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International Biogeography Society
7th Biennial Meeting
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Passing for press on December 14th.

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Seventh Biennial Conference of the International Biogeography Society

an international and interdisciplinary society contributing to the advancement
of all studies of the geography of nature
Bayreuth, Germany, 8– 12 January 2015

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Bayreuth | Germany

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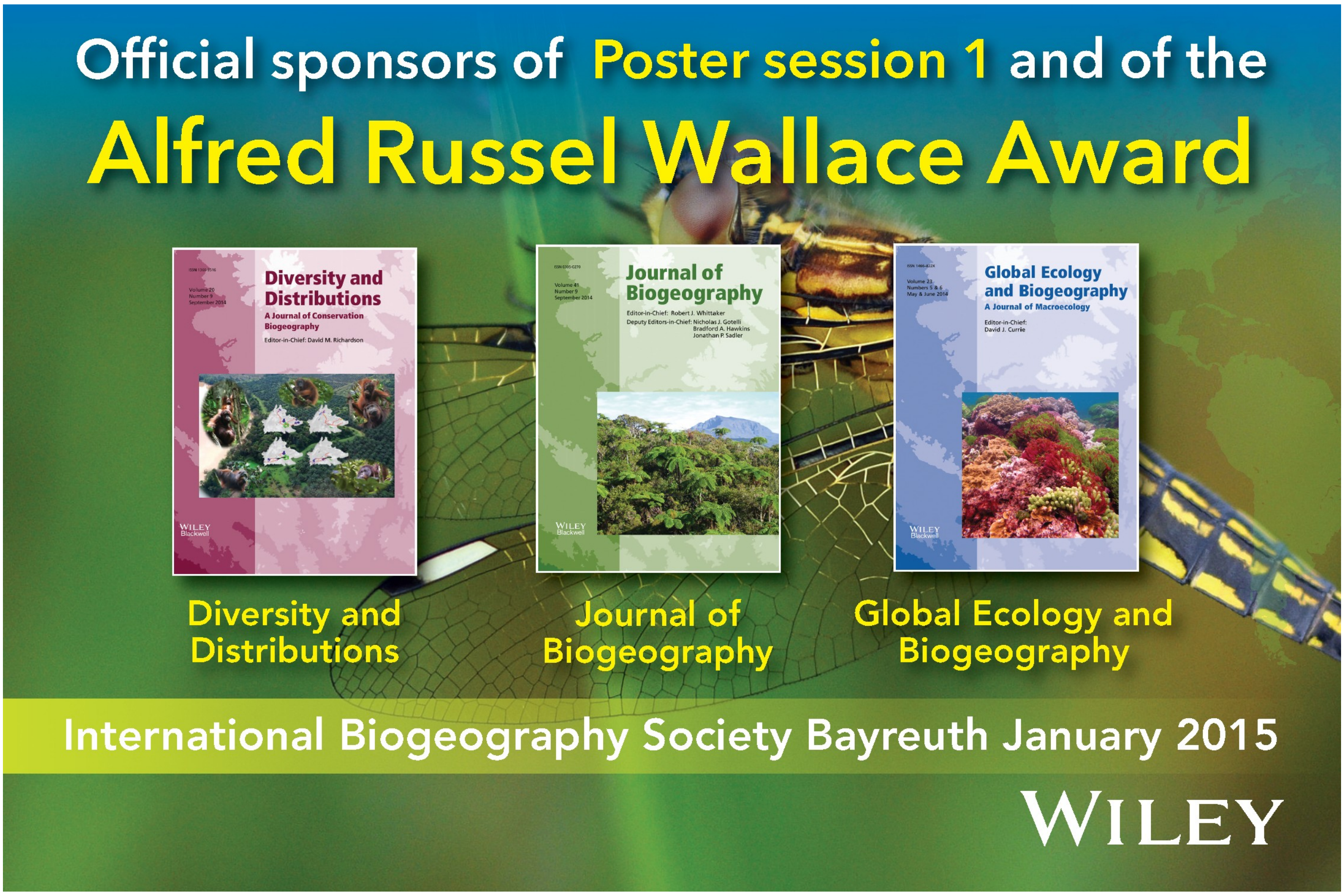
IBS Mission Statement

Biogeography, the study of the geography of life, has a long and distinguished history, and one interwoven with that of ecology and evolutionary biology. Traditionally viewed as the study of geographic distributions, modern biogeography now explores a great diversity of patterns in the geographic variation of nature — from physiological, morphological and genetic variation among individuals and populations to differences in the diversity and composition of biotas along geographic gradients. Given its interdisciplinary and integrative nature, biogeography is now broadly recognized as a unifying field that provides a holistic understanding of the relationships between the earth and its biota. Our abilities to develop more general theories of the diversity of life, and to conserve biological diversity may well rest on insights from the field of biogeography. Therefore, the International Biogeography Society (IBS) was founded in 2001, and incorporated as a non-profit organization in 2002, with the following mission:

- Foster communication and collaboration between biogeographers in disparate academic fields - scientists who would otherwise have little opportunity for substantive interaction and collaboration.
- Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers.
- Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the world's biota.

