Our study area is located in the Knersvlakte Nature Reserve (Western Cape, South Africa), comprising a unique and natural system of isolated quartz fields within a zonal semi-arid Succulent Karoo vegetation matrix. We sampled plant species abundance per subplot in 56 fine-scale transects of 6 × 1 m^2 plots across eight different boundary types (four quartz island – matrix, four between habitats on quartz islands). Soil depth and chemistry were analyzed for each plot. Differences in the two beta diversity components (turnover and nestedness) for each boundary type were tested by t-tests. We used GAMs and LMs to test relationships between species and environmental dissimilarity and for potential threshold detection. All boundary types showed high beta diversity. Species turnover was the prevailing component for six boundary types. Studying boundaries of habitat islands sheds light into the generation of diversity in island-like entities as a result of habitat-specific isolation and connectivity.

Engelbrecht, Hanlie (Presenter)

Session: CS22 – Biodiversity patterns, distribution & maintenance

Title: Open to all but to each its own: Miocene speciation patterns of Afrotropical colubrid snakes Crotaphopeltis and Philothamnus

Hanlie Madelein Engelbrecht (Hanlie.Engelbrecht@wits.ac.za), University of the Witwatersrand
Krystal Tolley, South African National Biodiversity Institute

Abstract:

The heterogeneous African landscape formed through long-term vegetation shifts as a result of the global cooling trend since the Oligocene. The overwhelming trend was a shift from primarily forest, to primarily savanna. As such, forest-savanna genera that emerged during the Paleogene-Neogene should show a genetic signature of the possible evolutionary impact of these biome developments. The widespread Crotaphopeltis and Philothamnus (Colubridae) were used to investigate whether timing and patterns of radiation are synchronous with biome reorganisation. A phylogenetic framework was used to investigate timing of lineage diversification in Bayesian Evolutionary Analysis Sampling Trees (BEAST), using two mitochondrial markers (cyt–b, ND4), one nuclear marker (c–mos), and incorporating three calibration points. Vegetation layers were used to classify species association with broad biome types ('closed' = forest, 'open' = savanna /other), and the ancestral habitat state for each genus was estimated. Philothamnus showed an ancestral state of closed habitat, while ancestral habitat type for Crotaphopeltis was equivocal. Both genera showed similar timing of lineage diversification from their sister genera during the Oligocene /Miocene transition (ca. 25 Mya), with subsequent species radiation in the Mid-Miocene. Philothamnus presumably undergone allopatric speciation during Mid-Miocene forest fragmentation. Habitat generalist and open habitat specialist species emerged as savanna became prevalent, while at least two forest associated lineages within Crotaphopeltis moved into Afromontane forest secondarily and independently. With similar diversification times, but contrasting ancestral habitat reconstructions, we show that these genera have responded very differently to the same broad biome shifts, likely due to distinct life-history traits.

Engelhardt, Eva Katharina (Presenter)

Session：CS08 – Biogeography of the Anthropocene

Title：Consistent signals of a warming climate in distribution changes of three insect taxa over 40 years in central Europe

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Matthias Biber, Technical University of Munich
Diana Bowler, German Centre for Integrative Biodiversity Research (iDiv)
Christian Hof

Abstract：

Changes in climate and land-use are considered to have considerable impacts on different levels of biodiversity. Most studies investigating biodiversity trends are limited by a lack of reliable fine-scale, long-term field data, especially in regions with highly heterogeneous habitats. In central Europe, heterogeneous regions are affected by different human pressures changing over short spatial distances, which increases the need for fine-scaled assessments of biodiversity trends.

We present long-term trends in three ecologically and physiologically different insect taxa (butterflies, dragonflies, grasshoppers), based on 40 years of survey data. For the first time we study survey data from Bavaria, southern Germany, a region representative for European landscapes and habitats. We use occupancy models to obtain reliable population trends, and link these trends to species' attributes, indicating possible drivers of change. We find that cold adapted species decline and warm adapted species increase across taxa, which may indicate that climate warming has already affected insect trends in general. In contrast, habitat specialists show slightly decreasing trends in terrestrial taxa (butterflies, grasshoppers), while dragonflies show no difference between habitat generalists and specialists. This might be an effect of improved habitat quality of waterbodies.

Our results highlight the effects climate change has already had on insect distribution trends across the past decades. Signals of other drivers are less clear, and especially those affecting habitat quality need more detailed analyses. Understanding past influences of climate and land-use change on species is the first step towards the mitigation of increasing human pressures on biodiversity in the future.

Etard, Adrienne (Presenter)

Session: CS04 - Functional Biogeography

Title: Do vertebrate species traits influence species' responses to land-use change?

Adrienne Etard (adrienne.etard.17@ucl.ac.uk), University College London

Abstract:

Land-use change is one of the most important drivers of biodiversity loss. Land-use change globally impacts vertebrate communities by reducing local species richness. Nevertheless, not all species respond similarly to land-use change. Species ability to cope with anthropogenic pressures is dependent on their functional traits: empirical evidence has shown that longer-lived, slow breeding specialist birds respond more negatively to land-use change than shorter-lived, generalist birds. By preferentially removing certain functional types, land-use change is reshaping the functional composition of ecological communities. Understanding how land-use change impacts the functional diversity of ecological systems is key to assess the potential consequences on ecosystem functioning. Moreover, assessing whether and which traits influence species' responses can help put into place efficient conservation measures. In this work, I investigate (1) how land-use change impacts the functional diversity of terrestrial vertebrate communities at global scales and (2) which traits are most important in shaping species responses to land-use change. I found that land-use change globally promotes the functional homogenisation of ecological assemblages by constraining the functional richness and the functional dispersion of local communities. Moreover, species sensitivity to land-use change differs according to their traits, explaining such changes in functional diversity under land-use change. As such, land-use change is likely to globally impact local ecosystem processes, and, consequently, services rendered by terrestrial vertebrates.

Ferguson-Gow, Henry (Presenter)

Session: CS08 - Biogeography of the Anthropocene

Title: Biodiversity and the competing demands on the British landscape: trade-offs or win-wins?

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Richard Pearson, University College London
Georgina Mace, University College London

Abstract:

Changes to patterns of food consumption are a component of global and national-level strategies to mitigate the effects of climate change. The replacement of animal-derived proteins with fruits and vegetables in human diets has been associated with several environmental benefits such as reduced greenhouse gas emissions and terrestrial pollutants, as well as with several public health benefits such as reduced mortality from cardiovascular disease. Such changes to diets are likely to be underpinned by changes to the agricultural system and thus will involve significant changes in patterns of land use and is likely to include the conversion of grazing land to horticulture. Here we use species distribution models to estimate impacts on biodiversity from converting grazing land in part to horticulture and in part to natural land covers. We estimate that each 10% of

cell area transformed from grazing to horticulture is associated with a 1-2% reduction in mean habitable area across 814 species, and each 10% of cell area transferred from grazing to natural land cover with an increase of 6%. Given that, calorie for calorie, horticulture makes more efficient use of the land surface this suggests that dietary change may bring not only public health and environmental benefits but benefits to biodiversity as well.

Finocchiaro, Marie (Presenter)

Session: CS19 – Biodiversity patterns, distribution and maintenance

Title: Systematic fine scale variations in temperature and community composition observed between putative microrefugia of Oxalis acetosella L. and nearby sites distant by only 50 m

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Frédéric Médail, Aix-Marseille University, IMBE
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Arne Saatkamp, Mediterranean Institute of Biodiversity and Ecology

Abstract:

Microrefugia are small areas with favorable environmental conditions enabling the survival of population outside their species range. In the context of global warming, a clear understanding of current microrefugia is crucial. However, there is a lack of knowledge to conclude whether, and to what extent, the climate encountered within existing microrefuges differed from the surrounding climate. We used the most abyssal and southernmost disconnected populations of the circumboreal herbaceous specie Oxalis acetosella in Southern France to study if populations matching the definition of current "microrefugia" benefit from particularly cold climatic conditions compared to neighboring sites (50-100m). Air and soil temperature were recorded every 15 minutes in microrefuges and their neighborhoods during approximately 2 years to quantify their thermal contrasts. Botanical inventories were performed to test if biological communities reflect microclimatic contrasts, based on Pignatti species-indicator values. We found systematic temperature variations with cooler conditions within microrefugia compared to nearby sites. This pattern was stronger for air temperature and verified throughout seasons, especially pronounced in summer. Abyssal populations showed stronger contrasts compared to neighboring sites than the southernmost populations occurring at high altitude. Community composition systematically differed, with species more adapted to cooler and moister conditions in microrefugia compared to nearby sites. Current microclimatic dynamics are genuinely at stake within abyssal sites, enabling the persistence of cold-adapted species into constrained limited surfaces. Microrefugium climate is cooler than its immediate surrounding landscape, and biological communities in place already translate strong spatial climatic variability, even at such microscale approach.

Fois, Mauro（Presenter）

Session：CS07 – Conservation Biogeography

Title：ItIsWet, an open source geodatabase for managers and researchers in biogeography, ecology and conservation of Italian island wetlands

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Eva Tankovic, Petites Iles de Méditerranée（PIM）
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Abstract：

ItIsWet is the Italian initiative of MedIsWet（Mediterranean Island Wetlands）MAVA project, which aims at investigating all areas with water cover seasonally, or permanently, with a minimum extent of 0．1 hectares．In Italy, the project is mainly focused on Sicily and Sardinia, the largest, most inhabited and endemic–rich islands of the Mediterranean biogeographical region．Over 12,500 wetlands were mapped and more than 500 scientific contributions inventoried, and, for the about 1,000 monitored sites, 10,000 plant, 2,000 bird and habitat occurrences are uploaded on the ItIsWet open–source web portal．These can be related to the recorded threats, uses and any retrievable information．Compared to previous knowledge, numbers are sensibly higher, mainly due to an underestimation of small wetlands, especially temporally or artificial ones connected with agricultural practices．As a result, even if more than 60% of the total wetlands surface falls into protected areas, about 80% of wetland sites, including places hosting several endangered species, is still unprotected．Furthermore, the underrated set of artificial and natural small wetlands should be re–considered as potential ecological corridors or stepping–stones．Among aspects that are still poorly investigated, potential interest could have researches on interspecific relationships between the high number of native and alien species that co–occur in island wetlands．First results are an example of how this information can be used by managers and researchers to improve the current state of the art．In this sense, collaborations among different specialists are encouraged to achieve more complete and effective outcomes．

Fonteyn, Davy (Presenter)

Session: CS07 – Conservation Biogeography

Title: Regionalization of mammal assemblages in central African forests: determinants, sampling gaps, ongoing threats and conservation priorities

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Adeline Fayolle, Université de Liège – Gembloux Agro-Bio Tech, Forest is Life, Terra Teaching and Research Centre

Abstract:

While central African forests shelter a diverse mammalian fauna, how assemblages are spatially structured is still barely known, though being crucial for setting regional conservation actions. Here, we applied a beta-diversity approach (dissimilarity in species composition) on an extensive compilation of forest-dwelling mammal species lists derived from wildlife and bushmeat-related surveys to identify and delimit zoogeographical districts for carnivores, primates and artiodactyls. While carnivores only form a unique and broad Congolian district with no clear further divisions, both primates and artiodactyls present spatially structured assemblages, leading to a highly congruent zoogeographical regionalization. Moreover, we employed a random forest approach to identify the environmental determinants driving the distribution of the 8 primate and 6 artiodactyl districts and our findings reveal the role of rivers (the Ubangui/Congo River system, Cross and Sanaga) for structuring both primate and artiodactyl assemblages and that of precipitation for primate. Lastly, we used our random forest classification model to build a wall-to-wall map of the mammalian districts across central African forests, highlighting the protection and threat levels faced by each district. Our findings can be used to locally evaluate the degree of species defaunation (in comparison to expected composition) and to provide support to regional conservation and rewilding efforts. While ongoing and future climatic changes and human population growth might further jeopardize forest-dwelling mammal species and their assemblages, our study also highlights that vast areas of the Congo basin still remain understudied, calling for more ground-based data collection in priority areas.

Foo, Jurry (Presenter)

Session: CS10 – Climate Change Biogeography

Title: Resilience of the Bagang Community towards Climate Change in Mempakad Laut, Pitas, Sabah, Malaysia

Jurry Foo (jurryfm@ums.edu.my),

Abstract:

Climate change is an extraordinary phenomenon that can occur in the natural environment that influences the condition of weather, temperature and humidity that will cause extreme weather, drought, floods, tsunamis and the rising of temperatures. This phenomenon occurs due to disruption of the natural process of the earth's system. The purpose of this article is to identify the coastal community's perception of climate change in Mempakad Laut, Pitas. The information was collected through in-depth interviews with the Bagang community, and then the information was analysed descriptively.

Keywords: Community, perceptions, climate change, Resilience

Forcina, Giovanni (Presenter)

Session: CS03 – Biodiversity patterns, distribution & maintenance

Title: Molecular taxonomy and acoustic data of the black francolin (Francolinus francolinus) support a reappraisal of the intra-Palaearctic boundary

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Filippo Barbanera, Department of Biology, University of Pisa

Abstract:

The debate about the transition zone between eastern and western Palaearctic is still ongoing, with some zoologist recently ascribing the whole Iran – a key crossroad of faunal biodiversity – to the latter as part of the "Great Western Palaearctic". Additional distributional and systematic information from low-vagile and sedentary taxa may help settle the dispute. For this purpose, we genotyped 221 samples of black francolin (Francolinus francolinus), a landbird distributed in the Middle East and southern Asia, comparing the genetic affinity of individuals from the entire range at nine microsatellite loci with vocalisations characterised in a recent study. A stunning overlap emerged between the two sources of information, both indicating the occurrence of an eastern and a western cluster consisting of four and two morphological subspecies, respectively, with a divide running north to south across central Iran. Interestingly, the same scenario was found between genetically dissimilar populations of other vertebrates. Palaeoclimatic and geological data from Iran indicated an overall

higher connectivity of the region thanks to milder and moister climatic conditions prior to the cold-arid climatic phase initiated by the last glacial stage and isolating most taxa to disjunct refuges. Subsequently, the temperature raise likely compounded this scenario by hampering gene flow between populations of species - black francolin included - located east and west of the Kavir and Lut deserts. Although the taxonomic significance of this split in the focal species awaits for further studies, these results produced weight for the occurrence of an eastern-western Palaearctic boundary crossing Iran longitudinally.

Foryuy, Fairo Dzekashu (Presenter)

Session: CS15 - Gradients, range-limits & diversity

Title: Seasonality in bee communities varies with elevation on East African mountain slopes

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Abdullahi Yusuf, University of Pretoria
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H. Michael Lattorff, International Center of Insect Physiology and Ecology (icipe)
Marcell Peters, University of Würzburg

Abstract:

While elevational patterns of insect diversity have been well covered in ecology, studies on the effect of seasonality on elevational diversity of tropical insects remain elusive. Across an elevation, several biotic and abiotic factors do influence community assemblages of insects leading to a shift in species distribution and functioning. We therefore set out to elucidate the contribution of seasonality to elevational biodiversity patterns of wild bees. Our study was set up on two mountains slopes (Murang'a and Taita Hills) in the Eastern Afromontane Biodiversity Hotspots (EABH) in Kenya, East Africa. A total of 50 study plots of 100 m x 100 m were all placed within regrowth vegetation, set across several elevation strata (ca. 515 m asl to 2600 m asl) for recording bee species and plant species visited by bees. We sampled bees over all major seasons of the year using sweep nets, aspirators and calculated α-, seasonal β- and γ-diversity. We used generalized additive models (GAM) to examine elevational patterns of bee and plant diversity and analyzed the drivers of seasonality with elevation using ordinary linear models in a multi-model-inference framework. We recorded a total of 185 bee species from 3127 bee samples visiting 314 plant species. We found a decreasing pattern for all three bee diversity measures (i.e. α-, γ- and β-diversity(seasonal)) with elevation and high turnover of species across seasons significantly accounted to higher γ- than α-diversity on study plots. We revealed that trends in seasonal bee diversity along the mountain slopes were largely determined by seasonality in climate and by the seasonal turnover of floral resources. We, therefore, conclude that climatic seasonality plays an important role in shaping bees' floral resources and consequently the observed seasonal patterns of bee species diversity along tropical elevation gradients. In addition to this, our study reinforces conservation arguments on the importance of regrowth vegetation for the protection and of the unique bee diversity on the Eastern Afromontane Biodiversity Hotspots.

Fragkopoulou, Eliza (Presenter)

Session: CS17 – Marine Biogeography

Title: Depth provides refugia for marine biodiversity during heatwave events

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Ester Serrão, CCMAR- Center of Marine Sciences, University of Algarve
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Jorge Assis, CCMAR University of Algarve

Abstract:

Marine heatwaves (MHWs) are increasingly causing mass mortality events, altering the structure and functioning of marine ecosystems globally. Driven by anthropogenic warming, projections estimate longer, stronger and more frequent MHWs, further threatening marine biodiversity in the future. Against this scenario, deep-colder habitats are hypothesized to present a refuge from environmental extremes. Despite extensive MHW research, a global overview of their potential impacts across depth ranges remains largely overlooked. Here, we compiled a comprehensive database of mortality events to assess the role of depth refugia for marine biodiversity, and compared it to the potential vertical distribution of each impacted species. Further, we estimated MHWs for different depth ranges to address potential reduction of thermal stress with depth. Our results show mass mortality decreasing with depth. Impacts are most severe in the upper 41m of the water column. Most impacted taxa were ecosystem structuring species of macroalgae, cnidaria and bryozoa, with mortality recorded over 60%, 53% and 48% of their potential vertical distributions, respectively. Mass mortality events agreed with the expectations of MHWs, and cumulative heat stress decreased with depth at global scales. Together, our results support that depth can provide refugia from MHWs, however, key structuring species of macroalgae and cnidaria with zooxanthellae with limited vertical distributions owing to light constraints for photosynthesis, remain vulnerable and might not escape environmental extremes, a hypothesis with large implications for ecosystems' functionality.

Fuentes-Castillo, Taryn (Presenter)

Session: CS10 – Climate Change Biogeography

Title: Chilean Mediterranean region: The role of Protected areas in a warmer future

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Rosa Scherson, Universidad de Chile
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Abstract:

Mediterranean Chile is one of the five recognized Mediterranean-type climates globally, harbouring a rich diversity of plants. Climate change has been reported as a significant threat to its biodiversity. Protected areas (PAs) are located mainly in the Andes Mountains and the coast, and the total area occupied by PAs does not exceed

2% of the entire territory. We evaluated the role of PAs in Mediterranean Chile according to two main questions (1) how biodiversity patterns will respond to climate change scenarios in the PAs? And (2) which type-size of PAs are more vulnerable to rapid climate change rates? To answer these questions, first, we estimated biodiversity metrics for the current and future climatic scenarios. Species distribution models for Chilean flora were done using Maxent for 1.727 species and 571 genera. Relationships between species/genera gain, loss, and turnover were evaluated under climate change scenarios within and outside Mediterranean Chile state PAs. Forward and backward climate change velocities for temperature and precipitation were also estimated, assessing PAs' climate change vulnerability. We found a general decrease in species richness toward future climate change scenarios. The highest average species and genus loss is predicted to occur outside the protected areas meanwhile species and genus gain are higher within them. Smaller PAs are more vulnerable to climate change as measured by climate-change velocity. Our findings enhance the importance of the current PAs to harbour future variation, despite their reduced number and size along the region.

Fungomeli, Maria (Presenter)

Session: Poster Presentation

Title: Species-area relationships and small-island effect of plant diversity in the coastal forests of Kenya

Maria Fungomeli (maria.fungomeli2@unibo.it), Coastal Forests Conservation Unit, Centre for Biodiversity, National Museums of Kenya
Piero Zannini, Alma Mater Studiorum - University of Bologna, Bologna, Italy
Fabrizio Frascaroli, Alma Mater Studiorum - University of Bologna, Bologna, Italy
Alessandro Chiarucci

Abstract:

In tropical areas, forest fragmentation is a primary driver of biodiversity loss due to habitats isolation, area reduction, deforestation and degradation. The coastal forests of Kenya are a biodiversity hotspot existing as fragmented forest islands, from a once continuous forest. In order to understand how species diversity is affected by area, we addressed: how forest fragment area controls plant species diversity; and the existence of a small island effect. Using a standardized vegetation survey, we examine the effect of forest fragment area in controlling plant species diversity by approaching a Species-Area Relationship (SAR) and Small Island Effect (SIE) using a range of alternative models applied to observed and rarefied species richness. Best-fit model was selected based on the lowest Akaike's Information Criterion corrected for sample size (AICc). We found that the area of forest fragment explained a significant portion of species richness variability with the best fitting model being the Arrhenius power model. We found a significant relationship between rarefied and observed values of species diversity, which suggests that species richness values were not inflated sampling effort across forest sites. Finally, a SIE was not evident in our study. We show the predominant role of forest fragment as a driver of plant species richness. Even for very tiny forest fragments, area revealed to have a major role in controlling species diversity. These results support the idea that, for conservation policies larger forest fragments are fundamental to preserve a high proportion of biodiversity of the highly fragmented Kenyan coastal forests.

Furness, Euan (Presenter)

Session: CS01 – Models & Methods in Biogeography

Title: The Jigsaw Model: modelling variable effects of habitat area and heterogeneity

Euan Furness (ef19@ic.ac.uk), Imperial College London

Erin Saupe, University of Oxford
Russell Garwood, University of Manchester
Philip Mannion, Imperial College London
Mark Sutton, Imperial College London

Abstract:

It is now generally accepted that the biodiversity of an area is controlled by both its area and its habitat diversity. Mathematical models that reflect this have multiplied in recent years, but have had difficulty in balancing empirical accuracy, biological meaningfulness, and ease of use. Furthermore, it has become clear that different models are best suited to different scenarios and, as such, the ideal model should have some degree of flexibility. To solve these problems, we have developed the Jigsaw Model: a simple but flexible biogeographical model, derived from existing biogeographic and ecological theory, which models species richness in areas as a function of their size and habitat diversity and can provide information about the processes controlling biodiversity in different scenarios. Tests with real-world datasets demonstrate that this model has a comparable goodness of fit to other models of similar complexity. However, this model's ability to partition the effects of habitat area from those of habitat heterogeneity presents an opportunity to investigate the conditions under which each of these factors are responsible for controlling biodiversity, and how each are affected by considerations such as spatial scale, in a way that other models do not.

Gabor, Lukas (Presenter)

Session: CS16 – Models & Methods in Biogeography

Title: Habitats as predictors in species distribution models: Shall we use continuous or binary data?

Lukas Gabor (gabor@fzp.czu.cz), Czech University of Life Sciences
Vítězslav Moudrý, Czech University of Life Sciences
Petra Šímová, Czech University of Life Sciences Prague

Abstract:

The representation of a land cover type within an area is often used as an explanatory variable in species distribution models. However, it is possible that a simple binary presence/absence of the suitable habitat might actually be the most important determinant of the presence/absence of some species and, thus, be a better predictor of species occurrence than the continuous parameter. We hypothesize that the binary predictor is more suitable for relatively rare habitats (e.g. wetlands) while for common habitats (e.g. forests) the amount of the focal habitat is a better predictor. We used the Third Atlas of Breeding Birds in the Czechia as the source of species distribution data and Corine Land Cover inventory as the source of the landcover information. To test our hypothesis, we fitted generalized linear models of 32 water and 32 forest bird species. Our results show that for water bird species, models using binary predictors performed better and explained more variability than models with continuous predictor; for forest species, however, the opposite was observed. Thus, future studies using habitats as predictors of species occurrences should consider the prevalence of the habitat in the landscape, and the biological role of the habitat type in the particular species' life history. In addition, performing a preliminary comparison of the performance of the binary and continuous versions of habitat predictors prior to modelling, during variable selection, can be beneficial. These are simple steps that will improve both the explanatory and predictive performance of models of species distributions in biogeography.

Gibert, Corentin (Presenter)

Session: CS02 – Paleobiogeography

Title: PER-SIMPER: a new approach to untangle the role of niche and dispersal within modern and deep-time biological assemblages.

Corentin Gibert (corentingibert@gmail.com), Université de Poitiers
Annika Vilmi, Finnish Environment Institute, Freshwater Centre
Olga Otero, Université de Poitiers

Abstract:

Understanding how assemblages are formed is a central and still very lively debate in ecology. The search for mechanisms behind assemblages formation led to the identification of a full spectrum of hypotheses. At one end of this spectrum, assemblages are seen as closed groups, in equilibrium, only constrained by the relationships of taxa to their biotic and abiotic environments (niche-assembly perspective). At the other end of this spectrum, assemblages are seen as open groups in perpetual change, resulting from the random dispersion, origination and

extinction of taxa seen as equal (neutralism) under natural selection (dispersal-assembly perspective). These two endpoints, once seen as opposite, are only conceptual since empirical assemblages are always the result of a more or less balanced combination of both perspectives. In order to position an assemblage along this niche-dispersal spectrum, we have developed a method called PER-SIMPER (Gibert & Escarguel 2019), which requires only a table of occurrence or abundance. Thanks to its straightforward modus operandi, PER-SIMPER can be used on a wide variety of datasets, such as paleontological datasets where the environmental information required in most other methods is usually missing or extremely sparse. Modern and paleontological datasets of varying temporal and spatial scales are used to illustrate PER-SIMPER's functioning. Such as modern communities of parasites and their mammalian hosts, or communities of freshwater fish and invertebrates in China and the USA. Finally, we show how the primary mechanisms underlying deep-time (Neogene and Pleistocene) mammalian assemblages are affected by major climate change.