More information at the IBS website: http://www.biogeography.org



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The International Biogeography Society

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	Thursday: 08.01.2015	Friday: 09.01.2015	Saturday: 10.01.2015	Sunday: 11.01.2015	Monday: 12.01.2015
08:00		Bus shuttle hotels, Registration	Bus shuttle hotels, Registration	Bus shuttle hotels	
08:30	Pre-conference Field Trips and Workshops	Welcome	**PS3**	**PS1**	Post-conference Field Trips and Workshops
08:45		Opening Lecture			
09:15		**PS4**			
09:55				Coffee Break (Foyer Audimax)	
10:00			Coffee Break (Foyer Audimax)		
10:10		Coffee Break (Foyer Audimax)			
10:25				**PS1**	
10:30			**PS3**		
10:40		**PS4**			
11:15			MacArthur & Wilson Award presentation and lecture (Audimax)		
11:30				Lunch (Mensa) with Student Discussion Groups	
11:45		Break (salty snacks)			
12:00			Lunch (Mensa)		
12:15		**PS2**			
13:00			**CT2** **CT4** **CT1** **CT3**	**CT5** **CT8** **CT6** **CT7**	
13:15		Lunch (Mensa)			
14:15		**PS2**			
14:30				Change of Rooms	
14:45				**CT10** **CT12** **CT9** **CT11**	
15:00			Coffee Break (Foyer RW I)		
15:30			Lightning talks #2:P4-14		
15:45		- CHANGE OF BUILDING - Coffee Break (Foyer RW I)		- CHANGE OF BUILDING - Coffee Break (Audimax)	
16:15		Lightning talks #1: PPS2+4 and P1-3		Business meeting (Audimax)	
16:30			Poster Session #2 with food and drinks	Awards Ceremony and Wallace Award Lecture (Audimax)	
17:15		Poster Session #1 with food and drinks			
17:30					
18:00	Welcome Reception (Ecological-Botanical Gardens) with Registration				
18:30			Shuttle transport to the location of the banquet dinner		
19:00			Banquet Dinner/Party		
19:15					
20:00					
22:00					

Sessions: PS – Plenary Symposia, CT – Contributed Talks, PPS – Posters from Plenary Symposia, P – Posters

Plenary Lectures

Introductory Lecture

Alexander von Humboldt as a role model for modern scientists and science institutions

Helmut Schwarz[1]
[1] President, Alexander von Humboldt Foundation

The accomplishments of Alexander von Humboldt as an explorer and universal scholar were pioneering for many scientific fields. His genius and curiosity were boundless, and his work and life border-crossing in many aspects; he set standards that shape our understanding of science until today. As a gifted networker he was in contact with scientists from all over Europe, and he supported with enthusiasm and emphasis young researchers. Following his example is a guiding principle for excellence in science - both for scientists and for science organizations.

MacArthur & Wilson Award Lecture

Speciation, extinction, and the geography of species richness

Daniel Rabosky[1]
[1] University of Michigan
Contact: drabosky@umich.edu

Species richness varies dramatically across the surface of the Earth. The latitudinal diversity gradient is a striking example of this variation, but many physiographically-comparable regions are characterized by disparate patterns of species diversity. Despite decades of interest in these patterns, we still do not fully understand why some regions contain more species than others. I will discuss the contribution of speciation and extinction rates to geographic variation in species richness, focusing in particular on the latitudinal diversity gradient in terrestrial vertebrates. I will describe the inference of these evolutionary rates from time-calibrated phylogenetic trees of extant species, and I will highlight some potential pitfalls in analyzing the geography of diversification. I will explain how new methodological tools and phylogenetic frameworks are providing unprecedented resolution into the causes of large-scale diversity gradients.

Alfred Russel Wallace Award Lecture

Character displacement and release in the small Indian mongoose and the stone marten

Daniel Simberloff[1], Arijana Barun[2], Shai Meiri[3]
[1] Department of Ecology and Evolutionary Biology, University of Tennessee, USA
[2] Ecology Department, Lincoln University, Canterbury, New Zealand
[3] Department of Zoology, Tel Aviv University, Israel
Contact: dsimberloff@utk.edu

In its native Asian range, the small Indian mongoose (Herpestes auropunctatus) coexists with larger carnivores, including congeners. Introduced to many islands worldwide, and to the South American mainland, it is the only carnivore except in South America, on Trinidad, and on several Adriatic islands. On all but Adriatic islands, it is generally larger than in Asia, consistent with the hypothesis of character displacement in its native range and character release on these islands. With the larger native stone marten (Martes foina), it co-occupies three Adriatic islands and is approximately the same size as in Asia, consistent with these hypotheses. Results from Trinidad and South America are ambiguous, perhaps because coexisting carnivores there are much larger. The marten, sole carnivore, is smaller on three Adriatic islands lacking the mongoose than on Adriatic islands with the mongoose and than in many other European locations, where it coexists with both larger and smaller mustelids, again consistent with the hypotheses of character displacement and release. Other hypotheses for these patterns seem less plausible, but several anomalies remain unexplained.

Plenary Symposia

PS1 Adaptation, migration, persistence, extinction

Plenary Symposium 1: Adaptation, migration, persistence, extinction: New insights from past climate changes – Conveners: Francisco Rodríguez-Sánchez and David Nogués-Bravo

1.1 The fossil record and the future: Using the past to assess climate-change vulnerability and adaptation

Steve Jackson[1]
[1] Southwest Climate Science Center, US Geological Survey, USA

Anticipating biodiversity consequences of ongoing and future climate change is richly informed by paleoecological records of biotic responses to past climatic changes. These records encompass past changes diverse in nature, rate, and magnitude, and varying also in specific ecological and biogeographic contexts. I will identify the gaps, challenges and opportunities in using the fossil record more effectively in global-change context. Important challenges include quantifying the biodiversity costs of past climatic change (extinctions, genetic bottlenecks), assessing climate sensitivity and adaptive capacity of natural populations, determining rates, patterns, and mechanisms of migrations and habitat shifts, and disentangling processes across multiple spatial and temporal scales. all pose daunting but surmountable challenges. They will require greater engagement with other disciplines (genetics, ecology, paleoclimatology), careful consideration of taphonomy, and rigorous examination of records inferences, and assumptions. In tandem with observation, experiments, and models, paleoecology can identify key vulnerabilities as well as adaptive capacities in a rapidly changing environment.

Keywords: biodiversity, climate change, fossil record, paleoecology

1.2 Testing the effect of past climatic changes on biodiversity

Hélène Morlon[1]
[1] Biology, Ecole Normale Supérieure
Contact: morlon@biologie.ens.fr

The history of life has been punctuated by periods of major environmental changes. Understanding how biodiversity responded to these past changes may help us predict how it will respond to current human-induced environmental changes. In this talk, I will present phylogenetic approaches for testing how diversification (speciation and extinction) and phenotypic evolution responded to past environmental changes. I will then present applications of these approaches across various taxonomic groups. Finally, I will discuss the relevance of these approaches for understanding and predicting the future of biodiversity in the context of current global changes.

Keywords: macroevolution; diversification; phenotypic evolution; environmental changes

1.3 A revolutionary way to reconstruct evolutionary dynamics in nature over centuries

Luisa Orsini[1]
[1] Biosciences, Environmental Genomics Group, University of Birmingham
Contact: l.orsini@bham.ac.uk

Understanding the consequences of environmental change on natural populations has been elusive because the causes and effects of such changes occur over many decades, and are therefore difficult to measure.

Currently, the study of evolutionary dynamics along extended time axes is most commonly addressed in species with short generation times easily propagated in controlled laboratory conditions. Here, I propose a revolutionary approach to generate longitudinal data from natural systems across the time-span of multiple human careers. This approach, "actuarial ecology", measures then predicts the risk incurred by natural ecosystems from human-driven changes. I will present the first genome-level study in which we identify adaptive responses to a suite of environmental stressors (e.g. land use changes) in populations of the waterflea *Daphnia magna* resurrected from a complex landscape of shallow ponds, and validated these findings in time, using sediment cores with known histories for specific stressors. Further, I propose the integration of these longitudinal data in forecast modelling to generate accurate predictions for species and ecosystems persistence in insipient climatic change.

Keywords: paleo"omics", forecast modeling, resurrection ecology, evolutionary dynamics

1.4 Reassessing extinction risk from anthropogenic climate change using fossils and molecular log books

Damien Fordham[1]
[1] The Environment Institute, The University of Adelaide
Contact: damien.fordham@adelaide.edu.au

Disregarding or misinterpreting biotic responses to past environmental changes could impede our understanding of future ecological dynamics under global change and make accurate predictions and effective solutions difficult to formulate. Current forecasts indicate that anthropogenic climate change will cause widespread biodiversity loss. However, the accuracy of these ecological predictions remains largely untested. I will discuss how biotic responses to past climate change, imprinted in species' genes and observed in fossil and historical records, can be used to establish if forecasts of extensive biodiversity loss from future climate change are a likely reality; and identify traits that make some species more prone to extinction from climate change. A tighter integration of genetic and fossil data into ecological models will generate more robust and validated predictions of the response of demographic and evolutionary processes to large-scale environmental change. These multidisciplinary methods will help conservation scientists to better connect theory to the on-ground design and implementation of effective measures to protect biodiversity.

1.5 Stability begets diversification: effects of climatic stability on the diversification of birds in the New World

Genoveva Rodríguez-Castañeda[1], Anouschka R. Hof[2], Roland Jansson[2]
[1] Section of Integrative Biology, University of Texas in Austin
[2] Dept. of Ecology and Environmental Science, Umeå University
Contact: roland.jansson@emg.umu.se

Variation in diversification rates among lineages has been suggested as an important mechanism explaining global diversity patterns, but the causes of diversification differences are poorly understood. We tested the role of climatic stability for species diversification by assembling sister genera of birds endemic to the New World. We found that diversification increased the more stable their geographic range had been between the present and the last glacial maximum, representing the warm and cold endpoints of temperature variation during the late Pliocene and Quaternary periods. The relationship was strongest for sister groups with representatives spanning both equatorial and extratropical latitudes, but was weak for temperate and equatorial sister genera. In contrast, we found no significant relationship between diversification and the productivity of ecosystems. The latitudinal gradients in diversification of birds reported in numerous studies could thus be explained by the latitudinal gradient in climatic stability.
Keywords: diversification, global, radiation, past climate change