Ginal, Philipp (Presenter)

Session: CS23 – Conservation & Invasion Biogeography

Title: Ecophysiology meets Invasion Biogeography: High Invasion Risk of the African Clawed Frog Xenopus laevis

Philipp Ginal (philipp.ginal@gmx.de), Zoological Research Museum Koenig

Abstract:

One main threat promoting the worldwide amphibian decline is the introduction of non-indigenous amphibians, like the African Clawed Frog Xenopus laevis, which is now one of the widest distributed amphibians occurring on four continents with ongoing expansion including large parts of Europe. Species Distribution Models (SDMs) and the concept of ecological niche are essential to predict the invasive risk of those species. Previous efforts to predict distributions of invasive amphibians have mainly focussed on correlative approaches but these can be vulnerable to extrapolation errors when projecting species' distributions in non-native ranges. Recently, more robust process-based models, which use physiological data like critical thermal limits, or hybrid models of both approaches were used for this purpose. Previous correlative SDMs for Europe predict different patterns in the potential distribution but it is likely that these models do not access the full invasive potential. Based on physiological performance trials we calculated size and temperature depending response surfaces, which were scaled to the species' range matching the critical thermal limits. These ecophysiological performance layers were used in a standard correlative SDM framework to predict the potential distribution in South Africa and Europe. We found thermal performance differed significantly among native and invasive populations indicating some degree of fundamental niche change, which lead to different potential distribution patterns for the native and invasive populations in the respective ranges. Our hybrid-SDMs revealed that X. laevis has a much higher invasive potential than previous correlative models predicted for Europe.

Hagen, Oskar (Presenter)

Session: CS12 – Paleobiogeography

Title: Deep-time environmental dynamics coupled with eco-evolutionary processes explains the uneven biodiversity across tropical moist forests

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Alexander Skeels, Landscape Ecology, Institute of Terrestrial Ecosystems, ETH Zürich
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Walter Jetz, ETH Zürich
Loïc Pellissier, ETH Zürich

Abstract:

The biodiversity found across tropical moist forests, the most species-rich terrestrial biome on the planet, varies broadly between the high diversity of the Neotropics and Indomalaya and the relatively lower diversity of the Afrotropics. Explanations for this variation across different regions, the "pantropicaldiversity disparity" (PDD), remain contested, due to difficulty teasing apart the effects of contemporary climate and paleoenvironmental history. Here, we assess the universality of the PDD across more than 150,000 species of terrestrial plants and vertebrates and investigate the relationship between the present-day climate and patterns of species richness. We then investigate the consequences of paleoenvironmental dynamics on the emergence of biodiversity using a novel spatially explicit model of diversification (gen3sis) coupled with a paleoenvironmental re-construction of plate tectonics, temperature and aridity. While contemporary climate is insufficient in explaining the PDD; a simple model of diversification coupled with paleoenvironmental constraints is successful in reproducing the variation in species richness and phylogenetic diversity seen repeatedly among plant and animal taxa, suggesting a prevalent role of paleoenvironmental dynamics. Our model indicates that high biodiversity in Neotropical and Indomalayan moist forests is driven by complex macroevolutionary dynamics associated with mountain uplift. Lower diversity in Afrotropical forests is associated with lower speciation rates and higher extinction rates driven by sustained aridification over the Cenozoic. Our analyses provide a mechanistic understanding of the emergence of uneven diversity in tropical moist forests across 110 Ma of Earth's history, highlighting the importance of deep-time paleoenvironmental legacies in shaping biodiversity patterns.

Hakkinen, Henry (Presenter)

Session: CS21 – Climate Change Biogeography

Title: Plants can naturalise in novel precipitation but not temperature regimes

Henry Hakkinen (hh375@exeter.ac.uk), University of Exeter

Regan Early, University of Exeter

Abstract:

Recent research has highlighted multiple examples of climate niche expansion in non-native species, in which species have colonised types of climate with which they have not been previously associated. This may suggest

that many species do not colonise climatically suitable areas in their native range, potentially due to non-climatic range limitations. Niche expansion creates challenges for predictions of invasion, as many predictive models assume that a species climatic preference will remain the same in its native and naturalised range. There is therefore a need to understand how common niche expansions are, and what processes drive niche expansions. We compare native and naturalised climatic niches in over 600 terrestrial plants, and find evidence of niche expansion in 45% of introductions. We further find that species predominantly expand into wetter climate than their native niche, and species that expand in this direction also expand further from their native niche. Species also expand into drier climate, but less frequently. Species only rarely show niche expansions towards hotter and colder climate. We also find that species are more successfully able to colonise the wettest and driest portions of their climatic niche. These results suggest that species do not occupy all climatically suitable areas in their native area. This could be because of biotic interactions at wet, productive range edges, which leads to enemy release in the non-native range, or the role of specific precipitation factors at species range edges.

Hedberg, Carson (Presenter)

Session: CS19 – Biodiversity patterns, distribution and maintenance

Title: Know thy neighbor: Unpacking mammalian functional and phylogenetic diversity gradients in the Anthropocene

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Felisa Smith, University of New Mexico

Abstract:

The latitudinal diversity gradient is one of the most ubiquitous patterns in species distribution on the planet, documented across diverse clades from trees to fungi to mammals. A mechanistic explanation has long fascinated scientists, spurring dozens of hypotheses drawing on both ecological and evolutionary explanations. However, human activities have enormously impacted the global distribution of fauna, particularly mammals, over the past millennia via extinctions, range contractions, and introductions. These profound 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 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. Preliminary results suggest tropical regions have greater redundancy among species and lower average functional distinctiveness for a given phylogenetic distance, potentially suggesting higher phylogenetic niche conservatism. Certain regions, particularly in temperate latitudes, currently exhibit higher functional distinctiveness than would be expected in the absence of human influence, suggesting patterns are generated by anthropogenic in addition to historical and ecological factors.

Heijink, Britte (Presenter)

Session: CS20 – Paleobiogeography

Title: Holocene increases in palm abundances in north-western Amazonia

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Crystal McMichael, University of Amsterdam
Dolores Piperno, Smithsonian National Museum of Natural History
Joost Duivenvoorden, Instituto Amazónico de Investigaciones Científicas Sinchi
Dairon Cárdenas, Instituto Amazónico de Investigaciones Científicas Sinchi
Álvaro Duque, Universidad Nacional de Colombia Sede Medellin

Abstract:

In Amazonia, 227 of c. 16,000 tree species account for half the individual trees (termed 'hyperdominants'), and a disproportionate number of these species are palms. Our objectives are to show how and whether palm abundance has changed through the Holocene. Here, we reconstruct a detailed fire and vegetation history from north-western Amazonia, with a focus on changes in palm abundances, and compare our results with regional data. We performed charcoal and phytolith analysis on soil cores, and obtained ages of past fires using 14C dating. We used these data to reconstruct changes in fire and vegetation, and compared these data with the species composition of palms in the modern forest. Seven 14C dates from charcoal in three cores provided fire ages ranging from 1630 to 2450 calibrated years before present. Charcoal was absent from one-third of the cores. Palm phytoltihs from genera such as Iriartea, Socrate, and Astrocaryum have increased through time, while genera such as Euterpe, Hyospathe, and Oenocarpus have remained relatively stable and similar to modern levels. Overall, palm abundances were negatively correlated with charcoal measurements. Palms have increased at Amacayacu and other forest plots through time, but the increases are largest in north-western Amazonia. The presence of fire, however, dampens the increase in palms through time. When comapred woth reconstructions from other Amazon regions, our results suggest that increases in palm abundances in the late Holocene occured both in the presence and absence of direct pre-Columbian human influence, and that response was strongest in north-western Amazonia when human influence was minimal.

Huang, Shuyin (Presenter)

Session: CS11 – Phylogeography

Title: Elevational sorting on phylogenetic assembly of plant species across East Asian islands

Shuyin Huang (huangshuyinwml@gmail.com), University of the Ryukyus

Abstract:

Tropical niche conservatism (TNC) hypothesis assumes some tropical lineages adapt to colder climate and diversify in temperate environment. TNC gains popularity in the last 20 years due to its elucidation on latitude and elevational diversity gradient with the availability of comprehensive phylogenetic tree. But its universality

requires more evidence from various organisms and ecosystems. Here we use angiosperm tree plants collected from 7 mountains on East Asia Islands to test TNC. The mountains are Lalashan(N 24°) on Taiwan, Miyanoura(N 30°) on Yakushima, Sampo(N 32°) on Kyushu, Shizuoka(N 35°), and Kurikoma(N 38°) on Honshu, Kariba(N 42°) and Taisetsu(N 43°) on Hokkaido which stretch form subtropical to temperate climate. Each mountain was divided into several elevation bands with 100 or 200m interval. 10 quadrats were surveyed on each elevational band. We extracted our phylogenetic tree from the GBOTB mega tree using R package V.Phylomaker. Mean family age (MFA) and mean pairwise distance (MPD) decline with increasing elevation in Yakushima, Shizuoka and Taisetsu which supports TNC, but not Kyushu, Kurikoma and Kariba. This may be due to the specific climate for Kurikoma and Kariba, such as the heavy snow in winter. MFA in Lalashan follows TNC, but MPD has no change with elevation. This may cause by the intense competition within close related species in subtropical climate. Phylogenetic turnover increased with elevational distance which is consistent across all mountains. Our study showed there is a general pattern for phylogenetic beta diversity pattern in the mountains on East Asia islands. But MFA and MPD indicate mountain specific community assembly processes are shaping East Asia plant biodiversity. More analysis needs to be done to find out what processes shape this mountain specific biodiversity pattern.

Huang, Huasheng (Presenter)

Session：CS25 - Paleobiogeography

Title：Eocene palms from central Myanmar, and their implications for paleoecology, paleoenvironment and biogeography

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Robert Morley, Palynova Ltd.
Alexis Licht, University of Washington
Guillaume Dupont-Nivet, University of Vienna
Friðgeir Grímsson, University of Vienna
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Jan Westerweel, Géosciences Rennes, CNRS and Université de Rennes 1
Zaw Win, Shwe Bo University
Day Wa Aung, University of Yangon
Carina Hoorn, Universiteit van Amsterdam

Abstract：

Palm and palm-like (PPL) taxa have been widely reported at low-mid latitudes in Paleogene pollen assemblages. Yet their occurrence in the Paleogene of Myanmar remains poorly documented. Here we investigate the morphology of PPL pollen along a middle to upper Eocene sedimentary sequence in the Central Myanmar Basin and discuss their nearest living relatives (NLRs). Principal components analysis indicates that Palmaepollenites kutchensis, Dicolpopollis, and Longapertites were dispersed from freshwater plants, while the parent taxon of Proxapertites operculatus was probably a member of the coastal vegetation in the manner of Spinizonocolpites. Together with sedimentological data, it suggests a paleoenvironmental change from a tidally-influence

environment to a fully freshwater setting through the late Eocene. Additionally, we mapped and compared the geographic distribution of selected Eocene palm taxa and their NLRs and found that their distributional ranges shrank after the Eocene. Moreover, in the Paleogene, species diversity of selected PPL taxa seems lower in Myanmar than in the Indian subcontinent and other regions in SE Asia. We hypothesize that in the Eocene the Indo-Asian collision zone formed a 'hotspot' for palm diversity, which is reflected in species-rich palynofloras. However, the local palm diversity declined after the Eocene, while at global level palm distributions were distinctly reduced between the Eocene and present. We propose that this reduction in range of many of the palms may have occurred as early as the Eocene–Oligocene Transition (EOT), during dramatic global cooling. This remains to be confirmed by the study of EOT pollen records in each of the tropical regions.

Hurtado, Fernando (Presenter)

Session: CS22 – Biodiversity patterns, distribution & maintenance

Title: Moss establishment success is modulated by temperature and interspecific interactions

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Lars Götzenberger, Faculty of Science, University of South Bohemia
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Pedro Aragón, Department of Biology (Botany), Universidad Autónoma de Madrid
Belén Estébanez, Department of Biology (Botany), Universidad Autónoma de Madrid
Joaquín Hortal, Department of Biogeography and Global Change, Museo Nacional de Ciencias Naturales (MNCN-CSIC)
Nagore G. Medina, Department of Biology (Botany), Universidad Autónoma de Madrid

Abstract:

Colonization regulates species distributions and is fundamental to the spatial dynamics of metacommunities. This is even more so for sessile organisms, such as mosses, since the establishment of propagules frames their success in colonizing new habitat patches. Mosses can produce vegetative propagules through fragmentation. After their dispersal, biotic and abiotic interactions may modulate the colonization of new areas during their establishment stage. We assessed the intra- and interspecific variation in colonization success and establishment in mosses using artificially fragmented vegetative propagules (leaves and shoots) of six species (Dicranum scoparium, Homalothecium aureum, Hypnum cupressiforme, Ptychostomum capillare, Syntrichia ruralis and Tortella squarrosa), cultured on rockwool cubes (530-675 mm2) at different temperature regimes, both individually and in pairwise combinations. In each sample, we measured colonization growth responses (colonized area and biomass). In pairwise combination samples, we also calculated interspecific spatial associations (ISA), checking the presence of both species across the cultured surface using grid cells (1 mm2). Combined, these two measures – ISA and growing responses for pairwise combinations – assess the effect of interspecific interactions. In terms of colonization potential, T. squarrosa was the most successful species, and D. scoparium the least. Our results show that the establishment success (biomass production and colonized area) of vegetative fragments in mosses is species-dependent and is also affected by both temperature and

interspecific interactions, leading to shifts in both colonization success and interspecific spatial associations. This experiment may help identify key processes during moss establishment and understand the spatial distribution of these species by providing meaningful information on their colonization potential.

Irl, Severin (Presenter)

Session: CS05 – Island Biogeography

Title: Climate controls plant life form patterns on a high-elevation oceanic island

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Alexander Obermeier, Biogeography, University of Bayreuth
Carl Beierkuhnlein, Biogeography, University of Bayreuth
Manuel Steinbauer

Abstract:

Plant life forms characterize key morphological strategies that enable large-scale comparisons of plant communities. This study applies Raunkiær's plant life form concept that was developed for temperate climate to a subtropical island flora (La Palma, Canary Islands), in parts, dominated by summer aridity. We quantify how plant life form patterns as well as patterns of important plant functional traits (PFTs) relate to important climate characteristics. We assigned each native plant species a plant life form as well as PFTs (succulence and N-fixer). We related richness and percentage values for each plant life form and PFT to climate characteristics using mean annual temperature and mean annual precipitation. Plant life forms and PFTs showed a clear pattern within geographic but also climate space. Phanerophytes mainly contributed to the flora in humid areas. Chamaephytes and hemicryptophytes most strongly contributed to the summit scrub flora and, to some degree, also to the arid coastal regions. Geophytes and therophytes were mainly found in dry coastal regions. N-fixers contributed mainly to warm-arid and cool-arid regions, while succulent species were mainly found in arid coastal regions. Raunkiær's plant life form concept can be comprehensively transferred to a subtropical island flora by adapting to local unfavorable growing conditions, i.e., aridity. The climate-driven variation in patterns of plant life forms and PFTs might be used for large scale comparisons in macroecological studies. Growth strategies reflected in Raunkiær's plant life forms suggest differences in species establishment and coexistence dynamics within different parts of the island's climate space.

Kass, Jamie (Presenter)

Session：CS03 – Biodiversity patterns, distribution & maintenance

Title：A global map of ant biodiversity, comparisons with vertebrates, and predictions of unknown hotspots

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Clinton Jenkins, Florida Institute of Technology
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Anne Chao, National Tsing Hua University
Steven Shattuck, CSIRO
Dave Lubertazzi, Harvard University
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Robert Guralnick, University of Florida
Nate Sanders, University of Michigan
Robb Dunn, University of North Carolina
Evan Economo, Okinawa Institute of Science and Technology Graduate University

Abstract：

Efforts to conserve biodiversity depend on our knowledge of where it is concentrated across the globe, but current strategies are based on maps that are highly biased toward vertebrates. This is problematic because most described species and a majority of terrestrial animal biomass are represented by invertebrates, which are also critical contributors to ecosystem functions and services but have biodiversity patterns that are largely unknown. Locating hotspots of invertebrate biodiversity is difficult because data are generally deficient, error-prone, and disparate in origin. Here, we present a high-resolution, global diversity map for ants, an exemplar invertebrate group. We used data from an extensive occurrence database covering all known species of ants and developed custom pipelines for data cleaning/georeferencing and species distribution modeling. We compare patterns of ant biodiversity to those of terrestrial vertebrates and find some unique differences and similarities. We also train random forest models on our biodiversity estimates and global ant sampling intensity to make predictions of undetected hotspots to guide inventory 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.

Keil, Petr (Presenter)

Session: CS14 – Biodiversity patterns, distribution & maintenance

Title: Estimating cross-scale biodiversity change from heterogeneous and incomplete data

Petr Keil (pkeil@seznam.cz), Czech University of Life Sciences
Jonathan Chase, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Abstract:

We need data-driven estimates of temporal change of biodiversity, and its components loss and gain. Ideally, these should be provided at local, regional, and global grains, and over geographic extents. However, such estimates are hard to get because of data incompleteness, heterogeneity, and lack of temporal replication. We introduce a tree-based machine learning approach that addresses these issues and estimates cross-scale biodiversity change and its components. The approach explicitly considers complex interactions between scale, geography, data types, and drivers of change. It can integrate inventory data from nature reserves or countries with data from atlases and local survey plots. We present two flavors which blend machine learning with advances in ecological scaling. The first combines machine learning with species-area relationships, the second with occupancy-area relationships. When applied to simulated and empirical data, our approach reliably captures temporal biodiversity change across a continuum of spatial scales. This can be done in spite of the lack of time series data, temporal biases in sampling, and highly uneven sampling area. The estimates can be mapped at any desired spatial resolution, with minimal computational cost.

Klöcker, Antonia (Presenter)

Session: CS13 – Biogeography of the Anthropocene

Title: Recovery Trajectories – Investigating how diversity responds to human disturbances in time and space

Antonia Klöcker (ckloecker@ethz.ch), ETH Zürich

Abstract:

In the last decades, natural ecosystems are experiencing unprecedented rates of anthropogenic disturbances, which contribute to the rapid biodiversity loss we are monitoring today. Such disturbances can impair community composition and associated functions long after the disturbance itself has been abated. Against this backdrop, an adequate quantification and projection of ecosystem responses to human disturbance is integral. In my PhD project, I use a process-based simulation framework in combination with empirical results from a meta-analysis, to investigate how abiotic and biotic parameters such as habitat heterogeneity and prior disturbance histories shape recovery trajectories across different disturbances, ecosystems, and biodiversity metrics. Thereby, we want to shed light on the lag effects in ecosystem response across systems and highlight the differences between community responses as well as the utilised response metric. By providing a comprehensive and system-wide picture, we want to contribute to closing extant gaps with regards to the diversity-stability relationship in ecological research and generate knowledge which can be applied in conservation or environmental engineering approaches to facilitate decision makers in taking the actions needed to bend the curve of biodiversity loss.

Koelemeijer, Irena (Presenter)

Session: CS18 – Invasion /Conservation /Climate Change

Title: Lower understory biodiversity of conservation concern in edge exposed boreal forest patches hit by a drought

Irena Adia Koelemeijer (irena.koelemeijer@su.se), Department of Ecology, Environment and Plant sciences, Stockholm University

Abstract:

Climatic extremes are strong drivers of local extinctions, and their impacts may be reinforced by other anthropogenic drivers, such as land use. For example, forestry practices significantly increase the proportion of forest edges in the landscape and alter thereby the climate experienced by forest understory organisms. Here we explore the hypothesis that extreme summer drought induced local extinctions of forest species of conservation concern, especially in forest patches with high edge exposure. Using a high-resolution precipitation dataset, we estimated drought intensity during the unusually dry year of 2018 for 60 old-growth boreal forest patches (woodland key habitats) in central Sweden that differed in their level of edge exposure. The year after the drought, we surveyed the distribution of forest species of vascular plants, lichens and bryophytes that are classified as red-listed or signal species. We assessed if species richness, community composition, and abundance, were related to drought intensity in 2018, edge exposure, and their interaction. Richness of red-listed and signal species was negatively related to drought intensity in forest patches with a high proportion of edge habitat, but not in more continuous forest structures. These patterns were mainly driven by cyanolichens and epiphytes on broad-leaved trees, as well as on species occurring on convex substrates such as trees and logs. Our study suggests that the combination of intense drought and edge exposure negatively affected biodiversity of conservation concern, indicating that understory biodiversity in small forest patches with high edge exposure is particularly at risk during extreme events. To mitigate such

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Koido, Ririko (Presenter)

Session: CS15 – Gradients, range-limits & diversity

Title: Population demographic history of Asian black bear in relation to the past distribution shifts of cool temperate forests in Japan

Ririko Koido (ririko0719@gmail.com), University of tsukuba
Naoki Ohnishi, Tohoku Research Center, Forestry and Forest Products Research Institute
Akane Kato, University of Tsukuba
Keisuke Yumoto, Swiss Federal Research Institute, WSL
Michael Nobis, Swiss Federal Research Institute, WSL
Yoshiaki Tsuda, Sugadaira Research Station, Mountain Science Center, University of Tsukuba

Abstract：

Wildlife species in forest ecosystems changed their habitats in response to the distribution shifts of tree species during past glacial–interglacial climate changes. Oak and beech forests provide habitat and food resources to many species, including Asian black bear (Ursus thibetanus). We hypothesized that genetic structure and demographic history of Asian black bear were influenced by past distribution shifts of cool temperate beech-oak forests. To test this hypothesis, we evaluated the genetic structure and population demographic history of Asian black bear in Japan using bi-parentally inherited nuclear DNA microsatellites and maternally inherited mitochondrial DNA sequences. Moreover, we reconstructed the inferred refugial areas of beech (Fagus crenata) and oak (Quercus crispula) populations in Japan during the last glacial maximum (LGM) using a modified species distribution model, KISSMIG. Genetic structure analysis (STRUCTURE) revealed that at least 15 local populations of Asian black bear exist in Japan. The largest genetic differentiation was detected between populations separated by mountainous areas in central Japan. Moreover, two diverged populations were detected in the northern part of Japan. The demographic inference suggested local divergence of these populations occurred before the LGM. Furthermore, directional admixtures from west to east occurred in central Japan after the LGM, suggesting post-LGM eastward expansion. The results of the KISSMIG model generally supported these patterns, including northern persistence of bear populations with oak forests during the LGM. These results shed new light on the interaction between the demographic history of Asian black bear and pre–post LGM recolonization of forest tree species.

Koo, Hongmi (Presenter)

Session：CS10 - Climate Change Biogeography

Title：Assessment and mapping of ecosystem services and biodiversity under different future scenarios in Ecuador

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Jin Noh

Christine Fürst, Martin-Luther-University Halle-Wittenberg, Institute for Geosciences and Geography, Dept. Sustainabl

Abstract：

Ecuador is known as home of diverse ecosystems including endemic species. Despite its ecological importance, these sensitive ecosystems are threatened by agriculture, invasive species, mining, pollution, timber extraction, and climate change, among others. This study aims at identifying potential impact of future development, and adapted land-use planning alternatives at biome and national levels of mainland Ecuador, based on a) the understanding of the relationship between human land-use and terrestrial ecosystem, and b) the assessment of the status of ecosystem services (ES) and biodiversity. Through participatory approaches such as surveys and workshops, the perspectives of regional experts in ecosystem conservation and environmental management were reflected in the ES assessment and scenario development. Specifically, most relevant ES to the Ecuadorian context and indicators to analyze the capacity of land-use and ecosystem types to provide ES and biodiversity were determined. Then, future scenarios related to deforestation, afforestation and climate change, and their simulation conditions were elaborated. A spatial explicit modeling approach that combines Geographic Information System (GIS) and Cellular Automaton (CA) was applied for analyzing the spatial impact of future scenarios on the provision of ES and biodiversity. The results presented a potential change in ES and biodiversity capacity maps and trade-offs or synergies between different ES and biodiversity. The results support the identification of adversely affected ES and areas that might experience biodiversity loss and ES decline in future. Furthermore, targeted recommendations can be formulated to strengthen the protection of vulnerable ES and biodiversity in Ecuador on biome and national level.

Krishnamoorthy Dharapuram, Bharti (Presenter)

Session: CS17 – Marine Biogeography

Title: Connectivity networks predict coastal provinces, connectivity hubs and barriers along the Indian coastline

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Abstract:

Ocean circulation drives the scale of connectivity in marine organisms, especially in marine invertebrates where dispersal primarily occurs during the pelagic larval phase. The time of spawning and pelagic larval duration influence the oceanographic context experienced by larvae and determine the extent of genetic connectivity between populations. Persistent oceanographic features can also shape patterns of diversity and distribution over evolutionary time-scales. The Indian coastline is a part of the Western Indo-Pacific biogeographic realm, where coastal circulation is driven by seasonally reversing monsoon winds and characterized by short-lived upwelling events. To understand the patterns of oceanographic connectivity in this region, we simulated the dispersal of over six million particles along the Indian coastline across different monsoonal seasons and El Niño–Southern Oscillation (ENSO) years. We assessed the variation in coastal connectivity across seasons, years and pelagic larval durations by analyzing connectivity networks built using simulated particle trajectories. We find that connectivity networks in the Indian coastline differ with season and pelagic larval duration, but do not vary significantly between ENSO years. Connectivity increases with pelagic larval duration resulting in larger and more well-connected clusters (ranging in number from 30-60) within the connectivity network. However, overall connectivity was low, where only a small proportion (0.5-3.4%) of all potential connections was actually realized. A few sites along the coastline were consistently recovered as connectivity breaks across comparisons and delineated four coastal provinces, which broadly overlap with empirical patterns of genetic connectivity and

biogeography. Coastal sites playing a key role in maintaining connectivity differed based on season and pelagic larval duration, indicating that temporally adaptive management measures guided by the dispersal traits of communities within each province are necessary.

Kühn, Nicola (Presenter)

Session：CS04 – Functional Biogeography

Title：Deeper roots to survive drier climates? A case study in the Cape Floristic Region

Nicola Kühn (nicola.kuhn@ouce.ox.ac.uk), University of Oxford
Carolina Tovar, Royal Botanic Gardens Kew
Kathy Willis, University of Oxford
Marc Macias-Fauria

Abstract：

Roots are responsible for essential plant functions including water uptake. However, the extent to which root traits (size and structure) determine plant presence in water-limited environments is still poorly understood. Here we analysed root variation across water availability gradients within a dry South African biome. We measured 6 belowground (root) and 8 aboveground (leaf+stem) traits of 124 individuals of nine dominant woody shrub species from wetter and drier sites (600-700 vs. 250-300mm annual precipitation) in the Fynbos biome of the Cape Floristic Region. Within sites, we sampled from recently burnt and unburnt/more mature vegetation and at three locations along topographical gradients. Drier regions showed greater maximum rooting depth, length, root dry matter content and root:shoot ratio. These trait patterns were consistent at an intraspecific level, along locally drier topographical locations and in post-fire environments. Roots accounted for significant whole-plant trait variation and significantly, in drier conditions, increased root allocation (at the expense of shoot allocation) deviated from expected allometric relationships. Our study also demonstrates that the combination of fire and drought on root systems in the drier site results in poor vegetation recovery in terms of plant size and cover – a finding that raises concern for future Fynbos resilience, particularly at its arid limits. Our results reveal that at drier sites within a biome, roots are not only deeper, but also longer, thicker, and more invested-in as compared with shoots. This is consistent across scales of water availability generated by regional precipitation gradients and local topographical gradients, as well as in post-fire conditions and within individuals of the same species. Our research suggests that root investment will be especially crucial for survival in a drier and warmer future and should be a focus of more research for global drylands.

Lambert, Joshua (Presenter)

Session：CS11 – Phylogeography

Title：Wrong but useful? The robustness of a simple phylogenetic model of island biogeography

Joshua W. Lambert (j.w.l.lambert@rug.nl), University of Groningen
Pedro Neves, University of Groningen
Luis Valente, Naturalis Biodiversity Center
Rampal Etienne

Abstract：

Models are important tools to understand the dynamics of biodiversity on Earth, yet, as the saying goes, “all models are wrong, but some are useful”. DAISIE (Dynamic Assembly of Island biota through Speciation, Immigration and Extinction) is a model of island biogeography that uses phylogenetic information to understand the colonization and diversification of island species over macroevolutionary time scales. As with all models, DAISIE makes simplifying assumptions：i) the island is assumed to be empty when it is formed, ii) the island does not undergo changes in area through time, and iii) the mainland source species do not undergo speciation or extinction on the mainland. In nature, all these assumptions are broken. Islands form via different geological processes (e.g. oceanic versus continental islands) and are not static entities. They have dynamically changing area, and some have species present on the island upon formation or transient connectivity via land-bridges. Species undergo speciation and extinction on the mainland. All these factors can potentially bias inferences made with DAISIE. We carried out robustness studies of the inference capacities of DAISIE, using simulation experiments to quantify the impact of violating the three abovementioned assumptions. We extended DAISIE simulations to include island ontogeny, sea-level fluctuations, different island types (oceanic, continental fragment, land-bridge), and also a dynamic mainland pool with extinction and speciation. We then applied DAISIE's inference model to simulated data. Here, we present the results, and discuss the robustness of DAISIE.

Lang, Karina (Presenter)

Session：CS10 – Climate Change Biogeography

Title：Environmental niche modeling of Fijian invertebrates and future potential distribution in response to climate change and sea level rise

Karina M Lang (klang03@syr.edu), SUNY College of Environmental Science and Forestry

Abstract：

As we learn more about the impacts global climate change and sea level rise will have on coastal communities, it is increasingly important to determine how these communities can begin to prepare for these changes. Oceania is a hotspot of biodiversity, and therefore we must prioritize actions that can be taken to maintain this diversity. We projected how the distributions of various culturally and biologically important Fijian invertebrate species and marine habitats may shift in the future, using the machine learning algorithm Maximum Entropy Species Distribution Modeling (MaxEnt). Using publically available data from the Global Biodiversity Information

Facility, the climatic niches of nine invertebrate species and three habitats present off the coast of Fiji and eastern Australia were evaluated, and then projected to future potential distributions based on several IPCC climate change scenarios. Our analyses suggest that most of the invertebrate species remain stable across the three scenarios, with changes in rainfall patterns allowing mud crabs (Scylla serrata) and mangroves to expand their ranges into areas that were previously too xeric. Relationships between projected distributions and climate severity were not linear, and some invertebrates, like Anadara antiquata and Holothuria edulis, lost or gained suitable habitat depending on the scenario. This suggests that climate change and sea level rise will influence these species in unique ways, so continued data collection and review will be necessary to best inform conservation decisions.

Larrue, Sebastien (Presenter)

Session: CS05 – Island Biogeography

Title: Human impact decreases the predictive ability of island biogeography models: the case of Pacific atolls

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Curtis Daehler, University of Hawaii
Jean-François Butaud, Private consulting (French Polynesia)
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Julien Chadeyron, University Clermont Auvergne (UCA)
Roger Oyono, University of French Polynesia

Abstract:

Humans may alter natural biogeographic patterns through increasing species extinction rates, but it is not documented whether this change now overwhelms expected natural biogeographic patterns across islands. Atolls provide a useful system to test the predictive ability of island biogeography models while also allowing us to explore the degree to which the current pattern of species richness across atolls depends on human influence. We used a stepwise regression model to test the relative influence of five biogeographic variables on native species richness on 111 coral atolls across the Pacific Ocean. An index of human impact was then estimated for each atoll, and residuals in the regression model predicting species richness from biogeographic variables were compared with the level of human impact. The regression model including atoll area, highest atoll elevation, stepping stone distance from the nearest raised atoll, and stepping stone distance from the nearest volcanic island significantly explained native species richness on the 111 Pacific coral atolls (adjusted $R^2=0.645$; $P<0.001$). Regression models for regional archipelago subsets were also significant. Residuals in the biogeographic regression model were not strongly related to human impact across all 111 atolls but were more significantly related to human impact in the Kiribati atolls. These results suggest that different levels of anthropogenic disturbance have altered the predicted biogeographic pattern of native species richness on atolls in some archipelagos of the Pacific. Human impacts should be further investigated for a better understanding of current biodiversity patterns in island biogeography.

Leroy, François (Presenter)

Session：CS13 – Biogeography of the Anthropocene

Title：Mapping biodiversity changes across a continuum of spatio-temporal scales

François Leroy (leroy@fzp．czu．cz), Czech University of Life Sciences
Petr Keil, Czech University of Life Sciences Prague (CZU)
Vladimir Bejček, Czech University of Life Sciences
Jiři Reif

Abstract：

Global biodiversity is facing increasing anthropogenic pressures． Being at the basis of many ecosystem services, it is important to document and understand its temporal trend． However, as an extensive variable, biodiversity and its dynamic are defined by both spatial and temporal scales that are closely related． While the links of biodiversity to area and time span are well known (i．e． species-area relationship, species-time relationship), it is still not clear how temporal changes of biodiversity are linked to spatial and temporal scaling． Even though global biodiversity is declining, we may not observe this decrease at local or regional scales． I will present the results of my PhD research in which I empirically document these relationships between biodiversity temporal trends and spatio-temporal scales (grains)． I used high-quality spatially and temporally heterogeneous data on bird diversity from the Czech Republic． A first dataset comes from an atlas and represent the highest spatial and temporal scales． The second one is composed of local time series with high resolution spatial and temporal scales． I found that avian species richness changes through time are negative at small spatial grains but positive at larger grains, showing that the intensity of macroecological processes varies with spatial scaling． I also found that biodiversity reaches a plateau with increasing temporal scale allowing inference of an optimal census time． In addition, I propose to use machine learning approaches (e．g． random forest) to predict biodiversity across a continuum of spatial and temporal scales． This will allow to predict biodiversity changes for locations and spatial and temporal scales which have not been sampled． Together with the unprecedented biodiversity data, these machine learning methods will show the link between species richness and spatio-temporal scales． These findings will be informative for estimation of biodiversity trends in data-poor regions．

Lewthwaite, Jayme (Presenter)

Session：CS19 – Biodiversity patterns, distribution and maintenance

Title：Biotic homogenization of Canadian butterflies over the past century

Jayme Lewthwaite (jlewthwa@sfu．ca), Simon Fraser University
Arne Mooers, Simon Fraser University

Abstract：

Recent studies have found that local-scale plots measured through time exhibit dramatic variation in the change in species richness． However, as some plots have gained species and some have lost them, the overall effect is

centered around 0, revealing no net change in species richness at the local scale. These studies thus far have largely been agnostic about the identities of the species lost/gained, as well as the processes that may lead to these changes. Generalist traits may be crucial in allowing species to colonize new plots or remain resilient in situ, whereas environmental filtering (whether it be climate change, land use change, etc.) may remove specialists from plots. As such, communities may be fundamentally different than they used to be – so that regionally, communities are becoming more similar (i.e. becoming homogenized) though they retain similar species richnesses. Using a curated distribution dataset of over 300 Canadian butterfly species and 500,000 records that span the past century, I tested this prediction. I found that communities are indeed becoming more similar to one another through time. Although there was no effect of mobility or diet breadth on plot-level colonizations or extinctions, we found that wide-ranged species are better able to colonize new plots than narrow-ranged species, and are disproportionately contributing to community homogenization. The degree of homogenization is not correlated with the amount of plot-level temperature warming through time, however may be linked to degree of land use change. This work will allow us to prioritize individual species at a heightened risk of extinction and highlight groups of concern.

Liddell, Luke (Presenter)

Session: CS01 – Models & Methods in Biogeography

Title: Polyploidy in the New Zealand Flora

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William Lee, Manaaki Whenua – Landcare Research
Esther Dale, University of Otago
Heidi Meudt, University of Auckland
Nick Matzke, University of Auckland

Abstract:

Many New Zealand plant groups contain a range of different ploidy levels, the result of historic whole-genome duplication (WGD) events. However, little is known about the ecological and biogeographic significance of these events. Globally, the distribution and abundance of polyploid plants is strongly biased towards higher latitudes and altitudes. Whole-genome duplication has also been linked to functional trait shifts and elevated rates of niche evolution. These trait and niche shifts may allow lineages to change their biome occupancy, a character that has traditionally been seen as highly conserved. Our research looks at the relationship between polyploidy and biome occupancy in two speciose New Zealand plant radiations, Coprosma (Rubiaceae) and Veronica (Plantaginaceae). Both are ecologically and morphology diverse, with species of different ploidy levels present across all three of New Zealand's major biomes (forest, open, and alpine). The ancestral range estimation software BioGeoBEARS is used to model the history of biome occupancy and whole-genome duplication in these lineages. We use this to test whether there is support for whole-genome duplication altering the rate of biome shifting, and the proportional change in this rate is quantified.

Lima, Herlander (Presenter)

Session: CS13 – Biogeography of the Anthropocene

Title: Hierarchical structure and the prediction of missing interactions in host-parasite networks

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Miguel Rodriguez, Universidad de Alcalá
Ignacio Morales-Castilla, Universidad de Alcalá (UAH)

Abstract:

When species interactions detection entails substantial sampling efforts, a comprehensive knowledge of complex ecological networks might be out of reach, particularly if it only depended on empirically observed interactions. Yet, this would be less of an issue if we were able to accurately predict undocumented interactions. In this vein, recent studies on host-parasite networks have tried to predict missing interactions using either species co-occurrence or trait data, which has two main limitations. First, using only co-occurrence data may hamper the prediction of potential future interactions among species that do not co-occur in the present, and may also lead to predictions that are impossible due to incompatible species traits. Second, predictions based only on trait data are constrained by limited knowledge of the traits underlying host-parasite interactions. As a solution, we propose a nonparametric, Bayesian network analysis framework based on graph-tool –a publicly available Python package– that does not depend on co-occurrences or traits, but on known links of the network. The framework generates a hierarchical classification of the network that is used to inform link probabilities. To test prediction accuracy, we analysed a global host-parasite dataset from which we removed interactions postdating 2006 as a testing set. True positive rate of predictions was 90%, thus supporting that network hierarchical structure can be safely used as predictive source of unknown interactions in host-parasite networks, which might have overarching implications for species conservation programmes and in the forecasting of disease emergence.

Liz, André Vicente (Presenter)

Session: CS06 – Phylogeography

Title: Integrative phylogeography to unveil historical biodiversity dynamics: a case study of Acanthodactylus lizards in arid regions

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Philippe Geniez, Centre d'Écologie Fonctionnelle et Evolutive
Pierre-André Crochet, CEFE/CNRS, Centre d'Écologie Fonctionnelle et Evolutive
Dennis Rödder, ZFMK, Zoological Research Museum Alexander Koenig

José Carlos Brito, CIBIO/InBIO, Research Center in Biodiversity and Genetic Resources

Abstract：

Integrating ecological modelling and phylogeographic analyses has a great potential to understand biodiversity dynamics across space and time. Desert ectotherms are excellent study systems to explore the role of past climate variability on biodiversity distribution patterns, due to the interplay of tight physiology-climate links and the fast and wide-ranging environmental shifts that historically occurred in arid biomes. The Afro-Arabian arid belt, integrated by the Sahara Desert, Sahelian savannah and Arabian Desert, experienced climate-driven extent fluctuations since the late Miocene, which prompted species range shifts and diversification through allopatric gene flow interruption. The present work assesses whether contemporary high genetic diversity areas are consistent with historical climatic refugia in the fringe-fingered lizard Acanthodactylus boskianus. We combined mtDNA and nuDNA phylogenies and climate-niche models, including paleoprojections, using a representative dataset covering most of the species range across North Africa and the Middle East. Four main mtDNA, spatially-structured lineages, embedding several parapatric sub-lineages, diversified throughout the Plio-Pleistocene, correlating with the regional dry/humid cycles. Foothills of mountains (Atlas, Central Sahara and Arabia) host great phylogenetic diversity, and these are the areas that likely acted as biodiversity refugia in unsuitable climatic periods. Low genetic diversity and past range shifts across vast regions, from Niger to Egypt, suggest recent connectivity across East Sahara-Sahel, while diverse and small-ranged lineages across West Sahara suggest past isolation. The nuDNA results suggest the existence of undescribed diversity, implying that this taxon may constitute an unresolved species complex. This work outlines the potential of integrative analyses to aid disentangling biogeographic questions.

Lu, Muyang (Presenter)

Session：CS09 – Biodiversity patterns, distribution & maintenance

Title：Complex relationships between beta diversity and dispersal in meta-community models

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Abstract：

Dispersal is one of the most important drivers of community assembly. Understanding how dispersal impacts spatial variations in community composition (beta diversity) is crucial for predicting biodiversity change during the Anthropocene. Classic theories and a large amount of empirical evidence have led to a common belief that increasing dispersal rate should lead to regional community homogenization (lower beta diversity). However, recent empirical studies show that increasing dispersal can also lead to regional community divergence when interacting with other processes such as disturbance and priority effect. The underappreciation of the complex relationship between beta diversity and dispersal rate might impede our ability to make accurate ecological forecasts. To address this concern, I examine the beta diversity-dispersal relationship through extinction and colonization dynamics in meta-community models. I find that a wide range of beta diversity-dispersal relationships (e.g. negative, positive, hump-shaped) can be generated by changes in species-level occurrence probabilities when meta-population dispersal (rather than mainland-island dispersal), disturbance and strong biotic interactions are at play. Specifically, reducing the variance of species-level occurrence probabilities leads

to community divergence and increasing the mean occurrence probability leads to community homogenization; a positive or hump-shaped beta diversity-dispersal relationship emerges when the effect of the decreasing variance is stronger than the effect of increasing mean. These findings highlight the intrinsic constraint of occupancy stochasticity on beta diversity changes; and echo the call for more realistic manipulations of stochastic dispersal and detailed understanding of the interaction networks to test various beta diversity-dispersal relationships in future empirical studies.

Lucchini, Nahla (Presenter)

Session: CS25 - Paleobiogeography

Title: Addressing the role of ecological processes in diversification of European vipers.

Nahla Lucchini (lucchini.nahla@gmail.com), CIBIO-InBIO / ICETA UP

Antigoni Kaliontzopoulou, Department of Evolutionary Biology, Ecology and Environmental Sciences, and Biodiversity Research In

Olivier Lourdais, Centre d'Etudes Biologiques de Chizé-La Rochelle

Fernando Martinez-Freiria

Abstract:

Climatic variation is among the major drivers of diversification, promoting the incidence of both geographical and ecological processes. In temperate regions, Pliocene and Pleistocene climatic oscillations are well-established as drivers of allopatric speciation in many taxa. The role of climatic adaptation in shaping species divergence, however, remains controversial. European vipers (genus Vipera) represent an excellent case study to infer the role of ecological and geographic processes in the diversification of temperate taxa. The genus is composed of three major clades (Pelias, Vipera 1 and Vipera 2) that diverged along the Miocene, with contrasting climatic niches (warm-adapted vs cold-adapted), and includes 27 lineages that distinctly diversified across the Palearctic since the Pliocene. Here, we integrated paleoclimatic models and niche overlap tests in a phylogenetic comparative framework to study the drivers of diversification of European vipers. We analyzed occurrence records for 24 lineages (n = 10,721) under a Maximum Entropy approach, reconstructing paleoclimatic scenarios for their diversification during the Pleistocene. In addition, we used 3D-hypervolume niche-overlap comparisons to investigate the occurrence of climatic niche shifts during the diversification of the group. Paleoclimatic models predicted distinct patterns of variation in the climatic space for the lineages across time, suggesting different responses to the cooling and warming events of the Pleistocene, even within the same clade. Niche overlap tests indicate that the divergence between several Pliocene lineages belonging to the three clades was accompanied by marked niche shifts. Our work therefore reinforces the importance of local adaptation in the geographic diversification of temperate taxa.

Luelmo-Lautenschlaeger, Reyes (Presenter)

Session: CS02 – Paleobiogeography

Title: The wood who lived. Relict landscapes in the Toledo Mountains (Central Spain)

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Sebastián Pérez-Díaz, Universidad de Cantabria
José Antonio López-Sáez, CSIC

Abstract:

The Toledo Mountains are a mid-mountain complex featured by a sharp relief and deep valleys, located between the Tagus and Guadiana rivers' basins, in central Spain. Due to the dominant Mediterranean climate, the particular topography and the oceanic influence felt on the westernmost side of these mountains they host wide plant diversity. Because of that, the Toledo Mountains arise as one of the best sceneries to run palaeoecological studies. In this environment covered by the typical Mediterranean vegetation is especially remarkable the scatter presence of Betula spp. and Corylus avellana, currently considered relict in this area and closely linked to humid spots. The aim of this work is to relate the contemporary populations with those extended in the past landscapes willing to understand their origin and development, as so the role played by the human being in this process. Some mires have been selected along the Toledo Mountains and the main results point to wider populations extended through these mountains, intimately linked to the peatlands spread in the ranges which acted as refugia for these species in a location where droughts are cyclic. Human activities over those spots have compromised the resilience of species like birch and hazel, and paradoxically nowadays only a change in human intervention could help to protect this particular and fragile ensemble. This wood should not be there but still resists and belongs to the Toledo Mountains vegetation history and identity and deserves to be protected as much as the main vegetation in these lands.

Machado Ribeiro Silva, Guilherme (Presenter)

Session: CS09 – Biodiversity patterns, distribution & maintenance

Title: Spatial structure of small mammal (Rodentia and Didelphimorphia) communities along Restingas of Southeastern-Southern Brazil

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Pablo Gonçalves, Instituto de Biodiversidade e Sustentabilidade (NUPEM), Universidade Federal do Rio de Janeiro
Caryne Braga, Laboratório de Ciências Ambientais, Universidade Estadual do Norte Fluminense Darcy Ribeiro

Abstract:

Restinga is a phytophysiognomy of the Brazilian Atlantic Forest (AF) Domain characterized by mosaics of shrublands and forests that evolved on sandy plains formed along the littoral during the Quaternary. It has been hypothesized that the colonization of animals and plants in the different areas of Restinga was recent, idiosyncratic, and involved only a subset of species from the adjacent forest. Thus, communities would be the result of recent and isolated colonizations and would bear high similarities with nearby biotas. In this study, we evaluated whether the spatial structure of small mammal communities (Rodentia and Didelphimorphia) from restingas in southern and southeastern Brazil is compatible with the recent colonization hypothesis, using an Elements of Metacommunity Structure (EMS) approach. A matrix of presence and absence of species was generated considering 20 published small mammal inventories in the south and southeast region, in addition to data from the mammal collection from NUPEM-UFRJ and the Species Link database. The EMS calculation was performed in the Metacom package, in the R environment. The resulting metacommunity structure was Clementsian, with two compartments, the first formed by restingas in the states of Espírito Santo, Rio de Janeiro, and São Paulo and the second by restingas from Santa Catarina and Rio Grande do Sul. This spatial structure reflects the AF's "Paulista" and "Southeast" biogeographic units, therefore, supporting the hypothesis of recent colonization. When evaluated independently, the compartments generated random structures, providing further support to the recent colonization hypothesis.

Makinen, Jussi (Presenter)

Session: CS16 – Models & Methods in Biogeography

Title: Spatial confounding in Bayesian species distribution modeling

Jussi Makinen (jussi.makinen@yale.edu), Yale University
Elina Numminen, Department of Mathematics and Statistics, University of Helsinki
Pekka Niittynen, Department of Geosciences and Geography, University of Helsinki
Miska Luoto, Department of Mathematics and Statistics, University of Helsinki
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Abstract:

Species distribution models (SDMs) may be subject to biased covariate effect estimates due to spatially structured processes that have not been accounted for in the model with covariate data. Biased estimates compromise the ecological interpretations of the species-environment relationships and possibly the predictive accuracy of SDMs. Spatial random effects (SREs) model the spatial autocorrelation of model errors and are assumed to account for the effects of the discarded processes. However, covariate effects and a SRE may be collinear, and models are subject to biased model estimates despite of accounting for spatial autocorrelation of model errors. We studied the estimation accuracy of spatially explicit SDMs with simulated and real data by varying the dependence between the observed and unobserved covariates and the spatial autocorrelation ranges of the covariates. We fitted models with Bayesian inference and applied different restrictive priors for the hyperparameters of the SRE to control the variation and confounding of the model components. Estimation bias increased when the observed and unobserved covariates were collinear, and the unobserved covariate varied in a shorter spatial autocorrelation range than the observed covariate. The bias could be slightly controlled by adding more prior probability for smoothly varying and relatively less important SRE. This was regardless of the actual spatial structure of the unobserved covariate. The common spatially explicit SDMs are unable to treat the

dependence between the observed and unobserved covariates, and modelers should be careful when interpreting model estimates from SDMs fitted with coarse scale environment data, such as climate variables.

Malem, Julien (Presenter)

Session: CS22 – Biodiversity patterns, distribution & maintenance

Title: Disentangling the origin of old lineages in New Caledonia: a geologically-informed test of the island-hopping hypothesis

Julien Malem (julien.malem@gmail.com), Sorbonne Université

Abstract:

In recent years, molecular dating along with geological evidence shifted the consensual hypothesis for the origin of the biota of New Caledonia (NC) from Gondwanan vicariance to relatively recent dispersal across the oceans. NC is now considered an oceanic island only 34 Myr old, according to the most recent geological studies. However, a small number of terrestrial taxa show ages incongruent with such a date, raising the question of the origin of "old" lineages on younger islands; classically, old lineages on recent islands are hypothesized to originate through a process of hopping on now-vanished islands (i.e. island-hopping hypothesis). Here we provide a dated phylogenetic and biogeographical framework for blattid cockroaches (Blattodea: Blattidae, Tryonicidae), showing divergence times much older than 34 Myr for two NC groups. We tested the role of an island-hopping process using ancestral area estimation in BioGeoBEARS. We considered the recent reviews regarding the palaeogeography of the Southwest Pacific region as well as posited the existence of yet-to-be-discovered past islands. We show that the presence in NC of "old" endemic lineages can partially be explained by indirect dispersal from Australia through now disappeared islands acting as refugia. Our results suggest that the Australian region was first colonized during the breakup of Gondwana in the Late Jurassic, and secondarily from Asia in the mid-Cretaceous. Our study highlights the importance of thorough inspection of paleogeographic evidence when studying old groups of organisms. Furthermore, the multiple colonization events deciphered for NC provide insight into the composite nature of NC's biota.

Malhotra, Rumaan (Presenter)

Session: CS07 – Conservation Biogeography

Title: Patch characteristics and domestic dogs differentially affect carnivore space use in fragmented landscapes in Southern Chile

Rumaan Malhotra (rumaanm@umich.edu), University of Michigan
Jaime Jiménez, University of North Texas
Nyeema Harris, Yale University

Abstract:

In an increasingly anthropogenic world, species face multiple interacting threats. Habitat fragmentation and domestic dogs are two perturbations threatening terrestrial mammals globally. Our aim was to determine if (1) the spatial use of domestic dogs increases with habitat destruction and (2) whether domestic dogs and habitat destruction drive the spatial use of native carnivores in a heavily degraded agricultural landscape. We implemented a camera trap survey in a fragmented landscape comprised of native forest patches amidst a matrix of pastureland in Los Lagos, Chile. We used single-species occupancy models to assess the impact of domestic dogs and habitat destruction on three mesocarnivores – the foxes, culpeo (Lycalopex culpaeus) and chilla (Lycalopex griseus) and the wild cat güiña (Leopardus guigna). Additionally, we compared temporal overlap of all study species (including domestic dogs). The occupancy of domestic dogs increased with habitat loss. Detection rates for both the foxes increased with domestic dog occupancy, while factors driving occupancy differed for each of the native species. We found that a 12% projected increase in domestic dog occupancy negatively impacted the spatial use of the culpeo. In contrast, domestic dog occupancy had no effect/was positively correlated with chilla spatial use. Fragmentation was a positive driver for chilla occupancy. The güiña did not respond to fragmentation and other habitat covariates or to domestic dog occupancy. All native carnivore species were primarily nocturnal, while the domestic dog was almost entirely diurnal. We highlight that the effects of domestic dogs or habitat destruction are not ubiquitous across the carnivore guild, with native species showing varied tolerance. However, future conditions of increased fragmentation and habitat loss will likely increase the potential contact between domestic dogs and native carnivores. Our work is an example of how landscape structure may impact native species while also mediating their interactions with an invasive species.

Mancino, Chiara (Presenter)

Session: CS22 – Biodiversity patterns, distribution & maintenance

Title: Going west: changing distribution of Loggerhead sea turtle nests in the Mediterranean Sea

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Luigi Maiorano, Dept. of Biology and Biotechnologies "Charles Darwin", Sapienza University
Daniele Canestrelli, Dept. of Ecological and Biological Science, Tuscia University

Abstract:

Global changes represent possibly the greatest threat to the future of biodiversity, and this can be especially true for species with both terrestrial and aquatic habitats during their life cycle. The problem is even greater when dealing with human dominated landscapes, e.g. the Mediterranean basin, occupied and exploited for centuries. No previous studies have focused on the effects of global change in terrestrial and marine environments together. Therefore, considering state of the art species distribution models (SDM), we used Loggerhead sea turtles (Caretta caretta) to explore the combined (marine and terrestrial) global change effects on coastal environments of the Mediterranean Sea. Sea turtles represent a good case study because they depend on both environments, have a migratory life stage, complex life cycle, and a sex determination based on temperature. Nesting areas for marine turtles are mainly concentrated in the eastern Mediterranean, with a trend in recent years towards an increased presence in the western basin. We calibrated a multi-temporal SDM considering nest locations and climatic and anthropogenic variables covering both the terrestrial and marine side of coastal areas.