1.6 Ecosystem response to climate change in the tropical island of Mauritius, SW Indian Ocean

Erik J de Boer[1], Henry Hooghiemstra[1]
[1] Institute for Biodiversity and Ecosystem Dynamics, Paleo & Landscape-ecology, University of Amsterdam, The Netherlands
Contact: deboer.erikjan@gmail.com

The '4200 yr BP megadrought' was an extreme event around the Indian Ocean. This period of monsoon weakening had a catastrophic effect on vertebrate populations in the lowlands of Mauritius. We demonstrate how extreme dry conditions 4000 years ago turned the freshwater basin of Mare aux Songes into a deadly cocktail, causing the death of 100,000s of vertebrates, including dodos and giant tortoises, that were dependent on this drink-water source.
Climate reconstructions record frequent extreme conditions in the Mauritian lowlands, indicating that its species were perfectly adapted to persist through these events. In the absence of human impact, species were able to withstand Quaternary climate change and survive population crashes and bottlenecks. Compared to the lowlands, high-resolution pollen records in the uplands show a different response to climate change. Rapid (<100 yr) turnover of montane forest compositions demonstrate non-linear responses to climate change advocating for strong drivers of internal forest dynamics. We hypothesize these dynamics are driven by a large niche overlap of canopy trees that stimulate interspecific competition in the montane forests of Mauritius.
Keywords: Paleoecology, climate extremes, population bottlenecks, ecological turnover

Plenary Symposium 2: Tracking changes from space: Advances of remote sensing in biogeography
Conveners: Mao-Ning Tuanmu, Kate He and Anna Cord

2.1 Remote sensing for biogeography: Networking our future

Woody Turner[1]
[1] Earth Science Division, NASA
Contact: woody.turner@nasa.gov

Airborne and satellite remote sensing provide observations of key biogeographic patterns at multiple spatial scales. They also provide vital information about broad-scale environmental drivers of these patterns, e.g.: climate, land use, and sea surface state. Evolving remote sensing approaches and increasing computational capacity are greatly enhancing the utility of remote sensing to biogeography. Airborne spectrometers identify canopy vegetation and marine phytoplankton to ecological functional type or species and are now capturing intraspecific variation. Airborne lidars provide three-dimensional views of vegetation structure with implications for habitat characterization. Our current ability to process large volumes of satellite imagery allows development of global satellite products at landscape scale, i.e. with pixel sizes of tens of square meters rather than hundreds of square meters to square kilometers. In parallel with airborne and satellite developments, *in situ* observation approaches offer a suite of techniques to measure biogeographically relevant parameters at organismal scales. Camera traps, acoustic sensors, small drones, and environmental DNA directly observe organism distribution and abundance, as well as behavior. Citizen science can engage legions of new observers in crowdsourcing fine-scale biodiversity observations. Today, our primary challenge lies in creating frameworks for the integration of observations across scales that foster data interoperability and generate inputs for ecological models. Development and improvement of biogeographic models will allow us to understand changes in the distribution and abundance of organisms in relation to changes in climate or human action. Networks of multi-scale observations driving biogeographic models promise a revolution in our understanding and sustainable management of the living world around us.

2.2 Advances in estimating species diversity by remote sensing: a challenge for biogeography

Duccio Rocchini[1]
[1] Dpt. Biodiversity and Molecular Ecology, GIS and Remote Sensing Unit, Fondazione Edmund Mach
Contact: ducciorocchini@gmail.com

Many geospatial tools have been advocated in spatial ecology and biogeography to estimate biodiversity and its changes over space and time. Such information is essential in designing effective strategies for biodiversity conservation and management. Remote sensing is one of the most powerful approaches to identify biodiversity hotspots and predict changes in species composition in reduced time and costs. This is because, with respect to field-based methods, it allows to derive complete spatial coverages of the Earth surface under study in a short period of time. Furthermore, remote sensing provides repeated coverages of field sites, thus making studies of temporal changes in biodiversity possible. In this talk I will discuss, from a conceptual point of view, the potential of remote sensing in estimating biodiversity using various diversity indices, including alpha and beta measurements. I will also review case studies that have improved the quality of species distribution models using remote sensing data as predictors. Lastly, I will address the prospective of using spectral information to effectively detect spatial autocorrelation when estimating species diversity among sites.

Keywords: biodiversity; distance decay models; remote sensing; species distribution modeling; spatial ecology

2.3 Benefits of multi-sensor remote sensing and image texture extraction for biodiversity mapping in the High Andes of Ecuador

Christine Wallis[1], Detlev Paulsch[2], Birgit Ziegenhagen[3], Roland Brandl[4], Nina Farwig[1], Jörg Bendix[5]
[1] Conservation Ecology, University of Marburg
[2] Gesellschaft für angewandte Ökologie und Umweltplanung mbH
[3] Conservation Biology, University of Marburg
[4] Animal Ecology, University of Marburg
[5] LCRS, Geography, University of Marburg
Contact: christine.wallis@biologie.uni-marburg.de

The linkage between biodiversity and habitat heterogeneity in forests derived by remotely sensed data is challenging due to multiple vegetation layers. To date, studies using statistical models with either discrete-return Lidar variables or satellite image textures explained only moderate variance for biodiversity predictions. Our objective was to identify the success of fitting models with a combination of Lidar surveys and high resolution image textures derived from multi-spectral imageries for predicting field data on birds from the mountain rainforest of southern Ecuador. We calculated three parameters of avian diversity: (i) species diversity, (ii) phylodiversity and (iii) community composition. We compared the explanatory power and performance of Lidar-only driven models with texture-only driven models, and with combined models to predict the above mentioned parameters. Our findings show that species diversity was best predicted by texture-only models, while we were not able to predict phylodiversity by any remote sensing driven model. Most importantly, bird community composition was best predicted by mixed models, containing both Lidar and texture measures.