We found that climate suitability increased by 80% over time in the western part of the basin, while it decreased in the East. Anthropogenic variables and sea surface temperature are the most important variables. The potential importance of the western Mediterranean beaches as possible nesting range for the sea turtles represents an important result to assist sea turtles' conservation during their range expansion towards West.

Marino, Clara (Presenter)

Session: CS18 – Invasion /Conservation /Climate Change

Title: Linking ecological strategies and impact of birds involved in biological invasions

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Céline Bellard, Univ. Paris Saclay
Camille Leclerc, Inrae

Abstract:

Biological invasions represent one of the major threat on biodiversity. Understanding how they affect native fauna is of upmost importance for anticipating potential functional shift within ecosystems. Here, we analyzed the ecological strategies of 800 birds that were either invasive or vulnerable to invasions. Using six ecological traits related to habitat exploitation, resource use and life-history, we distinguished three functional groups of birds: birds threatened by biological invasions, alien birds with a harmful impact and alien birds with no impact on native ecosystems. We found that birds threatened by invasive species were more likely to be terrestrial or water foragers and feed on invertebrates compared to birds threatened by other threats. By contrast, large-bodied species and habitat specialists were universally threatened. Our findings also revealed different alien bird profiles following their invasive mechanisms. For instance, birds acting as predators in invaded ecosystems were mostly habitat generalists with a terrestrial foraging strategy and a vertebrate-based diet. We used such a knowledge to classify the potential impact of data deficient alien species. This work offers a new point of view on the consequences of invasive alien species by addressing the functional aspect of threatened and threatening diversity.

Martín-Devasa, Ramiro (Presenter)

Session: CS15 – Gradients, range-limits & diversity

Title: Species range size shapes the distance decay in community similarity

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Sara Martínez-Santalla, Universidad de Santiago de Compostela
Carola Gómez-Rodríguez, Universidad de Santiago de Compostela
Rosa Crujeiras, Universidad de Santiago de Compostela
Andrés Baselga, Universidad de Santiago de Compostela

Abstract:

The decrease in community similarity with spatial or environmental distance (i.e. distance-decay) is a general property of biological systems. Adequately capturing the shape of this pattern is essential to characterize spatial turnover in community composition and its dependence on spatial or environmental distances. With this purpose, parametric functions implementing non-linear regressions of community similarity are usually employed, which are very useful because their parameters can be interpreted in biological terms. For example, highly vagile organisms tend to have flatter distance-decay slopes than dispersal-limited organisms. However, the links between distance-decay and key macroecological attributes such as species range size have received less attention, even though species range size determines to which extent two localities can share a given species. In this work, we aim to assess the dependence between the functional form of the decrease in biological similarity with distance and the species range sizes. To do so, we computed distance-decay curves from simulated communities to assess how the species range sizes shape the functional form of distance-decay patterns (i.e., negative exponential, power-law or sigmoidal [Gompertz] relationships). We also used European beetle species distribution data to explore the relationship between function parameters and compositional heterogeneity at a continental scale (multiple-site beta diversity) and study how each parameter capture the spatial structure in community composition at a large scale.

Matzke, Nick (Presenter)

Session: CS11 – Phylogeography

Title: Statistical comparison of DEC and DEC+J: the DEC model is statistically inadequate on typical datasets

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Wallis Bland, School of Biological Sciences, University of Auckland

Abstract:

Statistical model comparison has become common in historical biogeography, enabled by the R package BioGeoBEARS, which implements several models in a common framework, allowing models to be compared with standard likelihood-based methods of statistical model comparison. Ree and Sanmartín (2018) critiqued the comparison of Dispersal-Extinction-Cladogenesis (DEC) and a modification of it, DEC+J, which adds the process

of jump dispersal at speciation. DEC+J provides highly significant improvements in model fit on most (although not all) datasets. However, we show that DEC+J fits better on datasets because the DEC model is statistically inadequate in the common situation when most species have geographic ranges of single areas; the DEC model requires long residence times of multi-area ranges, and when these are not observed, a model that does produce such data patterns, such as DEC+J, prevails. More fundamentally, statistical comparison of DEC and DEC+J produces identical log-likelihood differences to statistical comparison of two submodels of ClaSSE where extinction rates are fixed to 0. We conclude with suggestions for more statistical sophistication and realism in phylogenetic biogeography.

Maureaud, Aurore (Presenter)

Session: CS17 – Marine Biogeography

Title: A global biogeography for marine benthic species

Aurore A. Maureaud (aurore.aqua@gmail.com), Yale University
Gabriel Reygondeau, University of British Columbia
Kate Ingenloff, Yale University
Kevin Winner, University of Hawaii
Les Watling, University of Hawaii
Jessica Vigneron, Yale University
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Abstract:

The regionalization of habitats into biogeographic units is the basis for understanding species' distributions and informing biodiversity conservation. Biogeographic and conservation research addressing global ocean environments has focused predominantly on characterizing coastal and pelagic regions, and largely ignored benthic environments. This oversight limits our ability to effectively study benthic marine species and communities. From shallow to deep waters, the ocean seafloor includes a high diversity of habitats and organisms of high conservation priority. By combining previously existing regionalizations of coastal and deep-sea ecosystems, we establish the first global seafloor biogeographic layer, divided into three main seafloor habitat categories: coastal (0–200m), bathyal (800–3,500m), and abyssal (3,500–6,500m). To ensure all ocean seafloor sites were associated with a region, we applied a three-dimensional nearest neighbor analysis to account for bathymetry. We then assessed the percentage of benthic habitats belonging to national and international waters and highlighted each countries' responsibilities in terms of seafloor habitat protection. Continental shelves do not extend similarly along coastlines, resulting in some exclusive economic zones that include more deep-sea regions than others. This is the case of island exclusive economic zones encounting more than 90% of abyssal zones in their waters. While most deep-sea regions extend beyond national jurisdictions, we also show that the seafloor biogeographic units are transboundary, requiring global cooperation for their conservation. This new seafloor biogeography is the first step towards understanding the global distribution of benthic species, and informing conservation prioritization by incorporating the bathymetric structure of the global ocean seafloor.

Medina, Wilderson (Presenter)

Session: CS19 – Biodiversity patterns, distribution and maintenance

Title: Elevational Shift of Endemic Birds in the Northern Andes: Effects of Climate Change and Deforestation

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Stuart Pimm, Duke University

Abstract:

Climate change and deforestation are two of the leading direct drivers of biodiversity loss in tropical forests. Some studies have compared historical and recent observations providing clues about Andean birds' movement patterns in response to climate change. Here we used crowd-sourced citizen-science data to assess altitudinal distribution patterns for 120 bird endemic species in the Northern Andes. We compared expected versus observed values in the extreme lower 5% and the upper 95% elevations between historical (<2000) and most recent data (>2000) using eBird and GBIF databases. Some species showed individual significant differences for the lower 5% limit and the upper 95% limit for historical records. Aggregated across all species, the data showed highly significant results for historical observations in the lower 5%. The evidence reveals a general trend of elevational shifting from lower to higher elevations after 2000. These findings provide widespread evidence of upward migration of birds from lower to higher elevations in the Northern Andes. These results are thought to be caused mainly as a response to temperature changes; however, other climate change proxies such as precipitation might help provide further insights. Likewise, deforestation may also contribute to these responses in birds' migration. Knowing these patterns will help in determining conservation priorities in the richest hotspot of the world.

Mendez Castro, Francisco Emmanuel (Presenter)

Session: CS04 – Functional Biogeography

Title: What defines insularity for plants in edaphic islands?

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Gianluigi Ottaviani, Institute of Botany of The Czech Academy of Sciences, Trebon
Luisa Conti, Czech University of Life Sciences, Prague

Abstract:

Isolation is not only a key concept of the Island Biogeography Theory but also the most essential parameter defining any island. Contrary to island size, increasing isolation translates into decreasing species richness due to a higher risk of extinction and lower colonization chance. Isolation also influences the genetic composition of island populations, generating unique eco-evolutionary histories leading island biota to develop distinct functional characteristics (i.e. traits). For example, high (Spatio-temporal) isolation is expected to gradually shape plant reproduction strategies and dispersal ability, favoring on-spot persistence (e.g. high incidence of clonality, production of large fruits and seeds). In highly isolated islands, sexual reproduction is riskier than vegetative reproduction and remaining close to the parent plant may constitute an eco-evolutionary advantage for the offspring. As a result, island plants are generally characterized by functional traits that differ from those found in non-insular systems. The predictable effect of isolation on plant traits is named island syndrome. Comparative trait-based approaches have great potential to answer important questions in island biogeography, including a more comprehensive identification of the island syndrome. Recently, a debate has opened as to whether terrestrial island-like systems function like true islands. Defining insularity is conceptually and methodologically challenging in terrestrial systems because recognizing species source(s) and measuring isolation is not as straightforward as for oceanic islands. We contribute to the debate by contextualizing the definition of insularity, and by proposing an approach to identify the role of isolation in the biota of edaphic islands. To test this approach, we explored the relationship between insularity predictors and the species richness of specialist plants in three edaphic island systems in Europe. Insularity affected edaphic island specialist richness through island size and target effect (i.e. an emergent property of islands depending on their isolation and size).

Méndez Cuéllar, Laura (Presenter)

Session: CS24 – Biodiversity patterns, distribution & maintenance

Title: Megafrugivores as fading shadows of the past: extant frugivores and the abiotic environment as the most important determinants of the distribution of palms in Madagascar

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Mijoro Rakotoarinivo, Département de Biologie et Ecologie Végétales, Faculté des Sciences, Université d'Antananarivo

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Abstract:

The extinction of all Madagascar's megafrugivores ca. 1000 years ago, may have left its signature on the current distribution of vertebrate dispersed plants across the island, due to the loss of effective seed dispersal. In this study, we dissect the roles of extinct and extant frugivore distributions, abiotic variables, human impact and spatial predictors on the compositional turnover, or beta-diversity, of palm (Arecaceae) species and their dispersal-related traits across 40 assemblages in Madagascar. Variation partitioning showed that palm beta-diversity is mostly shaped by the distribution of extant frugivores (eight lemur, three bird, two rodent and one bat species) and the abiotic environment (e.g., forest cover, slope and temperature), and to a lesser extent by the distribution of extinct megafrugivores (several giant lemur and elephant bird species). However, the

contribution of these variables differed between dry western assemblages and wet eastern assemblages, with a more prominent role, albeit still small, of extinct megafrugivores in the west. These results suggest that palm distributions in the dry west of Madagascar, where megafrugivores were probably most abundant in the past, still show signatures of past interactions. With a fourth-corner analysis we observed that the distribution of palm species with relatively large fruits and seeds was negatively associated with frugivore richness of both past and present communities and home range sizes of extant mammalian frugivores. This suggests that palm species with relatively large fruits tend to occur in places with fewer, small-ranged mammalian frugivores, which may indicate dysfunctional seed dispersal. Nevertheless, our results also indicate that several wide-ranging bird species with high dispersal ability (large hand-wing index) that also occasionally feed on fruits may compensate this potential dispersal loss. Our study sheds new light on dispersal anachronisms in Madagascar, and how defaunation and past species interactions may underlie current plant distributions.

Morris, Sarah (Presenter)

Session: CS06 – Phylogeography

Title: Historical biogeography of Blakeeae (Melastomataceae) in the hyper-diverse Chocó biogeographic region

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Abstract:

Nested between the Pacific Ocean and the Northern Andes, the Chocó biogeographic region is an extremely wet lowland tropical rainforest containing perhaps the greatest number of vascular plant species per unit area on Earth. This immense biological diversity poses a conundrum: geologic data has determined that the land comprising the Chocó is a recent formation that did not become fully terrestrial until 3.1 Ma – a short window of time to assemble a diversity hot-spot with high regional endemism. How can we explain the exceptional diversity of a region that was, until recently, under water? With its unique history at the nexus of South and Central America, disentangling the role of Andean orogeny and the rise of the Panama Isthmus on the formation of the Chocó flora remains a challenge. Lellinger and Gentry researched the floristics and phytogeography of the Chocó decades ago without the benefit of molecular data, and since then, the difficulty of accessing this region has prohibited further study. Using phylogenetic comparative methods and biogeographic models, we found new insights on the macroevolution of the Chocó flora using the melastome tribe Blakeeae as a focal group. Blakeeae contains about 200 species distributed throughout the Neotropics with a center of diversity in the Chocó-Andean region, making it an ideal group to explore the biotic and abiotic variables that impacted the diversification of the Chocó flora. We present here the first phylogenomic analysis of Blakeeae using sequence data from the Angiosperm-353 bait kit for 78 Melastomataceae species.

Morris, Thomas (Presenter)

Session: CS21 – Climate Change Biogeography

Title: Marine parasite distribution in a changing climate

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Nick Matzke, University of Auckland
Mark Costello, Faculty of Bioscience and Aquaculture

Abstract:

It is tempting to assume that parasites and their hosts have similar biogeographic patterns. However, studies have shown that external parasites have different spatial distribution patterns than their hosts. So, while marine species are generally expected to decline in the tropics and increase in the subtropics as climate change increases, current research indicates that changes in climate may be favourable for parasite distribution. This will have economic impacts on fisheries and aquaculture and biological impacts on the function and structure of marine ecosystems. In this study, we compiled the most spatially explicit marine dataset available for copepod parasites (downloaded from OBIS and GBIF databases) and projected their range shifts using MaxEnt. We propose that with increases in ocean temperature, parasite ranges may expand, potentially increasing their developmental rate, transmission, survival and pathogenicity. Parasites may also infest new hosts due to predicted parasite and/or host range shifts. By capturing the changes in the geographic ranges of parasitic species, these predictions give us a more holistic idea of the impact that climate change will have on global marine biodiversity, inclusive of parasites.

Murara, Pedro (Presenter)

Session: CS20 – Paleobiogeography

Title: Paleobiogeography and human occupation in the southern region of South America

Pedro Germano Murara (pmurara@gmail.com), Universidade Federal da Fronteira Sul
Gisele Lima, Universidade Federal da Fronteira Sul
Mirian Carbonera, Universidade Comunitária da Região de Chapecó
Ademar Graeff, Universidade Federal da Fronteira Sul
Arthur Bernardes, Universidade Federal da Fronteira Sul

Abstract:

Vegetation changes occurred in southern South America during the Last Glacial Maximum. Understanding the impact of these changes on the climate, on the biota and how these changes happened is essential to understand how migratory flows and human adaptations occurred after the Last Glacial Maximum. Sediment in wetlands of the Meridional Plateau, southern Brazil, have been collected and submitted to palynological analysis, in order to understand the vegetation dynamics in these areas. In parallel, botanical survey, description of current palynoflowers and pollen rain in surface materials have been implemented to support palynological analyses. Samples collected from archaeological sites and sedimentary cores will be submitted to radiometric carbon-14 dating for chrono-stratigraphic correlations. The data collected suggest that, compared to studies of the

Brazilian coast, the countryside presented a different vegetation distribution pattern, which contributed to a different migratory flow and occupation process by human beings. Due to the decrease in temperature and humidity, during the Last Glacial Maximum, the forest formations retreated to the valley bottom and refuge areas, giving up space for expansion of the Campos. With the gradual increase in temperature and humidity, the Forest expanded, but unlike what happened on the coast, this formation did not completely replace the Campos, which resulted in a vegetation consisting of a field-forest mosaic. In addition to this pattern in the distribution of these plant formations, the expansion of the Forest in these areas seems to have occurred earlier in the interior areas compared to those studied areas in the eastern strip.

Nemani, Shreya (Presenter)

Session: CS17 - Marine Biogeography

Title: Patterns of Species and Functional Diversity among Coastal Benthic Assemblages: Placentia Bay, Newfoundland and Labrador, Canada

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Katleen Robert, Memorial University - Marine Institute
Evan Edinger, Memorial University
David Cote, Dalhousie University
Benjamin Misiuk, Dalhousie University
Julia Mackin-McLaughlin, Memorial University - Marine Institute

Abstract:

Benthic species assemblages refer to species that co-occur in a region. Linking them to physical environmental variables allows us to model continuous maps assessing the spatial distribution of these habitats. The use of marine habitats as proxies for biodiversity is also becoming increasingly common to marine management efforts, however, studies mainly use a taxonomic approach based on species identity and abundance to assess their diversity. Considering functional traits, which capture the life history, physiology, and morphology of a species is important since benthic fauna are key drivers of various ecosystem services including nutrient cycling, maintaining biodiversity, and provisioning of food and habitat. This study used biological traits analysis (BTA) to compare five benthic species assemblages observed across two coastal sites in Placentia Bay, Newfoundland and Labrador, in addition to comparing the spatial patterns of taxonomic and functional diversity metrics. Trait data were compiled from databases and the following measures were calculated for both species and trait data: richness, diversity, and evenness. Trait composition was identified per assemblage using the community weighted mean, and functional similarity was assessed using co-inertia analysis(COI-A). Spatially, species and functional richness exhibited similar patterns, meanwhile species and functional diversity depicted contrasting patterns, indicating alternate hotspots for diversity. Taxonomically distinct assemblages exhibited similar trait compositions for two assemblages based on the COI-A ordination, meanwhile one assemblage exhibited a unique set of potentially sensitive traits which could limit its ability to resist disturbance. Overall, results indicate that incorporating both taxonomic and functional components may better inform management efforts.

Norder, Sietze (Presenter)

Session：CS05 – Island Biogeography

Title：Island Biogeography in the Anthropocene and Quaternary

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Abstract：

The realization that human activities have a major influence on ecosystems from local to global scales has given rise to the concept of the Anthropocene. However, although the influence of human activities on biodiversity is clearly significant, it remains unclear to what extent the rate and magnitude of biodiversity changes differ from pre-human dynamics. Islands are ideal model systems for understanding the relative contribution of environmental and societal variables to biodiversity because the onset of human activities on islands can generally be clearly defined. Here, I will present the two main parts of my PhD dissertation, in which I place human-environment interactions on islands in the context of environmental fluctuations over the Quaternary. First, I quantify how island area and isolation have changed over the Quaternary as a result of climate-driven sea-level fluctuations, and analyse how these dynamics have imprinted modern biodiversity patterns. Secondly, I study how human activities in the past and present shaped island ecosystems and landscapes, and compare their rate and magnitude to pre-human dynamics. Overall, the findings of my thesis indicate that modern biodiversity patterns show legacies of past human activities but are also imprinted by environmental dynamics in deep-time. Furthermore, the rate of change following human settlement on islands can largely exceed Quaternary background rates. Although human activities have become a major driver in affecting biodiversity worldwide, the ways in which environmental and anthropogenic variables have interacted to shape biodiversity at local to regional scales can be highly diverse.

Novella Fernandez, Roberto (Presenter)

Session：CS09 – Biodiversity patterns, distribution & maintenance

Title：Broad-scale patterns of geographic avoidance between species emerge in the absence of fine-scale mechanisms of coexistence

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Abstract：

The need to forecast range shifts under future climate change has motivated an increasing interest in better understanding the role of biotic interactions in driving diversity patterns. The contribution of biotic interactions to shaping broad-scale species distributions is however, still debated, partly due to the difficulty of detecting their effects. We aim to test whether spatial exclusion between potentially competing species can be detected at the species range scale, and whether this pattern relates to fine-scale mechanisms of coexistence. We develop and evaluate a measure of geographic avoidance that uses outputs of species distribution models to quantify geographic exclusion patterns expected if interspecific competition affects broad-scale distributions. We apply the measure to 10 Palearctic bat species belonging to four morphologically similar cryptic groups in which competition is likely to occur. We compare outputs to null models based on pairs of virtual species and to expectations based on ecological similarity and fine-scale coexistence mechanisms. We project changes in range suitability under climate change taking into account effects of geographic avoidance. Values of geographic avoidance were above null expectations for two cryptic species pairs, suggesting that interspecific competition could have contributed to shaping their broad-scale distributions. These two pairs showed highest levels of ecological similarity and no trophic or habitat partitioning. Considering the role of competition modified predictions of future range suitability. Our results support the role of interspecific competition in limiting the geographic ranges of morphologically similar species in the absence of fine-scale mechanisms of coexistence. This study highlights the importance of incorporating biotic interactions into predictive models of range shifts under climate change, and the need for further integration of community.

Oliveira, Matheus (Presenter)

Session: CS07 – Conservation Biogeography

Title: Woody Encroachment in the Brazilian savanna

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Vinícius Maia, Universidade Federal de Lavras
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Abstract:

The Woody Plant Encroachment (WPE) is increasing the woody cover and biomass across the tropical savannas, changing the composition and structure of the vegetation, and converting open-canopy ecosystems towards closed-canopy vegetation. These changes affect the ecosystem's functioning and promote biodiversity loss by reducing the herbaceous layer. Studies suggest that WPE is occurring in the Brazilian savanna (Cerrado), although many of them have been evaluated at a small spatial scale, making it difficult to evaluate the causes, extension, and impact of this phenomenon. We aimed to identify WPE prone regions throughout the Cerrado natural cover using trend analysis of the annual minimum Enhanced Vegetation Index (EVI) of MODIS images. We modeled the EVI trend as a function of climate variables, soil properties, and fire frequency, in order to evaluate which variables explain the WPE. Our study provides evidence that the WPE is occuring widespread in the Cerrado, although some peripheral regions with transitional climates are experiencing biomass reduction. The EVI trend is positively influenced by the mean temperature of wettest quarter, precipitation of driest month and precipitation of wettest quarter, as well as was negatively influenced by the initial EVI, fire frequency, isothermality, volumetric fraction of coarse fragments, and pH, and climate water deficit and maximum temperature trends. Because of the importance of the Cerrado for Brazilian biodiversity, we indicate the necessity to develop conservation policy for the biome in order to reduce the impact of WPE due to climate change and changes in the fire pattern.

Padullés Cubino, Josep (Presenter)

Session：CS06 – Phylogeography

Title：The phylogenetic structure of European forest plant communities

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Erwin Bergmeier, University of Göttingen
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Juan Antonio Campos, University of the Basque Country
Andraž Čarni, University of Nova Gorica
Mirjana Ćuk, University of Novi Sad
Michele De Sanctis, Sapienza University of Rome
Adrian Indreica, University of Brasov
Borja Jiménez-Alfaro, University of Oviedo
Larisa Khanina, Institute of Applied Mathematics of Russian Academy of Sciences
Ilona Knollová, Masaryk University
Jonathan Lenoir, Université de Picardie Jules Verne
Remigiusz Pielech, University of Agriculture in Kraków
Valerijus Rašomavičius, Nature Research Centre, Institute of Botany
Željko Škvorc, University of Zagreb
Jens-Christian Svenning, Aarhus University
Kiril Vassilev, Bulgarian Academy of Sciences
Wolfgang Willner, University of Vienna
Milan Chytrý, Department of Botany and Zoology, Faculty of Science, Masaryk University

Abstract：

Forests are a major component of terrestrial ecosystems in Europe. Yet, the phylogenetic structure of forest plant communities across the continent has not been quantified. We analyzed whether co-occurring angiosperm species in 61,816 georeferenced plots across Europe were more or less distantly related than under random expectation, and identified overrepresented clades in phylogenetically clustered plots. We also tested the effect of environmental variables on the phylogenetic structure of forest plots. Each plot was classified by an expert system into three forest types: coniferous, deciduous broadleaf, and sclerophyllous. We found a tendency for phylogenetic clustering in northern Fennoscandia that could reflect either environmental filtering by climatic harshness or species postglacial migration lag. Areas of phylogenetic overdispersion were located in the Baltic countries, interior regions of Russia, and on Iberian and Italian peninsulas, perhaps reflecting the effect of refugia and biome transition. Overrepresented clades in clustered plots varied among forest types and regions but mostly included Ericaceae and Poaceae for coniferous forests, Fagaceae and Poaceae for deciduous broadleaf forests, and Fagaceae for sclerophyllous forests. We found weak correlations between environmental variables and the phylogenetic structure of forest plots. These findings indicate that phylogenetic clustering or overdispersion of forest plant communities in different parts of Europe can be caused by different ecological processes, anthropogenic disturbances, and historical biogeographical events that ultimately select for particular sets of clades. Our findings underscore the need for considering the effect of historical evolutionary processes in community-assembly at large spatial scales.

Panchard, Thomas (Presenter)

Session: CS09 – Biodiversity patterns, distribution & maintenance

Title: Testing the power of remotely sensed snow cover duration to predict plant species distributions in alpine ecosystems

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Olivier Broennimann, University of Lausanne
Grégoire Mariéthoz, University of Lausanne
Mathieu Gravey, University of Lausanne

Abstract:

The impact of snow on plant distributions in arctic and alpine ecosystems has been known for decades. However, as major progress was made in the development of alpine plant species distribution models, snow cover was recurrently disregarded as predictor. Here we filled this gap by using a large set of satellite images to produce three snow cover duration indexes. One of them is using an online platform, allowing quick and easy replication anywhere in the world. We examined the increase in predictive power brought by addition of the snow predictor in species distribution models of 206 alpine plants, alongside other commonly used topoclimatic predictors. Despite the snow indexes containing redundant information with other climatic predictors, addition of each of the three indexes resulted in an overall increased accuracy of the models. Species being known for their interaction with snow seem to benefit especially from the additional information carried by the snow indexes. In the context of global warming, our findings suggest that scenarios of snow cover decrease should be considered when assessing the future distribution of snow-sensitive alpine plant species.

Pang, Sean (Presenter)

Session：CS24 – Biodiversity patterns, distribution & maintenance

Title：Clustering of spatially associated species：a statistical approach towards understanding and identifying patterns in species distributions

Sean E. H. Pang (s.pang@u.nus.edu), National University of Singapore
Ferry Slik, Universiti Brunei Darussalam
Damaris Zurell, University of Potsdam
Edward Webb

Abstract：

By classifying species based on their interspecific spatial associations (ISA), we can identify groups of species with uniquely similar geographical distributions. Such groupings would enable greater insights into the spatial structuring of species communities, their vulnerabilities to spatially relevant threats, and the formation of meaningful biodiversity units to better inform conservation and management priorities. Yet, largely absent from the literature are quantitative approaches or frameworks aimed at forming such groups. Here, we develop and illustrate the Clustering of Spatially Associated Species (CSAS) approach, and apply it to distributions of tree species in Borneo. We investigated how the choice of ISA index and clustering algorithm affects the clustering and performance of resultant dendrograms and identified methods that performed best. Based on the final clustering result, species were then classified into several distinct biodiversity units, where the impact of land-use change on each unit was evaluated. 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 based on Hellinger's distance (ISA) and WARD (clustering algorithm) 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 propose that such quantitative assessments of associations and species groupings are likely to offer opportunities for more nuanced inference in ecology, biogeography, and conservation.

Pepke, Michael (Presenter)

Session: CS11 – Phylogeography

Title: Reconciling supertramps, great speciators and relict species with the taxon cycle stages of a large island radiation

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Martin Irestedt, Swedish Museum of Natural History
Jon Fjeldså, Statens Naturhistoriske Museum
Carsten Rahbek, Statens Naturhistoriske Museum
Knud Jønsson, Statens Naturhistoriske Museum

Abstract:

The taxon cycle concept provides geographically explicit hypotheses for investigating the evolutionary processes underlying the distribution of species in space and time. Here, we explore taxon cycle predictions within a large avian island radiation and integrate the concepts of ‘supertramps’, ‘great speciators’ and relictualization. We constructed a new time-calibrated molecular phylogeny of the core Campephagidae (cuckooshrikes, cicadabirds and trillers) and used ancestral range estimation and diversification rate analyses to explore the biogeographical history of this group spanning the Indo-Pacific, Australia, Southeast Asia, and Africa. We tested for correlations between evolutionary age of species and dispersal capacity (based on wing morphology), diversification and distribution, while accounting for phylogenetic non-independence. Population-level analyses were used to understand the phylogeography of a ‘great speciator’, the Edolisoma tenuirostre complex. The Campephagidae represents a continuum of dispersal abilities; some species are widespread and undifferentiated (‘supertramps’) or show differentiation of local populations (‘great speciators’), and a few are endemic to single islands (relicts). We find that older species relative to younger species inhabit fewer and larger islands at higher elevations. The level of intraspecific variation decreases with species age and is highest in the ‘great speciators’, which have intermediate dispersal abilities and exemplifies gradual shifts in dispersal ability in relation to the geographical setting. We infer phases of range expansion and contraction over millions of years (taxon cycles), within a monophyletic group of birds. These observations demonstrate reconciliation of ‘supertramps’, ‘great speciators’ and relictual palaeoendemics within the temporal stages of the taxon cycle.

Pérez Chaves, Pablo (Presenter)

Session: CS08 – Biogeography of the Anthropocene

Title: Using forest inventories, remote sensing and machine learning to predict spatial floristic patterns in Peruvian Amazonia

Pablo Pérez Chaves (pablo.pch@gmail.com), University of Turku

Abstract:

Remote sensing provides spatially and temporally continuous information useful for predicting soil characteristics and biodiversity patterns in Amazonia. Field inventories are time-consuming, costly and often

have limited spatial coverage. Similarly, little is still known regarding the spatial patterns of floristic composition throughout Peruvian Amazonia. Therefore, the combination of field data from forest national inventories and satellite imagery can offer a cost-effective way to spatially predict floristic patterns in larger areas. Here, we combined remote sensing (Landsat satellite imagery and elevation) and environmental variables (climate and soil) with forest inventory data to predict floristic patterns in Peruvian Amazonia using machine learning. After summarizing the tree community data into a non-metric multidimensional scaling (NMDS) ordination, we found that the first axis of the floristic ordination (NMDS1) was strongly correlated with the spectral values of Landsat bands, whereas NMDS 2 and 3 were strongly correlated with both the remote sensing and environmental variables. We further spatially predicted each floristic ordination axis throughout Peruvian Amazonia using random forest algorithm (R2=0.63,0.57&0.39 for NMDS1,2&3 respectively). Therefore, it is possible to use remote sensing layers to predict spatial floristic patterns in areas beyond the location of the field data, which helps identifying suitable areas for sustainable management and conservation.

Pinilla Buitrago, Gonzalo (Presenter)

Session: CS16 – Models & Methods in Biogeography

Title: Wallace v2: Restructuring and new features for a modular and expandable species distribution modeling application

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Jamie Kass, Okinawa Institute of Science and Technology
Andrea Paz, ETH Zürich
Bethany Johnson, Universidad EAFIT
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Cory Merow, University of Connecticut
Sarah Meenan, City College of New York
Olivier Broennimann, University of Lausanne
Sara Varela, Universidad de Vigo
Brian Maitner, University of Arizona
Hannah Owens, University of Copenhagen
Peter Galante, American Museum of Natural History
Matthew Aiello-Lammens, Pace University
MARY BLAIR, American Museum of Natural History
Robert Anderson, City College of New York, CUNY

Abstract:

It is increasingly difficult for researchers to follow best practices for species distribution modeling, especially those without strong programming skills. For this reason, we released the Wallace Ecological Modeling Application in late 2017 and have worked to improve and expand it since then. Wallace is a GUI-based software that allows users to build, evaluate, and explore species distribution models (SDMs), while providing step-by-step guidance and features that enable reproducibility. Our development team has made many advancements:

a significant restructuring to promote modularity and metadata reporting, new enhancements of existing features, bug fixes with user-community feedback, and new modules co-authored by external collaborators. The main new features in Wallace v2 are: i) the ability to build and manage multiple species' models in a single session, ii) the addition of a new environmental space component capable of multispecies analyses, iii) the addition of new occurrence data sources, iv) more customized options to define areas of extent for model building and transfer, v) the opportunity to download extensive metadata, and vi) the choice to save and load working sessions. We expect that this version will be useful for researchers and will further encourage Wallace's adoption as a pedagogical tool for instructors in biogeography. Ongoing development (post v2) will allow users to post-process SDM predictions based on observations and remotely sensed data and calculate biodiversity change indicators (e.g., range size, percent suitable land cover). Wallace's future includes ongoing module addition and integration with other biodiversity tools, beginning with the Colombian Biodiversity Observation Network's BioModelos.

Platania, Leonardo (Presenter)

Session: CS06 - Phylogeography

Title: Microendemicity in a hotspot of biodiversity: speciation modes and microendemic patterns in New Caledonian leaf beetles.

Leonardo Platania (leonardo.platania@gmail.com), Institut Botanic de Barcelona (CSIC-IBB)
Jesús Gómez-Zurita, Institut Botanic de Barcelona (CSIC)

Abstract:

Microendemicity is a condition of endemicity referred to the relative small extension of a particular species range. Some regions of the world seem to concentrate more examples of species with narrow ranges across different taxa, as is the case of New Caledonia, where the levels of microendemicity are striking. We will present our recent work where, through a multifaceted approach, we use molecular phylogenies to investigate macroevolutionary processes including the diversification dynamics and the geography of speciation of two endemic genera of leaf beetles in New Caledonia, Taophila and Tricholapita. Most of the species in these genera are microendemic, locally distributed across the main island of Grande Terre. Our work revealed a decreasing rate of diversification rate in both genera following a time-dependent model, potentially related to accumulated effects of several ecological, environmental and geological factors. Furthermore, these genera diversified through cycles of allopatric speciation, probably enhanced by the same environmental and geological changes that affected New Caledonia during the late Cenozoic. The history of speciation and ecological interactions may contribute to maintaining small allopatric ranges for most species.

Prasetya, Audrey (Presenter)

Session：CS24 – Biodiversity patterns, distribution & maintenance

Title：Where Sunda Meets Sahul：Insights into biogeographical patterns in the Indo-Australian Archipelago from beta-diversity of bird assemblages

Audrey Miranda Prasetya (audrey.prasetya@anu.edu.au), Australian National University
Craig Moritz, The Australian National University
Paul Oliver, Griffith University & Queensland Museum
Leo Joseph

Abstract：

The Sunda-Sahul Biotic Interchange located in the Indo-Australian Archipelago is one of the many major biodiversity hotspots in the world and has been the setting of many biogeographical studies. Since the observations of Wallace's Line, many other biogeographical lines have been drawn throughout the region. It is unclear, however, how reliable these regionalization patterns are and how useful they are for investigating the evolutionary history of organisms in the region. Using calculated beta diversity indices, we investigate the consistency of regionalization patterns between taxonomic levels (species, genus, family) in birds and compare results to the current literature. Results show that regions within a continental shelf are consistently more similar to each other. Yet the regions that lie between Sunda and Sahul are less consistently grouped with either continental shelf. This was further highlighted by connectivity analyses, which showed that although dispersals occur throughout the island groups, most exchanges happened within the Sunda and Sahul continental shelf. The islands between Sunda and Sahul do not give any strong signal of belonging within either continental shelf group nor do they strongly follow previous biogeographical groupings. Overall, within-shelf barriers seem much weaker than between-shelf barriers suggesting some mechanisms of distance (geographical /environmental /biotic) were acting against dispersal between these inter-shelf barriers. Further analyses including using ancestral state reconstructions as well as incorporating geographic and environmental distance into the analyses will shed further light on the processes that may drive these biogeographical patterns.

Puglielli, Giacomo (Presenter)

Session: CS15 – Gradients, range-limits & diversity

Title: The cold-drought tolerance trade-off affects range size differences in temperate woody plants

Giacomo Puglielli (giacomo.puglielli@gmail.com), Estonian University of Life Sciences
Enrico Tordoni, University of Tartu
Aelys Humphreys, Stockholm University
Jesse Kalwij, University of Sussex
Michael Hutchings, University of Sussex
Lauri Laanisto, Estonian University of Life Sciences

Abstract:

A mechanistic explanation of the interspecific differences in plants' range size is yet to be uncovered. Physiological tolerances to cold and heat have provided the major means to expose such mechanism, but results are so far contrasting. We hypothesized that abiotic stress tolerance syndromes – i.e. trade-off axes among multiple abiotic stressors – instead of single stressors considered separately, could provide such a mechanistic explanation. We compiled a dataset including: actual range size (from range maps) and tolerance syndromes available as PCA axes (Stress Axis 1 and 2) representing a drought/warm-cold/wet trade-off and a shade tolerance spectrum respectively. The final dataset included information for 331 European and North American temperate woody plants. Phylogenetic generalized linear mixed models were used to analyze the range size-Stress Axes relationships, including latitude as additional main effect and phylogeny and plant functional types as random effects. Range size scaled only with Stress Axis 1, with the latter explaining 12-23% of range size variance depending on the continent. Overall, cold tolerant species had the largest ranges and drought tolerant species the smallest ones. The sign of the relationship was independent of latitude, continent, phylogeny and plant functional types, but deciduous species range size and tolerance syndromes distributions differed from that of evergreens. We conclude that the cold/wet-drought/warm trade-off is part of the mechanism generating interspecific differences in range size, but also that stress avoidance (deciduousness), more than tolerance, can also partly explain interspecific differences in range size, pointing to explicit inclusion of species' adaptations in range size analyses.

Reijenga, Bouwe (Presenter)

Session: CS15 – Gradients, range-limits & diversity

Title: The impact of biotic interactions on species diversity in space and time

Bouwe Rutger Reijenga (bouwe.reijenga.18@ucl.ac.uk), University College London

Alex L. Pigot, University College London

David Murrell, University College London

Abstract:

Priority effects can play a fundamental role in the assembly of ecological communities, but how they shape the dynamics of biodiversity over macroevolutionary timescales remains unclear. Here we develop and analyse a metacommunity model combining local priority effects with niche evolution, speciation and extinction. We show that by promoting the persistence of rare species, local priority effects cause the evolution of higher metacommunity diversity as well as major disparities in richness among evolutionary lineages. However, we also show how classic macroevolutionary patterns of niche incumbency—whereby rates of regional diversification and invasion slow down as ecological niches are filled—do not depend on local priority effects, arising even when invading species continuously displace residents. Together, these results clarify the connection between local priority effects and the filling of ecological niche space, and reveal how the impact of species arrival order on competition fundamentally shapes the generation and maintenance of biodiversity.

Ribeiro, Maria Margarida (Presenter)

Session: CS21 – Climate Change Biogeography

Title: MaxEnt modelling to predict current and future distributions of Arbutus unedo L. under climate change in the Mediterranean region

Alice M. Maria Marques Almeida (alicemalmeida@ipcb.pt), Universidade da Beira Interior

Maria Margarida Ribeiro, Instituto Politécnico de Castelo Branco-Escola Superior Agrária

Maria Martins, Forest Research Centre, School of Agriculture, University of Lisbon. Tapada da Ajuda

Manuel Campagnolo, Department of Natural Resources and Environmental Engineering, University of Vigo

Saki Gerassis, Department of Natural Resources and Environmental Engineering, University of Vigo

Paulo Fernandez, Mediterranean Institute for Agriculture, Environment and Development (MED) – Universidade de Évora

Teresa Albuquerque, CERNAS – Instituto Politécnico de Castelo Branco, Castelo Branco

José Gonçalves, CERNAS – Instituto Politécnico de Castelo Branco, Castelo Branco

Abstract:

Climate change will impact on the Mediterranean forest and species are expected to migrate northerly. Forests are in danger and may disappear in drier and hotter regions. Forest management policy should reflect the impact of climate change on usable areas for forestry, in particular considering species adapted to Mediterranean regions and to wildfires. In this study, our aim was to model a species widely distributed in the Mediterranean

region, the strawberry tree (Arbutus unedo L.) and, nowadays, well adapted to this region. MaxEnt, a presence-only species-distribution model, was used to model the strawberry tree' environmental suitability in present and future scenarios. The Bayesian network approach was used to determine the most relevant environmental features. The MaxEnt software was applied using 11487 species presence points, together with the matrix of environmental features (bioclimatic and physiographic). The current and future climate data were obtained from WorldClim. Acknowledgements: This work was supported by operation Centro-01-0145-FEDER-000019 - C4 - Centro de Competências em Cloud Computing, cofinanced by the European Regional Development Fund (ERDF) through the Programa Operacional Regional do Centro (Centro 2020), in the scope of the Sistema de Apoio à Investigação Científica e Tecnológica - Programas Integrados de IC&DT; and by Fundação para a Ciência e a Tecnologia I.P. (FCT) through the Forest Research Centre, Portugal, project UIDB/00239/2020 and through the CERNAS, Portugal, project UID/AMB/00681/2019.

Ringelberg, Jens (Presenter)

Session: CS06 - Phylogeography

Title: Dispersal limitation and phylogenetic niche conservatism shape the distribution of the pantropical mimosoid legume clade

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Erik Koenen, University of Zurich
Benjamin Sauter, University of Zurich
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Colin Hughes, University of Zurich

Abstract:

Although the uneven distribution of biodiversity across the globe is well-known, the processes shaping this distribution pattern are poorly understood, and detailed macroecological and macroevolutionary analyses of species-rich lineages that are both geographically and ecologically widespread are rare. Here we study mimosoid legumes, a large morphologically and functionally diverse pantropical clade of trees occurring across all major lowland tropical biomes, and often forming abundant or even dominant elements in rainforests, tropical dry forests and savannas. Using over 400,000 quality-controlled occurrence records for nearly all c. 3,400 mimosoid species, in combination with a robust generic backbone phylogeny based on phylogenomic analysis of 997 nuclear genes, we quantify and explain phylogenetic turnover both across the global lowland tropics and within each continent. These analyses reveal that mimosoid phylogenetic beta diversity is primarily structured by continents on a pantropical scale, but within continents phylogenetic turnover is largely associated with phylogenetic niche conservatism associated with precipitation. Furthermore, phylogenetic regionalisation of mimosoids closely resembles major vegetation types and regionalisations based on broader taxonomic datasets, suggesting that mimosoid legumes may serve as a proxy for overall turnover of woody plants across the lowland tropics. These results suggest that mimosoid legumes obtained their pantropical dominance through a combination of phylogenetic niche conservatism and evolvability, which allowed them to repeatedly adapt across rainfall gradients and subsequently radiate within these new niches.

Roeble, Lizzie (Presenter)

Session: CS22 – Biodiversity patterns, distribution & maintenance

Title: Diversity and biogeography of one of the most diverse plant families on islands: Asteraceae

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Patrick Weigelt, University of Göttingen
Rampal Etienne, University of Groningen
Holger Kreft
Luis Valente, Naturalis Biodiversity Center

Abstract:

Asteraceae are a megadiverse plant family, containing an estimated 25,000–33,000 species. On islands, it is one of the most diverse families of all, forming an iconic component of insular floras worldwide, including many spectacular island radiations, such as the Silverswords in Hawaii or the Bidens across the Pacific Islands. The question immediately arises why this family is so diverse. To answer this question, a complete picture of the diversity of this family on islands is needed, but much of the past research has focused only on individual archipelagos or single lineages. Here, we therefore compile a curated global checklist of Asteraceae native and endemic to islands and combine it with island and environmental data to explore global biogeographic and taxonomic patterns within the family as well as to infer diversity dynamics. We find that there are approximately 5,500 Asteraceae species native to islands, 2,000 of which are endemic. We present an overview of the insular hotspots of geographic and taxonomic diversity within island Asteraceae, and reveal the main macroecological drivers influencing diversity and endemism patterns in both continental and oceanic islands. With its global perspective, our analysis brings us one step closer to understanding the reasons for the remarkable macroevolutionary success of this plant family on islands.

Roilo, Stephanie (Presenter)

Session: CS23 – Conservation & Invasion Biogeography

Title: Measuring the effectiveness of Agri-Environmental Schemes and Ecological Focus Areas for farmland bird conservation across scales

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Jan Engler, Technische Universität Dresden
Thomas Vaclavik, Palacký University Olomouc
Anna Cord

Abstract:

Agri-Environmental Schemes (AES) and Ecological Focus Areas (EFA) are essential tools of the Common Agricultural Policy (CAP) to counteract the dramatic decline of farmland biodiversity in Europe. However, their effectiveness has been repeatedly doubted, as it seems to vary when measured at the field vs. landscape scale and to depend on the regional land-use context. Understanding the heterogeneity of AES/EFA performance and their scale of effect is thus important to develop management strategies that maximise their efficacy. Using ensemble Species Distribution Models (SDMs) and spatially-explicit field-level information from the Integrated Administration and Control System (IACS), we investigated the relative importance and the differential scale of effect of 5 AES/EFA groups (buffer areas, cover crops, extensive grassland management, fallow land and organic farming) on the occurrences of 15 farmland bird species in the Mulde River Basin, Germany. We then modelled how breeding habitat suitability would change if AES/EFA were removed and if their adoption increased following conservation-oriented recommendations. Models for all species had good predictive performance. Variable importance scores differed among species, reflecting species-specific differences in habitat requirements. While some measures (buffer areas, fallow land and extensive grassland) were beneficial for most species, land cover, topography and distance to forest edges and roads were better predictors of bird occurrences. Our results confirm the potential of AES/EFA to contribute to farmland bird conservation, but highlight that much higher adoption rates are necessary to aid farmland bird populations in central Europe.

Sayol, Ferran (Presenter)

Session: CS04 – Functional Biogeography

Title: Loss of functional diversity through anthropogenic extinctions in island bird communities is not offset by biotic invasions

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Robert Cooke, UK Centre for Ecology & Hydrology
Alex L. Pigot, University College London
Tim Blackburn, Department of Life Sciences, Imperial College London
Joseph A. Tobias, Department of Life Sciences, Imperial College London
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Alexandre Antonelli, Royal Botanic Gardens, Kew; University of Gothenburg; University of Oxford
Søren Faurby, Department of Biological & Environmental. Sciences, University of Gothenburg

Abstract:

Human impacts reshape ecological communities through the extinction and introduction of species. The combined impact of these factors depends on whether non-native species fill the functional roles of extinct species, thus buffering the loss of functional diversity. This question has been difficult to address because comprehensive information on past extinctions of species and their traits is generally lacking. Here, we compile morphological data for birds from across nine well-studied and biogeographically distinct archipelagos, including all extant native species as well as species that have become extinct since the Late Pleistocene, or were introduced by humans and established. We apply an imputation method to integrate trait data from extinct and extant species. We then assess which regions of functional space are (re-)filled by alien species and which remain empty, and the extent to which functional diversity among archipelagos has been homogenised by human impacts. We found that functional diversity decreased after anthropogenic extinctions. Even though established alien species often equaled or outnumbered anthropogenic extinctions, we still found a substantial and ubiquitous net loss in overall functional diversity, suggesting that alien species do not fully replace the lost functional diversity of the original avifauna. Moreover, these changes have caused functional homogenisation, as bird communities are becoming more functionally similar following anthropogenic extinctions and the establishment of alien species. Our study suggest that conservation effort should focus on functionally distinct species, trying to minimize further erosion of unique ecological functions.

Schafstall, Nick (Presenter)

Session: CS25 - Paleobiogeography

Title: From Dung Beetle to Bark Beetle: Using beetle remains to reconstruct long-term and short-term landscape dynamics in Central Europe

Nick Schafstall (nick.schafstall@gmail.com), Czech University of Life Sciences
Niina Kuosmanen, University of Helsinki
Vachel Carter, Charles University
Petr Kuneš, University of Glasgow
Nicki Whitehouse, University of Glasgow
Jennifer Clear, Hope University

Abstract:

Central European mountain forests are important ecosystems with unique communities of plants and animals. The long-term history of these forests can be studied by addressing paleoecological and archeological records. In many fields such as paleoecology, landscape archeology and biogeography, additional natural proxies to pollen include botanical macro remains, charcoal and also insect remains. Insect remains preserve well under anoxic conditions, especially Coleoptera (beetles) which possess extremely sclerotized exoskeletons. This allows for the identification of beetle remains up to species level and to reconstruct their preferred environment near the site of deposition. During my PhD project, beetle remains from Holocene lake sediments in Czechia were recovered

and correlated to pollen diagrams and charcoal diagrams. Due to the small volume of lake sediment samples, few individuals were recovered from these samples. However, single occurrences of bark beetle remains could be linked to disturbance events which were reconstructed from other proxies. From a forest hollow in Slovakia, bulk sediment was retrieved and subsampled for the last 1000 years; the beetle community was compared to a pollen record from the same site. The beetle record from the forest hollow shows a variety of species, including large amounts of bark beetles as well as synanthropic species which reveal clues about the naturalness of the site. These studies summarize a number of steps in the use of beetle remains to reconstruct vegetation dynamics and (natural) disturbances in central/eastern Europe.

Sciumbata, Matteo (Presenter)

Session: CS25 – Paleobiogeography

Title: Investigating modern-day relicts of a Miocene mangrove community of western Amazonia

Matteo Sciumbata (matteo.sciumbata@gmail.com), University of Amsterdam (UvA)
James T. Weedon, Vrije Universiteit Amsterdam
Giovanni Bogotá-Angel, Universidad Distrital Francisco Jose Caldas
Carina Hoorn

Abstract:

The Amazon drainage basin is home to the most biodiverse rainforest in the world, yet the origins of this diversification remain much debated. Miocene marine incursions into western Amazonia may have been one such driver of species diversity. During the Miocene Climatic Optimum (17.0–14.7 Ma), sea-level rise may have stretched coastal ecosystems, such as mangrove forests, onto a mega-wetland system (Pebas). Once the marine influence ceased, part of this mangrove community taxa could have adapted to freshwater conditions, becoming an integral part of modern Amazonian plant composition. However, to what extent Miocene marine incursions shaped the floral biodiversity of the Amazon drainage basin is currently unexplored. Here we show that relict species of associated Miocene mangrove taxa occur today in inland Amazonia and along the South American coastline. Using light microscopy (LM) and scanning electron microscopy (SEM), we found that pollen of the modern mangrove Rhizophora mangle is the nearest living relative (NLR) of the previously presumed fossil mangrove Zonocostites ramonae. Additionally, we applied clustering methods onto our pollen-record data and identified fourteen taxa closely associating with the fossil mangrove. Three of these taxa were assigned to NLRs that inhabit freshwater environments of the modern Amazon drainage basin. Together these taxa may form a legacy of species displacement and adaptation to new conditions during marine incursions into western Amazonia. Thereby, we conclude that the Amazonian flora, similarly to riverine fauna (e.g., pink river dolphin and selected fish taxa), likely carries an imprint of the Miocene coastal communities.

https://link.springer.com/article/10.1007%2Fs12549-020-00470-z

Serrano, Filipe (Presenter)

Session：CS09 – Biodiversity patterns, distribution & maintenance

Title：There and back again：when and how the richest Neotropical snake clade dispersed throughout the Americas

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Cristiano Nogueira, Universidade de São Paulo, Brazil
Matheus Pontes–Nogueira, Universidade Federal do ABC, Brazil
Felipe Grazziotin

Abstract：

The Neotropical region is a climatically diverse region, encompassing a wide range of habitats, such as lush rainforests, deserts and snow–mountains. This diversity of habitats is the result of a rich and complex paleogeographical history between and within two continental landmasses – Central and South America – and island systems, which widely shaped the evolutionary history of Neotropical biotas. Dipsadidae is the richest snake family in the Neotropical region, with over 700 species. Both the family's origin and its overall biogeographical history, such as timing and route of dispersal between Central and South America, remain uncertain. Our study aims to reconstruct the origin and historical biogeography of Dipsadidae snakes in the Neotropical region. To do so, we used a comprehensive molecular clock analysis calibrated phylogeny with a Bayesian estimation of the ancestral geographical ranges of this clade throughout the Neotropical region. Our results show that Dipsadidae has an Asian origin and that jump dispersal was the main process for the family's dispersal throughout the Neotropical region. Our results are congruent with paleogeographical events such as the Beringia Land Bridge, GAARlandia, Andean uplift and the formation of the Panama isthmus. The two main Neotropical subfamilies originated in Central America, but mostly entered South America at different periods. In more recent times there have been several events of dispersal to and from Central America. These different biogeographical histories thus likely influence current richness and regionalization patterns and highlight the importance of reconstructing the ancestral range of widespread diverse clades.