Keywords: Biodiversity, Birds, generalized linear models, gray level co-occurrence matrix, Lidar, Quickbird

2.4 Remote-sensing based prediction and monitoring of global species distributions

Walter Jetz[1]
[1] Yale University
Contact: walter.jetz@yale.edu

Remote sensing combined with biodiversity observation offers an unrivalled tool for understanding and predicting species distributions and their changes at the planetary scale. I will illustrate recently developed high-resolution remote-sensing based layers targeted for spatiotemporal biodiversity modeling, addressing climate, environment, topography, and habitat heterogeneity. Remote-sensing based capture of these putative predictors of biodiversity dynamics provides more a reliable signal than spatially interpolated layers and avoids inflated spatial autocorrelation. The layers result in more accurate models of species occurrence and are more readily able to address the scale of processes underpinning species distributions, e.g. when combined with emerging hierarchical, cross-scale models. I illustrate the multiple ways in which this type of information, based on continuously collected data, supports the prediction of not just spatial but also temporal variation in biodiversity. Using the global biodiversity point data record implemented in the Map of Life infrastructure I will showcase new indicators of species distribution and change that demonstrate these new opportunities.

Keywords: remote sensing; species distributions; global; models; monitoring; geographic range;

2.5 Invaders from space: Remote sensing of invasive plants

Bethany Bradley[1]
[1] Environmental Conservation, University of Massachusetts, Amherst
Contact: bbradley@eco.umass.edu

Analysis of remotely sensed imagery is increasingly being used for mapping invasive plant species. Resulting distribution maps are an important tool for understanding invasion biogeography and predicting invasion risk. Remote identification of invasive plants based on differences in spectral signatures is the most common approach, typically using hyperspectral data. But several studies have found that textural and phenological differences are also effective approaches for identifying invasive plants. I will present examples of remote detection of invasive plants based on spectral, textural and phenological analysis and highlight circumstances where the different approaches are likely to be most effective. Remote mapping of biological invasions is currently a relatively specialized research topic, but the unique cover, morphology and/or seasonality of many invaded ecosystems relative to uninvaded areas suggests that more species could be detected remotely.

Keywords: remote sensing, invasion biogeography, mapping

2.6 What you can't expect from remote sensing

Sebastian Schmidtlein[1]
[1] Inst. of Geography and Geoecology, Karlsruhe Institute of Technology (KIT)
Contact: schmidtlein@kit.edu

Remote sensing provides lots of new data sources for biogeographical research and it has, of course, natural limits. Like many fast evolving technologies it is often underrated but also a source of unfounded hopes. This talk aims at shedding some light on today's options, prospects and illusions regarding the use of remote sensing in biogeography. Most of the illusions relate to species and quantities derived from these while most of the hidden treasures relate to what can be derived for a better causal understanding of the observed patterns.

Plenary Symposium 3: Paleobiogeography: The importance of fossil data to species biogeography past, present, and future – Conveners: Alycia Stigall and Corinne Myers

3.1 Paleobiogeography: The importance of fossil data to species biogeography past, present, and future

Alycia Stigall[1], Corinne Myers[2]
[1] Department of Geological Sciences, Ohio University
[2] Dept of Organismic and Evolutionary Biology, Harvard University
Contact: stigall@ohio.edu

The fossil record is a rich source of data about the impact of environmental changes on biotic systems, including climate and habitat changes and species invasions. However, paleontological data have not been fully integrated within many aspects of modern biogeographic theory. Studies using Pleistocene and Quaternary fossils has resulted in innovative analyses with important implications, yet paleobiogeographic investigation into older parts of the fossil record are far less common. This under-utilization partly reflects methodological challenges and partly an historical expectation that detailed analyses were precluded by incompleteness in the fossil record. Both of these limitations have been mitigated over the past several decades. Recent efforts in stratigraphic correlation have provided a robust and detailed temporal framework for analysis in many time intervals. Furthermore, many “modern” biogeographic methods, such as species distribution modeling and phylogenetic biogeographic methods, have been adapted for use with deep time fossil data. These advances provide a framework within which an unprecedented level of synthesis may be achieved between paleo— and neo—biogeography.
Keywords: Paleobiogeography, deep time, fossil record, integrating, ENM, dispersal, plate tectonics

3.2 Origin of biogeography: 500 million years ago?

Thomas Servais[1], David A.T. Harper[2]
[1] CNRS - University Lille, France
[2] Durham University, United Kingdom
Contact: Thomas.servais@univ-lille1.fr