Servino, Leonardo Matheus (Presenter)

Session：CS14 – Biodiversity patterns, distribution & maintenance

Title：How different dimensions of body size of a common viper are related to climatic gradients in a tropical forest?

Leonardo Matheus Servino (leonardomservino@gmail.com), Universidade de São Paulo – USP
José Mario Ferrarini, Universidade Federal de São Paulo
Fausto Barbo, Instituto Butantan
Ricardo Sawaya

Abstract：

Spatial variation in animal body size groups has been explored since 19th century. Bergmann's rule predicts a larger body size of endotherms with increasing latitudes. This pattern has been explained by decreasing the environmental temperature in higher latitudes. Larger endotherms would conserve metabolic heat in cooler areas by having lower surface-volume ratios. However, ecthoterms have low capacity to generate metabolic heat and do not conserve it efficiently as endotherms. Therefore, several hypotheses were proposed to explain body size variation in ecthoterms along the climatic gradients Many ecthoterms are larger in dryer environments, to conserve water more efficiently. Alternatively, it has been suggested that squamate reptiles would reverse Bergmann's rule for a rapid heat gain in cooler areas. During these studies, various body size dimensions have been explored, including body length, mass, and stoutness. We explore the intraspecifical geographical variation in both body length and stoutness of one of the most common and widespread pitvipers of South American Atlantic Forest, the lancehead Bothrops jararaca. We found that body length was not related to climate. However, stoutness was negatively related to temperature, supporting the converse to Bergmann's rule for squamate reptiles. At the same time, stoutness was positively related to potential evapotranspiration, according to water conservation hypothesis. Therefore, different body size dimensions of forest ectotherms such as snakes should be constrained by distinct environmental constraints, including temperature and evapotranspiration. (Supported by CNPq, FAPESP, and CAPES).

Smith, Tessa (Presenter)

Session：CS11 – Phylogeography

Title：Phylogeography of a Southern-Hemisphere Cryptorhynchine Weevil

Tessa R Smith (tessa.smith@utas.edu.au), University of Tasmania

Abstract：

The influence of Pleistocene and Holocene glacial periods on species distributions has been well studied in the northern hemisphere where large ice sheets covered the large areas of continents. In the southern hemisphere, ice sheets formed in several areas during these periods, including the continental island of Tasmania. Previous phylogeographic studies of plants and skinks found a varying response to conditions after the Last Glacial Maximum (LGM). We studied one species of a widely distributed flightless leaf-litter inhabiting beetle endemic

to Tasmania: Decilaus striatus, Lea 1913 (Coleoptera: Curculionidae). mDNA from the COI gene was extracted from 71 newly collected specimens from 32 sites and 5 IBRA Bioregions. A SDM of current conditions using Maximum Entropy Modelling (Maxent) showed that current distributional areas were connected, except in the North-East. The genetic haplotype network showed the greatest difference between populations in the North-East, and aligns with Plomley's Island biogeographic region of endemism found in Millipdes.

Spiliopoulou, Konstantina (Presenter)

Session: CS07 – Conservation Biogeography

Title: Identifying Key Biodiversity Areas: The case of Greece

Konstantina Spiliopoulou (konaspilio@gmail.com), Hellenic Centre for Marine Research
Kostas Triantis, National and Kapodistrian University of Athens
Maria Stoumboudi, Hellenic Centre for Marine Research

Abstract:

On the rise of environmental exploitation and destruction, the need for acute and cost-effective responses are relevant more than ever. Global environmental goals push for the expansion of the protected area network to halt biodiversity loss. However, the designation of new sites needs to be thoroughly planned and the existing sites need to be evaluated in order to accomplice favorable conservation outcomes. Key Biodiversity Areas (KBAs) is a recent tool that can inform these actions. KBAs represent the globally most important sites for the persistence of biodiversity, and their importance has already been recognized, as their coverage by protected areas is an indicator to track progress towards Sustainable Development Goals (SDGs). This is one of the first attempts worldwide to identify KBAs at the national level using the "Standard for the Identification of KBAs". We present the potential KBAs of Greece, and a methodology to identify KBAs using multiple terrestrial and freshwater taxonomic groups (birds, mammals, amphibians, reptiles, mollusks, orthoptera, odonata, fish, 2 plant families and cave fauna). We show that using multiple taxonomic groups and especially invertebrates, adds new sites to the existing important sites identified using bird species only. We also show that many of these sites are partially or completely outside protected areas. We finally discuss that KBAs, in combination with other tools, can guide protected area designation and resources allocation for conservation actions in Greece, and they can help increase our chances to safeguard globally important biodiversity as more countries identify and update their KBAs.

Strandberg, Nichola (Presenter)

Session：CS02 – Paleobiogeography

Title：Drivers of past ecological change in Tonga and Vanuatu

Nichola Ann Strandberg (n.a.strandberg@soton.ac.uk), University of Southampton
Sandra Nogué, University of Southampton
David Sear, University of Southampton
Peter Langdon, University of Southampton
Mary Edwards, University of Southampton

Abstract：

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 islands along gradients of area, elevation and isolation in Tonga and Vanuatu we synthesised palaeocological 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 indicate 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 indicates increased vegetation turnover related to the cataclysmic Kuwae eruption of CE 1450s. Vegetation responses to disturbance vary between sites suggesting that island characteristics may be important when investigating the effects of disturbance.

Tan, Nicholas Wei Cheng（Presenter）

Session：CS23 – Conservation & Invasion Biogeography

Title：Turtle Trouble：A present and future assessment of the effectiveness of existing reserves in preserving three critically endangered freshwater turtles in Southeast Asia and South Asia

Nicholas Wei Cheng Tan（n．tan@leibniz–zfmk．de）, Research museum Alexander Koenig
Philipp Ginal, Zoological Research Museum Koenig
Anders Rhodin, Chelonian Research Foundation
John Iverson, ZFMK, Zoological Research Museum Alexander Koenig
Dennis Rödder, ZFMK, Zoological Research Museum Alexander Koenig

Abstract：

Tortoises and freshwater turtles are among the most threatened taxa of vertebrates in the world due to consumption, urban development, agriculture, and land and water pollution． About 50% of the currently recognised chelonian species are considered threatened with extinction according to the IUCN Red List． Asia is an epicentre for the turtle and tortoise extinction crisis, containing the highest diversity of threatened species． In this study, we used species distribution models（SDMs）to assess the effectiveness of existing protected areas across Southeast and South Asia for the conservation of three large critically endangered freshwater turtles（Batagur borneoensis, B． affinis, and Pelochelys cantorii）． We derived the models based on selected bioclimatic variables at the sites of known species records． Our SDMs showed that Indonesia is of particular importance in prioritising conservation for these three species, containing the largest areas of suitable habitat within protected areas． However, when considering water surface coverage, Thailand has the highest proportion of suitable areas under protection． Our results suggest that the present cover of protected network reserves seems inadequate in terms of size and should be expanded to sustain populations of the three target species． Therefore, we identified priority areas and reserves critical for further field surveys to the potential discovery of novel populations． To investigate the effect of climate change, we also projected potential distributions onto ensembles of four IPCC story lines． As a result, we found larger extralimital areas of suitable environment for all three species, particularly northwards and inland． However, high degrees of uncertainty in climate conditions indicate few reserves may provide long term protection． Lastly, we review the threats and propose recommendations for conservation of these poorly known freshwater turtles．

Trindade, Diego (Presenter)

Session：CS02 – Paleobiogeography

Title：Taxonomic and functional analysis of observed and dark diversity：dynamics over the last 14,500 years in Northern Europe

Diego Pires Ferraz Trindade (dpftrindade@gmail.com), University of Tartu
Carlos Carmona, University of Tartu
Triin Reitalu, University of Tartu
Meelis Pärtel

Abstract：

Global change (i.e. climate and land-use changes) is affecting species gains and losses worldwide. Pollen data allows examining vegetation dynamics over millennial scale and understanding the outcomes of current global changes. Biodiversity gains and losses can be more predictive if we also consider dark diversity - set of species present in surrounding regions, able to colonize and establish in a local site but currently absent. Dark diversity links local and regional scales by showing the missing part of the species pool for each local site. Functional differences between observed and dark diversity taxa can inform us why suitable species are absent. We examined both taxonomic and functional parameters of observed and dark diversity of pollen over time (14,500 years - time span) in 20 lakes in Northern Europe. Dark diversity was estimated using the Hypergeometric method (taxon co-occurrences) and functional dark diversity was calculated with the trait density probability. We found that observed, dark diversity and species pool size (observed+dark) increased over time, especially after late glacial and late Holocene, whereas community completeness decreased. Species in dark diversity were characterized by higher leaf area and lower height and seed mass. These results suggest that both warmer climates (after LG) and land-use have shaped colonization and extinction events at local and regional scales and species in dark diversity were mostly those with lower dispersal capacity and less able to cope with high temperatures. In conclusion, by examining both observed and dark diversity dynamics allows to better understand effects of global changes.

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van der Geer, Alexandra (Presenter)

Session：CS13 – Biogeography of the Anthropocene

Title：Changing invaders：Effect of isolation on skull size, skull shape and coat patterns in Polynesian rats

Alexandra van der Geer (geeraae@gmail.com), Naturalis Biodiversity Center

Abstract：

Populations of native island mammals regularly develop similar phenotypic changes, which is much more pronounced for populations with greater residence times on the islands. Palaeo-insular species include spectacular cases of ‘island evolution’, while introduced populations evolve minimal changes. To further understand the importance of time on evolution, I examined long-term phenotypic data on free-living populations of wild Polynesian rats (Rattus exulans) from 7 mainland countries and 106 islands, covering its native and introduced range. All insular populations exhibit increased skull sizes up to twice the ancestral size. Skull size is positively correlated with latitude, consistent with thermoregulatory predictions based on Bergmann's rule. Skull size is negatively correlated with number of co-occurring mammalian species, consistent with an ecological interpretation of island evolution. The largest rats live in temperate New Zealand, as well as on species-poor Oceanic islands. Carnivory in the form of predation on nesting seabird colonies promotes 1.4- to 1.9-fold skull size increases. Skull shape is mainly dictated by skull size (allometry): large skulls are long and tubular, small skulls are short and round. Finally, I found aberrant coat patterns in 12 island populations, against none in mainland populations, except for one albino. Observed coat colour polymorphisms included leucistic, melanistic and piebald coat patterns. Polynesian rat populations exhibited increased occurrence of white patches of fur. These phenotypic coat pattern changes are here explained as a neutral, non-adaptive process, as a result of genetic drift, little or no gene flow from the mainland and a relaxed selection.

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van Mazijk, Ruan (Presenter)

Session: CS22 – Biodiversity patterns, distribution & maintenance

Title: Environmental heterogeneity explains contrasting plant species richness between the South African Cape and southwestern Australia

Ruan van Mazijk (ruanvmazijk@gmail.com), University of Cape Town, Department of Biological Sciences
Michael Cramer, Department of Biological Sciences, University of Cape Town
George Verboom, Department of Biological Sciences, University of Cape Town

Abstract:

Given the importance of environmental heterogeneity as a driver of species richness through its effects on species diversification and coexistence, we aimed to account for the dramatic difference in vascular plant species richness per unit area between two similar Mediterranean-type biodiversity hotspots (the Greater Cape Floristic Region (GCFR) and Southwest Australian Floristic Region (SWAFR)) and whether this difference is explained by differences in heterogeneity. Comparable, geospatially explicit environmental and species occurrence data were obtained for both regions and used to generate heterogeneity and richness raster layers. Heterogeneity in multiple environmental variables and richness per unit area were compared between the two regions at a range of spatial scales. At each scale, richness was also regressed against these individual axes and against a major axis of heterogeneity, derived by principal component analysis. The GCFR is generally more environmentally heterogeneous and species-rich than the SWAFR. Richness per unit area is significantly related to the major axis of heterogeneity (PC1) across both regions, the latter describing ca. 38–50% of overall heterogeneity, the slope of this relationship differing between the two regions only at the finest scale. Multivariate regressions and regressions against PC1 revealed variations in the dependence of richness on heterogeneity between the two regions. Notwithstanding some region-specific effects, we present evidence of a common positive relationship between richness and heterogeneity across the GCFR and SWAFR. This is dependent on spatial scale, being strongest at the coarsest level of sampling. The generally greater richness per unit area of the GCFR is thus explained by the former's generally greater environmental heterogeneity.

Velasco Saragoni, Nicolás (Presenter)

Session: CS18 - Invasion /Conservation /Climate Change

Title: Supporting a potential old-introduction event for a Fabaceae in South America

Nicolás Velasco Saragoni (njvelasc@gmail.com), Univeristy of Groningen - Universidad de Chile
Ramiro Bustamante, Universidad de Chile
Patrick Baan, University of Groningen
Chris Smit

Abstract:

Acacia caven is a species with disjunct populations between both sides of the South American Andes. Some literature states that the species could be a potential archeophyte introduced to Chile, but pieces of evidence are few for past scenarios. To assess this idea, we test the morphological overlap between 32 populations distributed in two different ranges (west or east from the Andes mountains) by comparing traits in the field, herbaria, and seedlings growing in a climate room experiment. Additionally, we create ecological niche models (ENM) for both ranges, using current climatic conditions. Then we transfer the ENM to six different stages on the Pleistocene-Holocene, to check the reciprocal correspondence of the suitable occurrence areas through time. Our results found that morphology in Chile exhibits a close affinity to a strict part of the morphological variability present in Argentina, with a partial overlap in morphological traits. Vegetative traits have diverged more than reproductive traits, and these are kept in common growing conditions. ENM showed that the eastern niche has expanded in current conditions compared to the past. In all periods assessed, both range niches predict high suitability in central Chile. A common area of suitability east of Andes is depicted since 14.7 ka at northwest Argentina – south Bolivia. This area is more evident from 8.3 ka onwards, suggesting a potential area of introduction. Our results are in accordance to support an old introduction event, similar to other Fabaceae species potentially dispersed by man in pre-Columbian times.

Walentowitz, Anna (Presenter)

Session: CS08 - Biogeography of the Anthropocene

Title: How island ecosystems - the labs of biogeographers – are affected by outdoor recreational activities

Anna J. Walentowitz (anna.walentowitz@uni-bayreuth.de), University of Bayreuth
Manuel Steinbauer, University of Bayreuth

Abstract:

The high percentages of endemic species and large numbers of threatened taxa make islands key areas for global biodiversity conservation. Islands are also invaluable for research as their distinct boundaries and unique flora and fauna make them attractive for testing theory in biogeographic and evolutionary studies. However, islands do not only attract researchers but numerous tourists and athletes who value the vast range of sport activities that can be conducted on topographically complex islands – both as leisure and on the professional level.

Especially on islands, these developments are promoted to boost local economies. On the one hand, rising numbers of outdoor recreationists come with considerable threats for local terrestrial and near-shore marine ecosystems. Hyperendemic and highly endangered species with geographically very restricted occurrences can be imperilled dramatically by outdoor recreational activities, as these often don't stop at the borders of protected areas. On the other hand, well managed sustainable outdoor tourism can stimulate the local economy while preventing unregulated, destructive mass tourism. However, these dynamics have so far been addressed only scarcely in literature, especially when it comes to islands. We study the effects of sport activities on islands, review the literature and point out research gaps and challenges in the novel field of sport ecology.

Witteveen, Nina (Presenter)

Session: CS20 – Paleobiogeography

Title: 30,000 years of landscape and vegetation dynamics in a mid-elevation Andean valley

Nina Witteveen (nina.witteveen@hotmail.com), University of Amsterdam
Crystal McMichael, University of Amsterdam
William Gosling, University of Amsterdam

Abstract:

The mid-elevation Andean flanks are important biodiversity hotspots, yet little is known of their long-term ecology or environmental change. This study investigated 30,000 years of vegetation dynamics on a historic floodplain in a mid-elevation Andean forest in the Northern Andes (Campo Libre, Ecuador). Loss-on-ignition and particle size analysis were used to reconstruct past river dynamics, charcoal analysis to reconstruct past fire regimes and phytolith analysis to reconstruct vegetation through time. The results showed Campo Libre was part of the floodplain system of the Quijos River until 18,000 cal yr BP. After river incision left the floodplain inactive, Campo Libre transformed into a swampy marsh. CONISS and DCA analyses indicated that major ecological changes occurred at the onset of the Holocene (ca. 13,000 cal yr BP), when the site warmed and dried, transforming the swamp into a palm forest. Increasing levels of precipitation transformed the site back into a swamp around 7500 cal yr BP. It remained that way until maize agriculture began around 4600 cal yr BP. Local and regional fires were absent from the system until regional fires were detected ca. 3300 cal yr BP. Maize cultivation became frequent and regular by ca. 2700 cal yr BP. Ecological changes associated with maize agriculture were smaller than the ecological responses to climatic changes. Overall, these results demonstrate the ability of phytoliths to reconstruct vegetation change through time. These results also show that the mid-elevation Andean valley systems were highly dynamic, and highly responsive to climatic changes in the Pleistocene and Holocene.

Yang, Geng–Chen（Presenter）

Session：CS14 – Biodiversity patterns, distribution & maintenance

Title：Niche Differentiation Reveals Different Diversification Histories of Eastern and Western Clade of Angelica L． in East Asia

Geng–Chen Yang（1800017464@pku．edu．cn）, Peking University

Abstract：

Diversification is an essential biogeographic process underlying current biodiversity patterns． In general, there are two main diversification mechanisms, namely diversification by isolation and diversification by competition． Eastern and western part of East Asia are indicated to have experienced different biogeographic histories, while whether the dominant diversification mechanism differs in different parts of East Asia is still unclear． Here, we conducted a comprehensive analysis on niche differentiation of Angelica L．, a genus that diverges into two clades distributed in eastern and western part of East Asia respectively, based on species distribution model to infer diversification mechanisms． Results suggests that niche overlap within Western Clade of Angelica L． is significantly higher than that within Eastern Clade． Niche overlap is negatively correlated to phylogenetic distance in Western Clade, indicating niche conservatism, while an opposite correlation in Eastern Clade indicates niche divergence． Niche evolutionary rates in Western Clade is slower than those in Eastern Clade on most niche axes except for those environmental factors related to climatic characters of warmest quarter, suggesting that climatic characters in coldest season play a more important role in diversification process in East Asia． Results support our hypothesis that in western part of East Asia, diversification by isolation is the main mechanism, while in eastern part, diversification by competition plays the dominant role． Our research is the first empirical comparative study providing evidence for the difference of diversification mechanisms between western and eastern part of East Asia, while researches on other clades are needed to confirm our results．

Yumoto, Keisuke (Presenter)

Session: CS23 – Conservation & Invasion Biogeography

Title: Evaluation of the genetic structure and demographic history of a cicada species, Yezoterpnosia nigricosta, in Japan

Keisuke Yumoto (keisuke.yumoto.cicada@gmail.com), University of Tsukuba
Takashi Kanbe, Hokkaido University
Akane Kato, University of Tsukuba
Tomohiro Kando
Ririko Koido, University of Tsukuba
Taichi Umino, University of Tsukuba
Yoko Saito, The University of Tokyo
Shingo Kaneko, Fukushima University
Michael Nobis, Swiss Federal Research Institute, WSL
Yoshiaki Tsuda, University of Tsukuba

Abstract:

Species distributions are affected by geological and climatic events, as well as the evolutionary history and ecological traits of species. It is expected that the geographic range of species will shift due to recent climate change. To evaluate the impact of climate change on insects in subarctic and cool temperate forests in Japan, it is important to examine the population genetic diversity and structure, and demographic history of the species that inhabit them. In this study, we focused on a cicada species, Yezoterpnosia nigricosta, which is an environmental indicator species and widely distributed in subarctic and cool temperate forests in Japan. We evaluated the broad-scale genetic structure of this species in Japan by using maternally-inherited mitochondrial (mt) DNA sequences and biparentally-inherited nuclear DNA microsatellite markers. We inferred the population demographic history of Y. nigricosta and estimated the location of candidate refugia of host trees in cool temperate forests during the last glacial maximum (LGM, ca. 21 kya) by using species distribution modelling with migration (KISSMig). Our results showed that the genetic structure of Y. nigricosta was associated with past changes in the distribution of host trees and forests in relation to the LGM, suggesting that the population genetics and demographic history of the cicada is strongly influenced by the distribution of suitable habitat. Therefore, to evaluate the environmental adaptation of forest insects across spatio-temporal scales, it is important to evaluate not only the demography of single insect species, but also the evolutionary dynamics of host forest tree species and ecosystems.

Zamora Ospina, Camilo Ernesto (Presenter)

Session: CS08 – Biogeography of the Anthropocene

Title: Deforestation in protected areas and buffer zones of Ecuador´s mainland

Camilo Ernesto Zamora Ospina (cezo84@hotmail.com), Julius-Maximilians-University of Würzburg, Dept. Remote Sensing, Institute of Geography and Geology
Janina Kleemann, Martin-Luther-University Halle-Wittenberg, Institute for Geosciences and Geography, Dept. Sustainabl
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Pablo Cuenca, Martin-Luther-University Halle-Wittenberg, Institute for Geosciences and Geography, Dept. Sustainabl
Hongmi Koo, Martin-Luther-University Halle-Wittenberg, Institute for Geosciences and Geography, Dept. Sustainabl
Jin Noh, Ikiam (Universidad Regional Amazónica)
Christine Fürst, Martin-Luther-University Halle-Wittenberg, Institute for Geosciences and Geography, Dept. Sustainabl
Michael Thiel, Julius-Maximilians-University of Würzburg, Dept. Remote Sensing, Institute of Geography and Geology

Abstract:

Deforestation and forest degradation of tropical rainforests is of particular concern for the protection, sustainable use and management of biodiversity. Protected areas represent a key strategy to conserve biodiversity within its boundaries. However, escalating pressures of land use adjacent to these areas (i.e., leakage effect) significantly influence conservation effectiveness, hindering their purpose to maintain biodiversity and ecological functions. We analysed spatial patterns of deforestation in the protected areas and buffer zones (5 km and 10 km outwards the protected area boundaries) of Ecuador's mainland during the last 30 years (from 1990 to 2020) by using landscape metrics and geographical data provided by the Ministry of Environment and Water of Ecuador (MAAE). In addition, we assessed the differences of the level of deforestation regarding the protection status. Overall, a total of 21% of Ecuador's mainland natural forest total area is under protection. Approximately 12% of the accumulated deforestation occurred within the boundaries of protected areas, and up to 45% in buffer zones. The most proximate areas to the boundary of protected areas (5 km buffer zone) have been influenced by the major amount of degradation. Areas with high protection status were identified as the most deforested area adjacent to protected areas, with up to 75% of the total accumulated deforested area within their buffer zones. The results suggest that protected areas are generally effective to prevent deforestation within their boundaries. However, leakage patterns around protected areas can undermine conservation strategies to sustain biodiversity. Actions to address such dynamics and patterns of deforestation and forest fragmentation, and developing conservation strategies of their landscape context are urgently needed especially in the buffer zones of areas with the highest protection status.

POSTER PRESENTATIONS

Androski, Antonia (Presenter)

Session: Poster Presentation

Title: Rangewide phylogeography of Sorex monticola

Antonia Androski (aandroski@unm.edu), University of New Mexico
Joseph Cook, University of New Mexico

Abstract:

Sorex monticola, the montane shrew, is a small, insectivorous mammal that is widespread throughout western North America but poorly known. Genetic studies of S. monticola and the five other shrew species that make up the Sorex vagrans complex have revealed genetic structure within S. monticola that is inconsistent with current nomenclature and has not yet been clearly linked to morphology or ecology. We use a bioinformatics-based approach to understand drivers of genetic diversity among populations and species in this complex, and identify areas that harbor genetically distinct or endemic shrew populations to guide conservation efforts. This work especially focuses on isolated populations and contact zones. We will assess contact zones and compare island populations in the nearshore Alexander Archipelago of Southeast Alaska and in the high elevation boreal forests found on 'sky islands' in the American Southwest. More broadly, this project will provide insight into larger processes of faunal assembly and diversification, especially in insular systems. Responses to past environmental change will serve as a critical proxy for ongoing perturbation, including anthropogenic climate change.

Ashokan, Ajith (Presenter)

Session: Poster Presentation

Title: Neogene origin and diversification of ginger lilies in the Indo-Malayan Realm: a tale of mountains and monsoons

Ajith Ashokan (ajithashoksridhar@gmail.com), Indian Institute of Science Education and Research (IISER) Bhopal
Aleena Xavier, Indian Institute of Science Education and Research (IISER) Bhopal
Mark Newman, Royal Botanic Garden Edinburgh
Vinita Gowda

Abstract:

The Indo-Malayan Realm (IMR) is a biogeographic realm that extends from the Indian Subcontinent to the islands of Southeast Asia (Malay Archipelago) through southwest and southcentral China and mainland Southeast Asia. Tectonically, it is spread across three plates (Indian, Eurasian, and Philippine) and is known for hosting many biodiversity hotspots. Despite being megadiverse, evolutionary hypotheses explaining taxonomic diversity in

this region have been rare. Here, we investigate the diversification patterns and role of Himalayan orogeny and monsoon intensification in speciation events within the ginger lilies (Hedychium J. Koenig：Zingiberaceae). We built the first-ever time-calibrated phylogeny of Hedychium with ~ 75% taxonomic and geographic sampling. We found that Hedychium is a very young lineage that originated only in the Late Miocene (c. 10.6 Ma) of northern Indo-Burma, followed by a late Neogene and early Quaternary diversification, with multiple dispersal events to southern Indo-Burma, Himalayas, Peninsular India, and the Malay Archipelago. We also propose that the intensifications in the Himalayan uplift, as well as the Asian monsoon, played pivotal roles in the diversification of Hedychium. Within Hedychium, the occurrence of vegetative dormancy during the dry season was observed in both clades I and II, whereas the strictly epiphytic growth behavior, island dwarfism, lack of dormancy, and a distinct environmental niche was observed only in clade III. We conclude that Hedychium serves as an ideal model among perennial rhizomatous herbs that highlights the role of recent geoclimatic changes and environmental factors in the diversification of plants within the IMR.

Cosentino, Francesca (Presenter)

Session：Poster Presentation

Title：A dangerous fur：potential impact of American mink on the Pyrenean desman, an endemic and globally threatened mammal

Francesca Cosentino (francesca.cosentino@uniroma1.it), University of Rome "La Sapienza"

Ana Márcia Barbosa, Centro de Investigaçao em Ciências Geo-Espaciais

Lorenzo Quaglietta, CIBIO /InBio-Centro de Investigação em Biodiversidade e Recursos Genéticos; Associação Natureza

Abstract：

The Pyrenean desman (Galemys pyrenaicus), listed as Vulnerable by the IUCN and in the process of being updated to "Endangered", is restricted to mountainous watercourses and therefore particularly exposed to global warming. The invasive American mink (Neovison vison) is considered a potential threat. We assessed the potential influence of the mink on the desman distribution across its range (the Iberian Peninsula and southern France; 764,000 km2). We gathered occurrence data for the two species and climatic and anthropogenic data from online databases. We built two SDMs, one for each species, applying a favourability function at 10 km2 scale. We calibrated both models with the same variables, accounting for the spatial structure of the distribution data. We combined the favourability values (F) for the two species to map the threat posed by the presence of the mink on the desman distribution. After accounting for the spatial trend in species presences, the mean monthly evapotranspiration of driest the quarter and the mean temperature of the warmest quarter were the main factors influencing the mink and the desman respectively, the latter highlighting desman vulnerability to global warming. Desman and mink favourability's areas ($F \geq 0.5$) cover respectively 24% and 38% of the study area. Mink occurrence overlaps, and likely threatens, desman occurrence in 25% of the potential distribution of both species. This scenario highlights the need to undertake urgent actions for desman conservation, considering that mink distribution is expanding while the desman range is contracting. Our results point out the areas where the desman is most potentially threatened and the American mink should be more controlled.

Formoso Freire, Victoria（Presenter）

Session：Poster Presentation

Title：Predictive models of invasive species distribution：the case of Vespa velutina in Europe．

Victoria Formoso Freire（victoriaformoso．freire@usc．es）, Universidade de Santiago de Compostela
Ana Márcia Barbosa, Centro de Investigaçao em Ciências Geo-Espaciais
Andrés Baselga, Universidad de Santiago de Compostela
Carola Gómez-Rodríguez

Abstract：

Species distribution models are a key tool in the preventive fight against species invasion（one of the greatest threats to biodiversity today）, allowing to anticipate which places are most susceptible to invasion． Currently, one of the most worrying invasive species in Europe is the Vespa velutina, as it poses a threat to the stability of ecosystems due to its strong impact on pollinator populations． The main objective of this study is to evaluate the effectiveness of different species distribution models to estimate the risk of invasion of V． velutina in Europe． First, the climatic niche realised by V． velutina in both native and invaded areas will be characterised and compared in order to assess one of the basic assumptions of predictive distribution models：equilibrium between species distribution and climate． Thus, the bias potentially introduced by the fact that the species is currently expanding its distribution will be studied, which implies that part of the absence data used by the models correspond to potentially suitable sites that have not yet been colonised． This reliability of absences is, in principle, a critical element when building predictive models of invasive species distribution． In this work, we compared models built with presence-only data and models built with presence-absence data． In general, the models show that almost the whole European continent presents favourable conditions for the development of V． velutina, however, when incorporating absence data, the areas of probable invasion are reduced to the south-west of the continent． Thus, it is advisable to consider characteristics of the regions occupied in their native range and, above all, to assess whether the species is colonising areas with different conditions, which would violate the assumption of equilibrium with the climate and compromise the prediction of its expansion by statistical models．

Gabor, Lukas (Presenter)

Session: Poster Presentation

Title: Positional errors in species distribution modelling are not overcome by the coarser grains of analysis

Lukas Gabor (gabor@fzp.czu.cz), Czech University of Life Sciences
Vítězslav Moudrý, Czech University of Life Sciences

Abstract:

The performance of species distribution models is known to be affected by the analysis grain and the positional error of species occurrences. Coarsening of the spatial analysis grain has been suggested to compensate for positional errors. Nevertheless, this way of dealing with positional errors has never been thoroughly tested. Here, we examined the trade-offs between positional error and analysis grain and provided recommendations for best practice. We generated virtual species using tree canopy height, topography wetness index, and altitude derived from LiDAR point clouds at 5 x 5 m fine-resolution. We simulated the positional error in the range of 5 m to 99 m and evaluated the effects of several spatial grains in the range of 5 m to 500 m. We used three common modelling techniques and four discrimination metrics to evaluate model performance. We found that model performance decreased with increasing positional error in species occurrences and coarsening of the analysis grain. Most importantly, we showed that coarsening the analysis grain to compensate for positional error did not improve model performance. Our results reject coarsening of the analysis grain as a solution to address the negative effects of positional error on model performance. We recommend fitting models with the finest possible analysis grain even when available species occurrences suffer from positional errors. If there are significant positional errors in occurrence data, users are unlikely to benefit from making additional efforts to obtain higher resolution environmental

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Grattarola, Florencia (Presenter)

Session: Poster Presentation

Title: Integrative models for geographic range dynamics of carnivores in the Neotropical region

Florencia Grattarola (grattarola@fzp.czu.cz), Czech University of Life Sciences Prague (CZU)
Petr Keil, Czech University of Life Sciences Prague (CZU)

Abstract:

Abiotic and anthropogenic changes such as climate and land-use affect species' distribution ranges by shifting, reducing, or expanding their areas. To assess these changes there are increasingly more data openly available around the world – e.g., derived from museum specimens' data mobilization, eDNA, camera-traps, acoustic data loggers, and citizen-science records. However, in many regions, data are still highly insufficient, spatially, and temporally biased, hindering evidence-based conservation actions. Our aim is to integrate different types of data on carnivore mammals from the Neotropical region to model species distribution and provide a temporal view by assessing their geographic range variations in two time periods (pre- and post-2010). We have compiled a

robust database of presence-only and presence-absence data from 48 species, together with potential environmental predictors of geographic distribution, and have setup a model based on Poisson point process that integrates these types of data, while accounting for sampling bias. Tests of the model on simulated data indicated that the model is fit for purpose. We present preliminary results from select species Neotropical carnivores, illustrate practical application of the integrative model using JAGS and /or INLA, and discuss the potential of the approach to address data gaps and biases in other taxa and regions.

Groner, Vivienne (Presenter)

Session: Poster Presentation

Title: What is the role of rare and endagered species in supporting agricultural production?

Vivienne Groner (v.groner@ucl.ac.uk), University College London
Jessica Williams, University College London
Richard Pearson, University College London

Abstract:

While biodiversity undoubtedly underpins ecosystem services that support human wellbeing, it remains open to debate whether benefits to people are robust arguments for the conservation of rare and endangered species. The emphasis on benefits to people, rather than the intrinsic value of species, has become a popular argument in the context of agricultural production, which is a main driver of biodiversity change and, at the same time, could suffer largely from the loss of species. We critically assessed the evidence for the quantitative contribution of rare and endangered species to agricultural production in a systematic review and identified areas where further research may be needed.

Haesen, Stef (Presenter)

Session: Poster Presentation

Title: ForestTemp – gridded sub-canopy microclimate temperatures of European forests

Stef Haesen (stef.haesen@kuleuven.be), KU Leuven
Jonas Lembrechts, University of Antwerp
Pieter De Frenne, Ghent University
Jonathan Lenoir, KU Leuven
Koenraad Van Meerbeek, KU Leuven

Abstract:

Ecological research heavily relies on coarse-gridded climate data based on standardised temperature measurements recorded at 2 m height in open landscapes. However, many organisms experience environmental conditions that differ substantially from those captured by these macroclimatic (i.e. free-air) temperature grids. In forests, for instance, the tree canopy functions as a thermal insulator, and buffers sub-canopy microclimatic conditions, thereby affecting biological and ecological processes. To improve the assessment of climatic conditions and climate change-related impacts on forest biodiversity and ecosystem functioning, temperature grids reflecting forest microclimates are thus urgently needed. Combining more than 1,200 time series of in situ near-surface forest temperatures with topographical, biological and macroclimatic variables in a machine learning model, we predicted the mean monthly offset between sub-canopy temperature at 15 cm above the surface and free-air temperature over the period between 2000 and 2020 at a spatial resolution of 25 m across Europe. This offset enabled us to calculate mean annual and monthly temperatures for European forest understories. We found that sub-canopy air temperatures differ substantially from free-air temperatures, being on average 2.1°C (standard deviation ±1.6°C) lower in summer and 2.0°C higher (±0.7°C) in winter across Europe. Additionally, our high-resolution maps expose considerable microclimatic variation within landscapes, not captured by the gridded macroclimate products. The provided forest sub-canopy temperature maps will enable future research to more accurately model biological processes and patterns, as well as species distributions affected by climate change.

Jäkle, Katja (Presenter)

Session: Poster Presentation

Title: Species distribution modelling of selected grasshopper species in Europe and Bavaria

Katja Jäkle (katja.jaekle@tum.de), Technische Universität München

Christian Hof, Technical University Munich

Abstract:

Land use and climate change cause declines in populations and distributions of many insect species, such as grasshoppers (Orthoptera). To understand these trends and to develop projections of future range shifts, species distribution modelling (SDM) is a popular approach. However, the uncertainties of SDMs are well-documented, too. Here we assess some of them, specifically we try to answer the questions of (1) whether accurate predictions are possible even with simple approaches, (2) whether model outcomes and performances differ between different scales, and (3) how land-use and climatic variables differ in their importance as factors influencing the distribution. To answer these questions, we conducted SDMs at the continental (European) and the regional (Bavarian) scale under current conditions for the grasshopper species Chorthippus apricarius, Phaneroptera falcata, Phaneroptera nana and Psophus stridulus. We found that while the models were often accurate (indicated by high values of model performance measures), their outcomes depend strongly on a variety of factors such as the species in question, the scale level, the input data, the modelling algorithms, and the selection and implementation of model parameters. We also found that even though land use does not necessary enhance model performance, there may be reasons for including it, depending on the purpose of the study.

Kemppinen, Julia (Presenter)

Session: Poster Presentation

Title: Geomorphological processes shape plant functional traits in the Arctic

Julia Kemppinen (julia.kemppinen@oulu.fi), University of Oulu

Abstract:

Geomorphological processes profoundly affect plant establishment and distributions, but their influence on functional traits is insufficiently understood. Here, we unveil trait-geomorphology relationships using field-quantified vegetation, geomorphological processes, microclimate, and soil data from 5280 plots and 200 species across three Arctic regions. We combined these data with database trait records to relate local plant community trait composition to dominant geomorphological processes of the Arctic, namely cryoturbation, deflation, fluvial processes, and solifluction. Our results demonstrate that community-level traits are related to geomorphological processes, with cryoturbation most strongly influencing both structural and leaf economic traits. These results were consistent across regions, suggesting a coherent biome-level trait response to geomorphological processes. These geomorphological processes may potentially constrain changes in traits in response to future climatic shifts. Yet, large uncertainties remain how these processes and potential biogeomorphic feedbacks will evolve along climate change in the Arctic.

Konowalik, Kamil (Presenter)

Session: Poster Presentation

Title: Phylogeography and ecological niche modeling reveal migration routes of the Carpathian endemic plant Leucanthemum rotundifolium (Compositae, Anthemideae)

Kamil Konowalik (kamil.konowalik@upwr.edu.pl), Wrocław University of Environmental and Life Sciences

Abstract:

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. 250 plant taxa. A small but interesting part of that number are subendemics (ca. 15 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 rotundifoium (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.

Krishnamoorthy Dharapuram, Bharti (Presenter)

Session: Poster Presentation

Title: What are the drivers of genetic diversity in soil predatory arthropods?

Bharti Krishnamoorthy Dharapuram (bharti.dharapuram@gmail.com), CSIR-Center for Cellular and Molecular Biology
Pooja Pawar, CSIR-Centre for Cellular and Molecular Biology
Jahnavi Joshi, CSIR-Centre for Cellular and Molecular Biology

Abstract:

Soil arthropods have an important role in ecosystem functioning and nutrient cycling, but their biodiversity remains poorly documented. Within-species genetic diversity, an important component of biodiversity, helps us understand the ecological and evolutionary processes shaping populations. A dearth of studies from the soil ecosystem prompted us to investigate the patterns and drivers of intra-specific genetic diversity in centipedes, a group of ancient predatory soil arthropods. To do this, we assembled a database of over 1100 mitochondrial cytochrome c oxidase subunit I sequences representing 126 species (with atleast three sequence representatives each) from all the five orders under Chilopoda. For a subset of these species with complete information (83 species, 836 sequences) we derived estimates of genetic diversity and studied its variation with sample size, geographic distance, latitudinal range and life-history traits, while controlling for shared evolutionary history of species within a family. We observed a wide variation in genetic diversity across species (average pairwise genetic distance=0-0.1641, haplotype diversity=0-1). Genetic diversity decreased with body size and latitudinal position of sampled localities, indicating the role of ecological strategy/dispersal ability along with environmental/historic correlates of latitude. Species with vision had greater genetic diversity, which might be explained by habitat specialization or low population abundances. Our results show a rich heterogeneity in patterns of intra-specific genetic diversity, making centipedes an interesting system for comparative population genetics and phylogeography studies.

Lema, Danielle (Presenter)

Session: Poster Presentation

Title: Identifying population structure in African leopards (Panthera pardus) across sub-Saharan Africa

Danielle Lema (dgrace999@gmail.com), Fordham University
Corey Anco, Draper Natural History Museum
Evon Hekkala, Fordham University / American Museum of Natural History
Alexis Neffinger

Abstract:

The African leopard (Panthera pardus) occupies the largest distribution of all Felids. In recent decades, however, its distribution has alarmingly been reduced by up to 75%. Yet this decline has been largely ignored, owing to the

leopard's seemingly ubiquitous occurrence and notably adaptable nature. Efforts to understand patterns of partitioning across the leopards' distribution have been limited in the past by poor sampling, or minimal genomic representation. This has led to the classification of all sub-Saharan leopards as a single continent-wide panmictic group. However, our laboratory's recent work has identified five genetically and geographically distinct lineages from the mitochondrial NADH-5 locus. Alarmingly, two of these lineages occur in regions facing relatively high threats of local extinction, West Africa and the Congo Basin, warranting reassessment of current classifications, and individualized management strategies for regionally distinct groups. Here we use DNA extracted from archival museum specimens representing broad sampling across sub-Saharan Africa to infer genomic relationships of leopards. 150bp paired-end sequencing was performed on an Illumina HighSeq4000. SNPs were called across reduced representation genome and complete mitogenome and analyzed for various indices of genome evolution and population differentiation. We expect that geographic and genomic distances are positively correlated, and that there exists both genomic and mitogenomic structure, as well as low (or no) migration and introgression between groups. We expect this investigation will reveal previously unrecognized depth of divergence across the genome, and unravel cryptic diversity within the species across its distribution. Data analysis in progress.

Lima, Jacqueline (Presenter)

Session: Poster Presentation

Title: Range dynamics of broadleaved tree species in Sweden: towards climate change adaptation?

Jacqueline Souza Lima (jac.slima@gmail.com), Stockholm University
Jonathan Lenoir, Université de Picardie Jules Verne
Kristoffer Hylander, Stockholm University

Abstract:

As a consequence of climate warming and to avoid extinction, species are expected to shift their geographical ranges poleward and upward on mountain slopes. For sessile organisms like plants, this dynamic occurs through sexual reproduction, with recruits dispersing and establishing in newly suitable places where their parents could not able to grow. Furthermore, the current warming trend pronounces the lags in biotic responses on such organisms. To better understanding the effect of climate change on forest biodiversity and the response of the trees, here we examined the range dynamics of Acer platanoides (maple) and Quercus robur (oak), broadleaved trees species which has their northern range limit occurring across central Sweden. We collected presence-absence data from the Swedish National Forest Inventory across a set of 61,552 forest plots. Then, using a novel species distribution models framework, we modeled both realized and potential distribution of each species and life stages, to identify areas of the potential range and if the species already started to expand their latitudinal distribution northward. For both species, we found that the potential range is wider and northward than realized distribution. However, when we compared the realized distributions of adults and juveniles, we observed differences between the two species. For maple, the juveniles distribution is northward than adults. On the other hand, for oak, the juveniles range is centralized and adults distribution is in the northward direction. Our results suggest that different environmental variables and climate change can affect the distribution of the two species in different ways.

Makinen, Jussi (Presenter)

Session: Poster Presentation

Title: Utilities of combined data approach for species range wide SDMs

Jussi Makinen (jussi.makinen@yale.edu), Yale University
Walter Jetz, Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA

Abstract:

Combining systematically surveyed presence-absence and opportunistically sampled presence-only data in a species distribution model (SDM) holds a promise of providing more information about the species-environment relationship and improving model predictions compared to fitting models solely with presence-only data. However, this is usually compromised by the systematic sampling bias of the presence-only data and relatively small amount of the systematically sampled presence-absence data. Here we tested the utilities of the combined data models for 48 Central and South American hummingbird species over their whole geographical ranges. We show that combined data approach improves predictive accuracy and precision of the model compared to the model fitted solely with presence-only data. The improvement is based on the update of the spatial random effect of the model, and thus the further the prediction points are located from the presence-absence sampling points, the less there are improvement in the predictions. The combined models do not provide more information about the species-environment relationship and may still be confounded by the collinearity between environmental variables and the spatial random effect. Model predictions improve especially for species which have little presence-only data and large geographical ranges. Our results support the use of spatially explicit models for fitting SDMs with combined data sets. This allows utilizing the information of presence-absence observations and treating spatial clustering of the presence-only locations related to the sampling effort. We also encourage careful interpretation of the estimated species-environment relationships of the combined data models.

Matten, Damaris (Presenter)

Session: Poster Presentation

Title: Phylogenetic diversity of Fennoscandian vascular plants: Do we protect the relevant areas?

Damaris Matten (damaris.m.matten@ntnu.no), Norwegian University of Science and Technology (NTNU)

Abstract:

Protecting phylogenetic diversity conserves valuable properties of ecological communities. In this ongoing study, we test how well currently protected areas conserve phylogenetic diversity of the Fennoscandian vascular flora.

We expand an existing molecular phylogeny of Norwegian vascular plants by including the native floras of Sweden and Finland. Combined with occurrence data, we compare measures of phylogenetic diversity and endemism inside versus outside protected areas. We test if the variation of phylogenetic diversity conserved between protected areas and unprotected areas can be explained by environmental variables.

This study will investigate the importance of using estimates of phylogenetic diversity for decision making in nature management. It will also assess how successfully current management conserves the phylogenetic diversity of native vascular plants.

Mereghetti, Alessandro (Presenter)

Session: Poster Presentation

Title: Investigating the community structure of extinct Arctic herbivores through multiproxy coprolite analysis

Alessandro Mereghetti (alessandro.mere@gmail.com), University of Maine
Mikayla Mason, University of Maine
Valery Plotnikov, Academy of Sciences of Sakha Republic
Albert Protopopov, University of Maine
Jacquelyn Gill, University of Maine

Abstract:

During the late Quaternary, the largest biome on Earth world was the so-called "mammoth steppe", a cold mosaic of grassland, tundra and boreal parkland widespread across the Northern Hemisphere. This biome was characterized by a diverse community of cold-adapted herbivores that disappeared over the course of the last 20,000 years. The mechanism that allowed the coexistence of a high biomass of different herbivore species (including Mammuthus primigenius, Bison priscus, Equus sp., Rangifer tarandus) in an environment supposedly low in plant diversity and productivity is still a subject of debate. According to niche theory, coexistence between different herbivore species is promoted by dietary specialization, with different species feeding preferentially on specific food items. However, due to low taxonomic resolution, isotopic studies based on fossil bones give us conflicting results on the degree of overlap of Arctic herbivore diets. To better understand how extinct herbivores from the same region partitioned their diet, I will analyze a unique set of 60 coprolites (sub-fossil feces) from Yakutia, Siberia, dating back to the Late Pleistocene. I will use a multiproxy approach combining both traditional (macrofossils, pollen, starch grains) and cutting-edge (ancient DNA) paleoecological tools to achieve a high-resolution environmental and dietary reconstruction. The unprecedented number of samples coupled with the use of complementary dietary proxies will allow me to reconstruct the diet of extinct Arctic herbivores with greater accuracy than any other previous work on the subject, shedding light on the mechanisms that allowed their coexistence and potentially informing the reasons of their extinction (or survival) during the Pleistocene/Holocene tranistion.

Monroy, Fernando（Presenter）

Session：Poster Presentation

Title：An ancient shift in the distribution of the invasive species Scyphophorus acupunctatus （Coleoptera：Dryophthoridae）

Fernando Monroy（fernando．monroy@crea．gov．it）, CREA – Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria

Chiara Ferracini, Department of Agricultural, Forest and Food Sciences, University of Torino

Abstract：

Range expansion of invasive species can be driven by multiple factors, but little is known about the kind of adaptive events that increase the chances of a species becoming more invasive than others． In many cases, species are considered relatively similar in their invasiveness potential, leaving ecological opportunity – either environmental changes that become favorable for a particular species or fortuitous dispersal in new suitable habitats– as a main explanation for the rapid spread of an invader beyond its native distribution area． In the case of the curculionid beetle Scyphophorus acupunctatus Gyllenhaal, 1839, known as the agave weevil, the human-mediated spread of its suitable host species（mainly from the genus Agave, but also including species from Yucca, Dracaena, Beaucarnea, Polianthes and Dasylirion）is considered the main cause of the expansion of this pest all around the world． However, the other species of the clade, S． yuccae Horn, 1873 –which morphologically resembles S． acupunctatus and can also feed on several species of yucca and agave– does not show an invasive behaviour and occurs in a smaller distribution area． In this study, we compared the available distribution records of the agave weevil in its native and invaded range, and those of their main plant hosts as well, to define the main events shaping its original geographic distribution． The analysis of both recent and historical records of live individuals suggests that the Mexico region is the main distribution center of the species, where S． acupunctatus is found on a higher number of host species in natural conditions． The native range also covers large areas to the north of the distribution center, overlapping with the distribution of its main plant host species in parts of California, Arizona and Texas． On the other side, the analysis of the few available fossil records revealed that S． acupunctatus, together with two currently extinct congeneric species, was present in a location more to the north than expected（Florissant, Colorado）, outside of both its native range and the native range of its main plant hosts．

Musil, Martin（Presenter）

Session：Poster Presentation

Title：Phytogeographical division of the Czech Republic：statistical analysis of a large-plant distribution database

Martin Musil（musil．martin@volny．cz）, Department of Geography, Faculty of Science, Masaryk University

Jan Divíšek, Department of Geography, Faculty of Science, Masaryk University

Milan Chytrý, Department of Botany and Zoology, Faculty of Science, Masaryk University

Jiří Danihelka, Institute of Botany, The Czech Academy of Sciences

Zdeněk Kaplan, Institute of Botany, The Czech Academy of Sciences

Jan Wild, Institute of Botany, The Czech Academy of Sciences
Petr Novotný, Department of Biology Education, Faculty of Science, Charles University

Abstract:

The aim of this study is to map the distribution of vascular plant diversity in the Czech Republic and provide statistically based phytogeographical division of the country. The data on plant distribution come from the Database of Czech Flora and Vegetation (Pladias). The Pladias database is the largest set of data on vascular plant occurrence in the Czech Republic, which is subject to continuous quality control. We used information on presence /absence of 3139 vascular plant species in 2370 grid cells, each of them spanning 5' × 3' (∼6 × 5.55 km at 50°N latitude). Based on this data, we calculated and mapped the number of species occurring in each grid cell. Beta diversity was calculated using the Sørensen and Simpson indices and the resulting dissimilarity matrix was then subjected to principal coordinate analysis. Grid-cell scores on the first three ordination axes were mapped. Based on the dissimilarity in species composition, grid cells were clustered using the Ward's method. Alpha diversity maps showed that biodiversity hotspots are located in White Carpathians, south of South Moravian Region and around big cities (Prague and Brno). The highest species turnover was observed between locations with the highest and lowest altitude (a gradient of climatic, geologic and land use factors). The second highest turnover was indicated between eastern and western part of the country, corresponding with bedrock and continentality index. Results of cluster analyses projected on the country map suggested various phytogeographical divisions based on species composition of native species or all species.

Owens, Hannah (Presenter)

Session: Poster Presentation

Title: New R Tools to Efficiently Acquire, Visualize, and Cite Occurrence Data

Hannah L. Owens (hannah.owens@gmail.com), CMEC, University of Copenhagen; Florida Museum of Natural History, University of Florida
Cory Merow, University of Connecticut
Brian Maitner, University of Connecticut
Jamie Kass
Vijay Barve, University of Floried; Purdue University
Robert Guralnick, University of Florida

Abstract:

Available observational and specimen-based biodiversity data is increasing at an exponential rate, but the ability to manage and document the resulting large, complex biodiversity datasets is not keeping pace. This gap costs valuable time for researchers when working to cite their data, for downstream users when attempting to reproduce analyses, and for primary data publishers when tracking how their data are used. These obstacles, if unaddressed, ultimately harm the long-term sustainability of truly repeatable biodiversity science using big data. Here, we present an R package, occCite, to aid researchers in querying large species occurrence data aggregators (specifically the Global Biodiversity Information Facility, GBIF, and the Botanical Information and

Ecology Network, BIEN). Results are stored as data objects that also contain detailed metadata (e.g. primary data providers, database accession dates, DOIs, and the taxonomic sources for search terms). occCite also includes tools to summarize and visualize query results and generate citation lists of all data providers and software packages used during the query process. Our aim is to efficiently close the gap in the citation cycle between primary data providers and final research products, allowing researchers to meet best-practice dataset documentation standards without sacrificing time and resources to the demands of providing increasing levels of detail on their datasets

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Pacheco Riaño, Laura Camila (Presenter)

Session: Poster Presentation

Title: Modeling the lag of plant communities to climate warming using phytosociological and occurrencedata

Laura Camila Pacheco Riaño (sciurus.pacheco@gmail.com), University of Bergen
Jhon-Arvid Grytnes, University of Bergen

Abstract:

Many species have experienced a latitudinal and altitudinal shift in their distribution driven by climate change. Lags between biodiversity and current climate changes have been reported around the world. In order to understand the correlations between ecological communities and the environment, modeling approaches strongly depend on the availability of historical, recent, and accurate plot scale data. However, this kind of data has received lower attention than the species occurrence data, this last kind of data is widely available through large databases as the Global Biodiversity Information Facility (GBIF). Here, we reconstructed floristic temperature based on plant assemblages from phytosociological vegetations plots (720 plots) and GBIF occurrence data (7731 artificial plots) in Norway. We compared the floristically and climatically reconstructed temperature trends over 105 years. We found that the use of occurrence data might underestimate the lag between the ecological communities and climate. However, the integration between phytosociological and occurrence data might improve the model, especially for those areas with a lack of data. This work exposes that the combination of high-quality data as the phytosociological data and occurrence data might improve the estimation accuracy of the models and help us to understand the plant communities' responses to climate change.