The Early Palaeozoic was a critical interval in the evolution of marine life on our planet. Through a window of some 120 million years, the Cambrian Explosion, Great Ordovician Biodiversification Event, End Ordovician Extinction and the subsequent Silurian Recovery established a steep trajectory of increasing marine biodiversity that started in the Late Proterozoic and continued into the Devonian. Biogeography is a key property of virtually all organisms; their distributional ranges, mapped out on a mosaic of changing palaeogeography, have played important roles in modulating the diversity and evolution of marine life. The recent researches of some 130 authors from over 20 countries, on distributional and in many cases diversity data for all the major biotic groups plotted on current palaeogeographic maps (Geological Society Memoir 38, edited by Harper and Servais), has provided major advances in our understanding of Early Palaeozoic biogeography and palaeogeography. We have now a greater potential to identify oceanic circulation and migrational patterns, zones of upwelling and species pumps and the phylogeography of the major animal groups.
Keywords: Cambrian, Ordovician, Silurian, palaeobiodiversity

3.3 Biogeographic structure of marine benthic assemblages over the last 300 Million years

Wolfgang Kiessling[1], Adam Kocsis[2]
[1] GeoZentrum Nordbayern, Friedrich-Alexander Universität Erlangen-Nürnberg
[2] Eötvös University, Budapest
Contact: wolfgang.kiessling@fau.de

Although important analyses have been published on deep-time biogeographic patterns, no attempt has yet been made to quantify fossil biogeography over longer stretches of geological time. The Paleobiology Database, a community-wide effort to compile fossil occurrence data, renders this now possible. We assessed the biogeographic structure of shallow-marine shelf faunas using hierarchical cluster analysis and multidimensional scaling of well-sampled paleogeographic grids and found that (1) at the broadest scale a significant latitudinal zonation is often evident, whereas longitudinal structure was usually less prevalent than today; and (2), there is little agreement between inferred paleoclimate and provinciality and even mass extinctions had limited effect on biogeographic structure. We also found that there is no substantial difference in the delineation of provinces between species and genus level, supporting the common use of genera in paleobiological studies.
Keywords: paleobiogeography, paleoclimate, marine systems

3.4 Do we need fossils for historical biogeography?

Thomas Denk[1]
[1] Palaeobiology, Swedish Museum of Natural History
Contact: thomas.denk@nrm.se

Historical biogeography is closely linked to the evolutionary history of a plant group. To understand historical and modern biogeographic patterns taxonomic relationships must be known. Generally, taxonomic relationships are best explained by molecular differentiation patterns. If a good phylogenetic framework is available, one may argue that the evolutionary unfolding reflects the biogeographic history of a group. This has been used as an argument against the inclusion of fossils in historical biogeographic studies. In my talk I will show that palaeobotany and recent botany equally depend on each other if a realistic biogeographic reconstruction is to be reached. Specifically, I will examine the effect of fossils on biogeographic scenarios under different premises: (*i*) a straight-forward phylogenetic framework is available, the “easy case”, (*ii*) a complex phylogenetic framework is available including conflicting signal in molecular data, and (*iii*) no phylogenetic framework is available.

3.5 Integrating fossils, phylogenies, and niche models into biogeography to reveal ancient evolutionary history: The case of *Hypericum* (Hypericaceae)

Andrea Sánchez Meseguer[1], Jorge M. Lobo[2], Richard Ree[3], David J. Beerling[4], Isabel Sanmartín[5]
[1] The Center for Biology and control of Populations (INRA)
[2] Museo Nacional Ciencias Naturales-CSIC
[3] Field Museum of Natural History
[4] University of Sheffield
[5] Real Jardín Botánico de Madrid-CSIC
Contact: asanchezmeseguer@gmail.com

Uniformitarianism assumptions imply that the processes acting in the present are the same as those operating in the past. Biogeographers used this assumption to reconstruct ancestral ranges from present data. However, under scenarios of high extinction, the biodiversity we observe today will not be representative of the historical diversity. The fossil record can help us escape this trap. We introduce a method to incorporate the temporal, spatial and climatic information provided by fossils into biogeographic inference; the distribution of the fossil is used to constrain the inference of ancestral areas. We also use fossil distribution data and ecological niche modeling to reconstruct the niche and potential distribution of the ancestors over time, building a biogeographic model that takes into account ecological connectivity through time. We use this approach to reconstruct the biogeographic history of the angiosperm genus *Hypericum*. Our study highlights the need for an integrative approach to biogeography and reveals the confounding effect of differential extinction across regions, which may lead to ancestral areas being erroneously inferred as resulting from recent colonization

Keywords: Biogeography, Cenozoic climate change, ecological niche modelling, extinction, fossils, Hypericum, phylogeny

3.6 Continental gateways and the dynamics of mammalian faunal change

Catherine Badgley[1]
[1] Dept of Ecology & Evolutionary Biology, University of Michigan
Contact: cbadgley@umich.edu

Tectonic changes interact with climate to open or close narrow “gateways” to passage of organisms from one region to another. First recognized in the marine realm, these gateways have continental counterparts where mountain ranges and changing sea level open or close corridors to dispersal. The interaction of open vs closed gateways with changing vs stable climate yields four biogeographic modes, each predicting changes in origination and extinction rates and ecological structure. For example, open corridors and climatic stability result in low rates of immigration and extinction, elevated endemic speciation, and stable ecological structure. Three examples from the mammalian fossil record test these scenarios. (1) In Miocene faunas of Pakistan, immigration rates peak and faunal proportions change during an interval of cooling and open corridors. (2) Miocene faunas of Spain show elevated extinction and origination rates and changing trophic structure during regional aridification with open corridors. (3) In Quaternary faunas of South Africa, during interglacials with closing corridors and warming climates, ungulates show range reductions and extinctions as grasslands contracted.

Keywords: mammals, paleobiogeography, macroevolution

PS4 Global functional diversity in a data-rich era

Plenary Symposium 4: Global functional diversity in a data-rich era
Conveners: Björn Reu, Miguel Mahecha, Jens Kattge and Christian Wirth

4.1 Traits, niche occupancy, coexistence, and geographic distribution

Robert Ricklefs[1]
[1] Department of Biology, University of Missouri-St. Louis
Contact: ricklefs@umsl.edu

The increasing availability of trait and distribution data is providing new possibilities for analyzing the assembly of ecological communities on local to regional scales. However, quantifying niche space and its filling by species, as well as understanding the relationship between local niche occupancy and geographic distribution, continue to challenge ecologists. Using examples from plants and birds, I will assess relationships between traits, local abundance, and geographic distribution. These analyses suggest that species are broadly competent over large regions of ecological space and that competitive impacts within local and regional assemblies are diffuse and do not impose strong constraints on community membership.

Keywords: Global Functional Diversity in a Data-Rich Era, traits, niche occupancy, coexistence, geographic distribution

4.2 Long-term historical effects on functional diversity and potential impacts on ecosystem functioning

Alejandro Ordonez[1], Jens-Chsitian Svenning[1]
[1] Biosciences, section of Ecoinformatics, Aarhus university - Denmark
Contact: alejandro.ordonez@biology.au.dk

An emerging unanswered in functional biogeography question is if historical legacies in biodiversity patterns translate into contemporary functional diversity and ecosystem functioning. Here, we hypothesize that they do so, as shallow- and deep-time historical drivers may shape effect-trait diversity and thereby ecosystem functioning. This notably could occur via response-trait mediated effects on species ranges and community assembly, but may also involve other processes. Here we describe how three interacting history-linked processes may partly determine functional diversity: lineage biogeography determined by evolutionary and diversification dynamics and colonization from areas of origin; Historic range dynamics defined by environmental and non-environmental constraints; and lasting imprints in the local community assembly due to competition or habitat species filtering, immigration from the regional pool, and perhaps less often priority effects. These considerations suggest a need to rethink how ecosystem functioning should be expected to respond to near-future global change.

Keywords: climatic stability, disequilibrium dynamics, functional traits, historical biogeography, historical legacy, paleoclimate, response lags, spatial non-stationary

4.3 Large-scale distribution of pollination systems in Europe

Aveliina Helm[1], Argo Ronk[1], Markus Franzén[2], Oliver Schweiger[2], Luisa Carvalheiro[3], Robert Szava-Kovats[1], Meelis Pärtel[1], Martin Zobel[1]
[1] University of Tartu
[2] Helmholtz Centre for Environmental Research - UFZ
[3] University of Leeds
Contact: aveliina.helm@ut.ee

We used the most comprehensive large-scale distribution data of European vascular plant species to depict and analyse the distribution of pollination systems. We tested which climatic, land-use and biodiversity drivers shape the relative richness of insect-pollinated plant species compared to pollinator-independent species and whether there are any differences in distribution patterns for plant species with strict versus intermediate dependence on insect pollination. Insect-pollination was prevailing in compositionally diverse landscapes, in regions with higher temperatures, larger wind-speed and with larger diversity of both plants and pollinators. The relative distribution of intermediate vs. strictly pollinator-dependent species was additionally determined by land-use patterns: there were relatively more intermediately pollinator-dependent plant species in open landscapes with higher human population density, less precipitation, higher annual temperatures and larger wind-speed. Our results provide the first evidence of what drives the distribution of pollination systems in large scales.

4.4 Projecting traits, communities and functional diversity: novel approaches to ecosystem modeling

Simon Scheiter[1], Liam Langan[2], Steven I. Higgins[3]
[1] Biodiversität und Klima Forschungszentrum (BiK-F), Senckenberg Gesellschaft für Naturforschung
[2] Institut für Physische Geographie, Goethe Universität Frankfurt am Main
[3] Department of Botany, University of Otago
Contact: simon.scheiter@senckenberg.de

The ability to project patterns of traits, community composition and diversity is an important challenge in ecology and it is required to understand how climate change and disturbances may influence vegetation. Models are powerful tools to investigate vegetation under past, present and future conditions and at large spatial scales. Their development depends on empirical data and large amounts of ecological data available to modelers allow the development of novel approaches. Here, we present a novel dynamic vegetation modeling approach, the aDGVM2. Plants in the model are characterized by an individual combination of trait values; traits are linked by trade-offs. Successful plants can pass their trait values to the next generation whereas other strategies are filtered out. The aDGVM2 assembles plant communities that are well adapted to the environment. This approach allows to simulate trait patterns, vegetation distribution and diversity and it allows to study the process that drive these patterns. The aDGMV2 links data and models in a way not possible in most alternative models and it provides a framework to integrate Earth system modeling and functional biology.