Pladevall-Izard, Eulàlia (Presenter)

Session: Poster Presentation

Title: Roles of environment and geographic distances to taxonomic, phylogenetic and functional beta diversity of vascular plants in Pyrenean mires.

Eulàlia Pladevall-Izard (eulalia.pladevall@gmail.com), University of Barcelona
Aaron Pérez-Haase, University of Barcelona
Janne Alahuhta, University of Oulu
Josep M. Ninot

Abstract:

In the Central Pyrenees, mires occupy small areas but contribute substantially to gamma diversity at landscape scale. Plant communities in mires have been broadly studied through ordination methods. Here we studied the contribution of beta diversity components (total, replacement and abundance difference) in 422 plots from 56 mire systems in the Central Pyrenees. Besides taxonomic beta diversity, we address phylogenetic and functional beta diversity. We analysed the entire plant communities—which implied over 250 species in total—and then plant communities of wet habitat specialists—103 species. We found high rates of total taxonomic beta diversity, while phylogenetic and functional beta diversities were similarly lower. This result points to strong environmental filters that foster different plant communities to share phylogenetic plant relatives and similar ecological strategies. Beta diversity of specialist species showed almost the same results, denoting similar biogeographic patterns, but the abundance difference compartment was proportionally higher. We then related beta diversity indices with geographic distances and local and landscape scale environmental variables carrying out variance partitioning analyses. Against expectation, the locality effect (i.e. the fact that two plots belonged to the same mire system) explained about 24% of the total beta diversity variance, while environmental variables and spatial distances showed secondary relevance for all beta diversity computations. This fact reveals the importance of dynamic immigration and successful settling processes in Pyrenean mires, which are characterized by constrained connectivity through landscape. There, the establishment of new species would be limited by niche occupancy by species with similar characteristics.

Rahman, Md. Habibur (Presenter)

Session: Poster Presentation

Title: Trends of Woodfuel Production and Consumption in South Asian Countries: Implications of Energy Policy for Sustainable Development

Md. Habibur Rahman (habibmdr@gmail.com), Kyoto University
Kaoru Kitajima, Kyoto University

Abstract:

Traditionally woodfuel is used for cooking and heating purposes by the residential and commercial consumers in South Asian countries. However, reliable assessments of woodfuel demand, production, and consumption, as

well as their temporal trends are limited. In this study, we used FAOSTAT and UNdata to compare the trends of woodfuel production and consumption of eight South Asian countries between 2000 to 2018. South Asia has 19% forests coverage while Bhutan has the highest land covered by forest (71.4%). Woodfuel consumption peaked around 2010 with a total estimated consumption of 289.5 million t, then slightly declined to about 282 million t. Over this time period, woodfuel production has increased along with the forest area in Bhutan and Nepal but decreased in Bangladesh. In case of India, woodfuel production changed in a Zigzag pattern in relation to the forest area. Annual woodfuel production steadily increased with the population sizes in Afghanistan, Bhutan, Nepal, and Maldives, but decreased in Bangladesh. Similarly, woodfuel consumption steadily increased with the population sizes in Afghanistan, Bhutan and Nepal but decreased in Bangladesh. Annual changes in woodfuel production and consumption were associated with each other with large noises in Afghanistan, Bhutan and Nepal. In Bangladesh, it is clear that with decrease of woodfuel production is accompanied by the woodfuel consumption. In these countries, population size and the alternative fuels demand continue to increase, whereas the forest area decreased. Moreover, rigorous evidence-based data are lacking for informing national energy policies and strategies for achieving the country's sustainable development goals.

Rana, Suresh (Presenter)

Session: Poster Presentation

Title: Role of freezing line in driving the plant species richness difference between tropical and temperate regions of the Himalaya

Suresh K. Rana (envsuresh09@gmail.com), GB Pant National Institute of Himalayan Environment, India
Trevor Price, Department of Ecology and Evolution, University of Chicago, IL, USA

Abstract:

At the macroscale, climate strongly correlates with species richness gradients, resulting from differences in in-situ diversification and dispersal. Temperate climates contain few species because past disturbances have generated high extinction rates, and species from tropical regions are unable to easily colonize. We used grade of membership models on distribution of the Himalayan plant to cluster species according to locations shared and conducted phylogenetic analysis to evaluate diversification rates. Species fall into four cohesive biotas, organized by climate. Points of turnover between biotas occur where the mean minimum temperature of the coldest month is approximately 0oC (2,000 m - 2,500 m), and at the point of occasional annual freezing (1,000 m - 1,500 m); these boundaries run the length of the Himalaya. The patterns are retained when we consider whole clades rather than species. All plants (and the subsets trees, herbs and shrubs) belonging to the biota above the 2,000 m - 2,500 m line have higher recent speciation rates than those lower down. We attribute the high rate of recent speciation in temperate climates to high rates of turnover, creating ecological and geographical opportunity. The high elevation biota has few species, but spans the largest area, implying species numbers are far from any carrying capacity, at least with respect to accumulation of allopatric forms. This study thus links climatic restrictions of clades to differences in diversification rates, and by inference species numbers.

Reyes-Puig, Carolina (Presenter)

Session: Poster Presentation

Title: Linking static allometries to macroevolutionary patterns in green lizards

Carolina Reyes-Puig (creyesp@usfq.edu.ec),
Urtzi Enriquez-Urzelai, Czech Academy of Sciences, Institute of Vertebrate Biology
Antigoni Kaliontzopoulou, Department of Evolutionary Biology, Universitat de Barcelona

Abstract:

The increase in sexual dimorphism (SD) with body size in male-biased clades, or decrease in female-biased ones, is known as Rensch's Rule (RR). RR has been almost exclusively examined for size and not for other characters, despite being initially formulated for a diversity of traits. The trend of increased SD with increasing body size represents a case of evolutionary allometry, and it has been linked to sexual selection. Similarly, sexual differences in intraspecific static allometry have been associated with the tendency to exaggerate the relative size of body parts under sexual selection. As such, intraspecific allometric variation could underlie RR. Here we evaluate RR in different body parts of Mediterranean green lizards (Lacerta and Timon) and examine whether intraspecific allometries shape the evolutionary allometry of SD. We quantified five morphological traits: body size (SVL), head size (HS), trunk length (TRL), forelimb (FLL), and hindlimb length (HLL). To assess RR we carried out a phylogenetic generalized least-squares regression analysis between SD and species size. Additionally, we tested if sexual differences in intraspecific allometric slopes contributed to RR. We found a positive relationship between SD in SVL and HS relative to species size, consistent with RR. By contrast, SD of HLL exhibited a negative relationship with species size. The difference in slopes between the sexes had no contribution. This is the first detailed evaluation of RR in traits other than body size. By doing so we confirm RR for body and head size and explore the relevance of sexual selection in producing macroevolutionary trends.

Rozzi, Roberto (Presenter)

Session: Poster Presentation

Title: Causal explanations for the evolution of "low gear" locomotion in insular ruminants

Roberto Rozzi (roberto.rozzi@idiv.de), German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Sara Varela, Universidad de Vigo
Pere Bover Arbós, Universidad de Zaragoza
Jeff Martin

Abstract:

What triggers the particular anatomy of island species, compared to their mainland relatives, is one of the key questions in island biogeography. The so-called island syndrome is a suite of evolutionary pathways, including shifts in body size towards that of intermediate-size taxa, which have been linked to the geographic isolation and ecological simplicity of island environments and communities. Mammals on islands often undergo remarkable evolutionary changes in cranial, dental, cerebral, and postcranial morphology. For instance, extinct and extant insular ruminants often evolved a peculiar structure of the limbs by shortening distal limb elements – most markedly the metapodials, increasing their robustness, and occasionally developing bone fusions. This evolutionary pathway has been explained as an adaptation for what some authors described as “low gear” locomotion – a frequent phenomenon believed to be advantageous, in the absence of predators, for low speed walking in mountainous environments. Bovidae is a highly diverse clade of large mammals, which provides an excellent opportunity to study how locomotion on different terrains affects loading regimes experienced by distal limb elements and, consequently, their morphology. Here, we focus on extant and fossil insular bovids to assess whether the most common morphological features associated with “low gear” locomotion, that is shortening and thickening of metapodials, are independent of body size and body size divergence. Furthermore, we explore the role of several topographic and ecological predictors in driving the evolution of this type of locomotion.

Rutina, Lucas (Presenter)

Session: Poster Presentation

Title: Potential importance of agricultural landscapes surrounding Trans Frontier Conservation Areas in the conservation of large African carnivores

Lucas Rutina (lprutina@gmail.com), Department of Wildlife Management and Tourism Studies, University of Namibia

Abstract:

Southern African governments have been engaged in creating Conservation Areas, consisting of mosaic of different land uses. Within this mosaic agricultural landscapes play an important role as habitat and corridors for wide-ranging wildlife such as large carnivores. In particular, less competitive and endangered species are expected to use agricultural landscapes to avoid competition with dominant species. In this study I examined the potential of three agricultural landscape in northern Botswana in promoting co-occurrence among three sympatric carnivores; lion, leopard and wilddog. The three landscapes acts as corridors between protected areas. I used confirmed cases of livestock predation by these carnivores as a measure of their distribution and relative abundance. I calculated multidimensional niche overlap with three axes (location of predation, month of predation and livestock predated upon). The results showed that in all agricultural landscapes niche overlap between lion-leopard and lion-wilddog were low ($P < 0.001$ for all pairwise comparisons), suggesting potential co-occurrence of lion and the other subordinate carnivores in these areas. Niche overlap between leopard-wilddog was relatively higher ($P < 0.01$ for all pairwise comparisons) and increasing with decreasing wildlife /livestock ratio. Leopard and wilddog significantly shared the location of predation and the prey preyed upon ($P = 0.002$), suggesting potential co-occurrence far from wildlife areas. The study suggests that the three species can co-occur in agricultural landscapes. However, it is recommended that studies to determine the utilization of wild prey by these carnivores be conducted to compare with livestock predation.

Schenkel, Elisa (Presenter)

Session: Poster Presentation

Title: Thermal tolerances and biogeography of Central European dragonfly species

Elisa Schenkel (Elisa.schenkel@tum.de), Technichal University Munich
Roberto Novella Fernandez, TUM
Christian Hof, Technical University Munich

Abstract:

In the face of climate change, species reactions to varying temperatures are important to understand to predict their potential responses to temperature increases. As species range is of key importance for species survival, its drivers are of particular interest for ecology, biogeography, and conservation. For odonata, multiple drivers of range size have been identified previously, including ecological and life history traits (such as habitat preference or duration of the adult flight period). Temperature can influence some of these traits; e.g. the timing of adult stages will advance with increasing temperatures in springtime. We are particularly interested in the effects of temperature on species ranges, therefore we aim to assess the intra- and interspecific variation of experimentally measured thermal tolerances of damselflies (Zygoptera) and how these thermal tolerances correlate with attributes of the distributional range.

We collected adult Zygoptera across the State of Bavaria. Different levels of thermal tolerance maxima were measured using a thermocycler. Distribution data was compiled from the "Atlas of the European dragonflies and damselflies" by Kalkman et al. (2015). Environmental data like temperature and humidity was measured at each collection site and day. With these data we assessed whether the abiotic environment accounts for the intraspecific variance in Zygopteran thermal tolerance. Furthermore, we tested whether thermal tolerance range, average and limits correlate with characteristics of the European distribution such as its size, average location or limits. We expected that species with higher thermal tolerance maxima will also have a more southern range. In our poster we will present our conceptual approach as well as results.

Serrano, Filipe (Presenter)

Session: Poster Presentation

Title: Snakes on a puzzle: regionalization patterns of the richest snake family in the Neotropical region

Filipe C Serrano (filipe.serrano@usp.br), Universidade de São Paulo
João Paulo Vieira-Alencar, Universidade de São Paulo, Brazil
Cristiano Nogueira, Universidade de São Paulo, Brazil

Abstract:

The search for coincident regionalization patterns is a central quest in biogeography since biogeographical units are essential to understand the distribution and evolutionary history of biotas. Furthermore, biogeographical

units are important targets to spatially informed conservation action. These units are the result of processes such as vicariance, where barriers divide ancestral ranges, which can alter their species richness and composition. One of the most widely used methods is Biotic Element (BE) analysis, which tests a central tenet of the vicariance model: the presence of non-random sets of co-occurring species. Herein, we map BEs for Dipsadidae, the richest snake family in the Neotropical region, home to a megadiverse snake fauna. To do so, we used a dataset of 731 species ranges over 2º x 2º grid cells in Central and South America for the whole family and its two main subfamilies, Dipsadinae and Xenodontinae. Non-random patterns of regionalization were obtained only for Dipsadinae, with a total of 12 BEs representing 206 species. Most BEs were distributed in Central America and delimited by major geomorphological features such as mountains and isthmus. BEs not obviously delimited by these features are apparently shaped by ecological features such as major biomes or ecoregions. Our results show that historical constraints on species distributions, such as elevation and geomorphology, are major drivers of regionalization patterns, forming biotas with different ranges and evolutionary histories. Thus, conservation efforts might benefit from using BE analytical units, and BEs may be important surrogates of evolutionary or phylogenetic diversity.

Studnicka, Eva (Presenter)

Session: Poster Presentation

Title: The influence of climate and land-use on dragonfly distributions at different spatial scales

Eva Studnicka (ge34xon@mytum.de), Technical University Munich

Christian Hof, Technical University Munich

Abstract:

The importance of factors influencing and limiting species distributions varies at different spatial scales. While climate usually plays a dominant role at the larger scale, topography or land-use play an important role at smaller scales, with land-use and its intensity being particularly relevant as they determine the availability and suitability of habitats. Here, we examined the relative role of climate and land-use variables as determining factors of dragonfly distributions at different spatial scales (with Europe as the continental and the State of Bavaria as the regional scale level). In particular, we assessed whether and how different land-use variables influence the degree to which dragonfly species fill there climatically suitable range at the regional scale level. To do so, we calibrated species distribution models (SDM) at the European scale level based on climatic variables for all 72 Bavarian dragonflies. To identify the potential range at the regional scale, we then projected the SDMs to the map of Bavaria and compared the potential with the actual distribution for each species. By overlaying these distribution maps with spatial data of land-use type and intensity, we quantified the differences in land-use between the actual and the potential distribution. Preliminary results indicate that land-use and probably mainly its intensity does influence dragonfly occurrences at the regional scale, as apparently the amount of cropland is consistently larger in areas where the dragonflies do not occur despite a potentially suitable climate. These findings could be helpful to develop more detailed SDMs at the regional scale in order to guide the conservation of dragonflies.

Tajudeen, Tawakalitu (Presenter)

Session: Poster Presentation

Title: Effect of climate change on food crop production in Lagos State.

Tawakalitu Titilayo Tajudeen (tajudeentawakalt547@gmail.com), Lagos State University, Ojo

Abstract:

Climate change is set to be particularly disruptive in poor agricultural communities. Agriculture in Lagos Nigeria is largely rain-fed. It, therefore follows that any unfavorable climate change is likely to have a negative effect on food productivity which could be in terms of crop yield, availability of soil moisture, soil erosion and flooding, the incident of weed, pest and diseases, and decrease in soil fertility. This study examined the effect of climate change on food crop production in Lagos. The data were sourced from Lagos State Ministry of Agriculture and Co-operative, the National Bureau of Statistics and, the Central Bank of Nigeria (CBN) bulletin on climate variables (1986-2015) and crop production (1995-2014). Descriptive Statistics, Regression Analysis and, ANOVA were adopted. The finding reveals an unsteady climatic pattern with peak points across the periods under review. The Simple Linear Regression Analysis indicated that cassava production is related to rainfall but not significant statistically ($p=0.776$) and to temperature but statistically significant ($p=0.033$) with an F-value of 2.703. Maize production is also related to rainfall and temperature but not significant statistically at $p=0.807$ and $p=0.252$ respectively with F-value=0.778 where $p>0.05$. Also, a total of 180 Questionnaires were administered across the 3 selected locations (Badagry, Ikorodu, and Epe). The result shows insignificant variations in sex, household size, and educational qualification distributions across the locations. It further reveals that the majority of the farmers were old men with long years of farming experience. Many of the respondents adopted some strategies depending on the type of crop grown and there were insignificant variations across the locations with regards to measures adopted. It is therefore recommended that adequate mitigation and adaptive measures should be put in place to reduce the effect of climate change to achieve appreciable agricultural productivity.

Tsianou, Mariana (Presenter)

Session: Poster Presentation

Title: Functional redundancy and functional vulnerability in British avifauna

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Danai-Eleni Michailidou, Department of Ecology, Aristotle University of Thessaloniki

Maria Lazarina, Department of Ecology, Aristotle University of Thessaloniki
Konstantinos Touloumis, Department of Ecology, Aristotle University of Thessaloniki
Aristi Andrikou-Charitidou, Department of Ecology, Aristotle University of Thessaloniki

Athanasios Kallimanis, Department of Ecology, Aristotle University of Thessaloniki

Abstract:

Beyond the loss of species, the ongoing biodiversity crisis may alter key ecosystem processes through the loss of particular functions. When several species perform similar functions, this functional redundancy may ensure that ecosystems will continue to function despite environmental changes or species losses (functional insurance). We use recently published presence/absence data on British avifauna to explore functional redundancy and functional vulnerability of avian communities. We firstly identified functional entities based on five categorical functional traits (body mass, clutch size, activity time, foraging location, diet type). We then assessed the level of functional redundancy (mean number of species per functional entity) and functional vulnerability (percentage of functional entities having only one species) with species richness. We found that the richest communities have the highest functional redundancy. In most cases, there is low functional vulnerability in the richest communities although in a few cases of grid cells with lower species diversity, functional vulnerability ranges 50%. Our results show that functional insurance might not be as applicable in British avifauna as we expected.

Turner, Laura (Presenter)

Session: Poster Presentation

Title: Roots in the Tundra – Belowground Plant Traits Under Varying Environmental Conditions at Multiple Arctic and Alpine Sites

Laura Turner (laura.turner@nottingham.ac.uk), University of Nottingham

Franziska Schrodt, University of Nottingham
Richard Field, University of Nottingham
Gabriela Schaepman-Strub, Oak Ridge National Laboratory

Colleen Iversen, Oak Ridge National Laboratory

Abstract:

Roots in the Tundra – Belowground Plant Traits Under Varying Environmental Conditions at Multiple Arctic and Alpine Sites 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.

Velasquez-Franco, Susana (Presenter)

Session：Poster Presentation

Title：Biodiversity legacies from conflict zones in tropical Andean forest and potential management opportunities

Susana Velasquez-Franco (susanavfranco@gmail.com), University of Utah
Mitchell Power, University of Utah

Abstract：

Andean Tropical Forest has been experiencing the conflict/post-conflict scenario for many decades. Land-use changes linked to this social phenomenon include a mosaic of deforestation and rewilding through gains and losses during these socio-ecological processes. Ultimately, long-term conflict zones have a human landscape legacy that can be linked to changes in biodiversity. After the peace agreement between FARC and the national government in Colombia in 2016, illegal occupation in protected areas has increased rates of deforestation and armed conflict. These conflict zones can be considered unique ecological entities, and provide an opportunity for understanding human-environment interactions through time. Building a bridge between scientists studying Andean Forest ecosystems and management agencies charged with governance provides an opportunity in the Colombian post-conflict era. The goal of this research is to use historical archives, including satellite imagery and historical records, as well as proxies from ancient sediments, to capture the human legacy effects on local biodiversity. Information on natural and human processes that influence biodiversity through time will be used to empower local decision-makers. Specifically, this work seeks to answer two questions; 1) what is the human legacy impact to modern biodiversity within Andean Tropical forest/watersheds and 2) how can long-term ecological processes can be integrated into land-use planning and future management strategies? The study sites occur in two post-conflict Andean watersheds, Samaná and La Miel located in the Central Cordillera in Colombia. Currently, research is lacking in this region to inform decision making as the returning post-conflict populations accelerate biodiversity loss.

Wayman, Joseph（Presenter）

Session：Poster Presentation

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

Joseph Paul Wayman (JPW830@student.bham.ac.uk), University of Birmingham
Jonathan Sadler, University of Birmingham
Thomas Pugh, Lund University
Thomas Martin
Joseph A. Tobias, Department of Life Sciences, Imperial College London
Thomas Matthews, University of Birmingham

Abstract：

Spatial variation in community assembly can be driven by many different processes. While there are many examples of analyses exploring the drivers of spatial variation across different taxa and resolutions, analyses of high-resolution empirical data at large scales are lacking. Here we used a dataset consisting of the presence/absence of birds in 10km x 10km quadrats across Britain. Taxonomic and functional pairwise beta diversity and their constituent components (turnover and nestedness resultant dissimilarity) alongside two other measures of functional change (mean nearest taxon distance and mean pairwise distance) were calculated between all assemblages. These measures were used in generalised dissimilarity models (GDMs) with various environmental predictor variables (climate, land use and land cover (LULC), elevation, human influence index (HII), and habitat diversity), as well as geographic distance. We then calculated the amount of variation explained by 1) the environmental variables, 2) Geographic distance only, and 3) the amount of variation shared between the two. Results showed that there was a unique proportion of variation explained by distance alone for all measures of dissimilarity, except for MPD and the nestedness components, suggesting a role in dispersal limitation in assemblage dissimilarity. However, a large proportion of the variation explained by geographic distance was shared with the environmental variables. MPD and the nestedness components were 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 implications in the face of a warming climate and future LULC change.

Xie, Shu (Presenter)

Session：Poster Presentation

Title：Robustness of a simple island biodiversity model to trait dependency in diversification and colonization rates

Shu Xie (s.xie@rug.nl), Gelifes, University of Groningen
Rampal Etienne, University of Groningen
Luis Valente, Naturalis Biodiversity Center

Abstract：

To reveal the causes of variation in species richness among clades and geographical regions, biologists have long been interested in quantifying whether species traits have an impact on evolutionary and biogeographical rates. The application of state-dependent speciation and extinction (SSE) models to a variety of clades has revealed an important role for traits in general. However, the role of traits in diversification remains comparatively unexplored in insular communities, which can include multiple independent clades resulting from different colonization events. Here, we perform a robustness study to identify under what conditions trait-dependence in rates of island colonization, extinction and speciation (CES rates) can impact the estimation accuracy of the island biogeography inference model DAISIE (Dynamic Assembly of Islands through Speciation, Immigration and Extinction), which is silent on traits, that is, it assumes no rate variation between trait states. We extend the DAISIE simulation model to include state-dependent rates, and evaluate the robustness of the DAISIE inference model by comparing the error distribution between data simulated with and without the effects of trait dynamics on CES rates. Our results show that when the CES rate differences between states are moderate, inference with DAISIE shows negligible error for a variety of island diversity metrics (number of species, endemic and non-endemic species through time, the total number of species and colonists, distribution of island clade sizes and colonization time). However, for large differences in cladogenetic speciation rates (the rate for one state is more than three times larger than the rate for the other state) errors become large, especially for clade size variation and the number of non-endemic species through time, and when diversification is diversity-independent. We conclude that for many biologically realistic scenarios where traits play a role in insular diversification and colonization, island diversity dynamics can be accurately estimated based on phylogenetic data without the need to explicitly model trait dynamics.

Zeb, Shakil (Presenter)

Session：Poster Presentation

Title：Classification and Ordination studies of the Phytogeographic Elements of the Riparian Vegetation along the River Panjkora of Hindu Kush Mountains Range

Shakil Zeb (shakilahmadzeb@gmail.com), Quaid-i-Azam University Islamabad

Abstract：

Distributions of plant species over the earth's surface are neither random nor even, but are geographic specific and characterized by specific sets of environmental and climatic factors. The current study aimed to classify the

vegetation along the River Panjkora of the district Dir Lower, Khyber–Pakhtunkhwa, Pakistan into different phytogeographic units via exercising the Multivariate statistical techniques. Vegetation sampling was carried out through quadrat quantitative ecological techniques. Quadrats of various sizes i.e. 1 × 1 m2, 5×5 m2 and 10 × 10 m2 were taken for herbs, shrubs and trees, respectively. Inclusively 215 plant species belong to 22 different phytogeographic elements were analysed and documented. The most dominant category of phytogeographic element was Irano–Turanian with 77 species, followed by Cosmopolitan 25 species, Holarctic 23 species, Pluriregional 19 species, Mediterranean 16 species, Western Himalayan 14 species, Paleotropical 12 species and Eastern Asiatic 6 species. Eurasian, Euro–Siberian and Saharo–Arabian were represented by 3 species, Tropical, Sub–cosmopolitan and Pantropical contribute by 2 species while Paleotemperate, South American, Australian, American, African and central Asian element by a single species. The relationship of various phytogeographic elements with different environmental variables such as pH, EC, TDS, Mn, Ni, Co, Cr, Cu, Cd, Zn, Fe, Na, Ca, Mg and K were determined via Canonical and Detrended Correspondence Analyses. We have observed that with the increase in nutrients concentration i.e., Mn, Co, Mg & Ni the number of Irano–Turanian, Cosmopolitan, Holarctic, Mediterranean & Western Himalayan elements increases while with the decrease in nutrients Cr, Cu, Cd and Na concentration the number of Australian, Sub–Cosmopolitan, Sahro–Arabian, Euro–Siberian, Tropical, American, and Pantropical phytogeographical elements. There is a direct relationship between phytogeographic elements and soil nutrients that is obviously coupled with the genetic mechanism and natural selection of the species. The area hosting a diverse flora and having a strong correlation with a specific sets of edaphic and climatic factors.