Keywords: trait based model, community assembly, aDGVM2, dynamic vegetation model

4.5 Does functional diversity modulate demographic responses to stand structure and climate in European forests?

P. Ruiz-Benito[1], S. Ratcliffe[2], A.S. Jump[1], L. Gómez-Aparicio[3], J. Madrigal-González[4], C. Wirth[2], G. Kändler[5], A. Lehtonen[6], J. Dahlgren[7], M. A. Zavala[4]
[1] Biological and Environmental Sciences, School of Natural Sciences.University of Stirling. FK9 4LA, Stirling, United Kingdom.
[2] University of Leipzig. AG Spezielle Botanik und Funktionelle Biodiversität. Johannisallee 21-2. 04103 Leipzig, Germany.
[3] Instituto de Recursos Naturales y Agrobiología de Sevilla (IRNAS), CSIC, PO BOX 1052. 41080. Sevilla. Spain.
[4] Forest Ecology and Restoration Group, Department of Life Sciences, Science Building, University of Alcala, Campus Universitario, 28805, Alcalá de Henares (Madrid), Spain.
[5] The Forest Research Institute
[6] Finnish Forest Research Institute, Vantaa Research Centre, PO Box 18, 01301 Vantaa, Finland.
[7] Department of Forest Resource Management, Swedish University of Agricultural Sciences, SE-90183 Umeå, Sweden.
Contact: palomaruizbenito@gmail.com

Diverse forests are crucial for the carbon cycle and forest productivity, but increased tree mortality and decreased growth could be aggravated by the negative effects of drought and high temperatures. Despite its importance for understanding and predicting climate change effects in forest ecosystems, it is not well understood how diversity loss may alter growth and mortality responses to elevated climatic stress. We used data from *c.* 55,000 plots across Europe and maximum likelihood techniques to quantify the effect of stand structure, climate and diversity on stand growth and mortality, and to explore whether functional diversity can modulate demographic responses to climate and competition. Diversity had a strong effect on stand growth and mortality in Mediterranean forests. Furthermore, functional diversity had indirect effects through modification of growth and mortality response to evapotranspiration in broad-leaved deciduous forests and to tree density in Mediterranean forests. We suggest that the positive effects of functional diversity may have been underestimated because high functional diversity may also ameliorate stressful conditions in different forests

Keywords: climate change, community-weighted means, functional dispersion, indirect effects, maximum likelihood, national forest inventory, plant functional traits

4.6 Community diversity and structure in geographical space: the roles of functional diversity and all other intrinsic properties may be very challenging to evaluate

Bradford Hawkins[1], Xiangping Wang[2]
[1] University of California
[2] Beijing Forestry University
Contact: bhawkins@uci.edu

Understanding spatially structured ecological and biogeographical patterns must rely on evaluating a combination of extrinsic and intrinsic drivers; the former using variables generated independently of the focal species/communities [e.g., climate; geological history, island size], and the latter using variables derived from the target organisms themselves [e.g., all morphological, physiological and ecological traits; functional diversity; phylogenetic metrics]. For both types of variables the aphorism ‘pattern does not identify process’ is well known, but for the latter the pattern itself is problematical. In this talk I will illustrate an issue that greatly complicates analyses of spatially structured data and the inferences than can be drawn from them. I will also offer an alternative method of analysis that is not plot- or cell-based that appears at this time to at least partially resolve the problem.

Keywords: Community structure, community phylogenetics, diversity gradients, null models, spatial autocorrelation, spatial structure

Contributed Talks

Contributed Talks 1: Island biogeography
Convener: Manuel Steinbauer

1.1 Global patterns and drivers of phylogenetic structure in island floras

Patrick Weigelt[1], W. Daniel Kissling[2], Yael Kisel[1], Susanne A. Fritz[3], Dirk Nikolaus Karger[4], Michael Kessler[4], Samuli Lehtonen[5], Jens-Christian Svenning[6], Holger Kreft[1]
[1] Biodiversity, Macroecology & Conservation Biogeography Group, University of Göttingen, Germany
[2] Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, The Netherlands
[3] Biodiversity and Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung, Germany
[4] Institute of Systematic Botany, University of Zurich, Switzerland
[5] Department of Biology, University of Turku, Finland
[6] Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Denmark
Contact: weigelt.patrick@gmail.com

Islands are ideal for investigating the processes shaping assemblage composition. We examine three of these processes - dispersal, environmental filtering and in-situ speciation - across 393 islands and 37,041 vascular plant species worldwide (representing angiosperms overall, palms and ferns) by linking phylogenetic assemblage structure to island characteristics: isolation, area, geology, age, environmental heterogeneity, past and present climate, source pool size and biogeographic history. Together, physical and environmental factors explain more variation in phylogenetic structure for angiosperms (49%) and palms (52%) than for ferns (18%). Signatures of dispersal, environmental filtering and in-situ speciation markedly differ among taxonomic groups according to their dispersal- and speciation-related traits, adaptations to climate and biogeographic history. Furthermore, different measures of phylogenetic structure capture traces of different speciation patterns (radiations in single vs. multiple lineages). Our results show the value of comparing phylogenetic assemblage structure between different lineages for studying the processes shaping global plant diversity.
Keywords: Dispersal, Diversification, Ferns, Environmental Filtering, Flowering plants, Island Biogeography, Macroecology, Palms, Phylogenetic Diversity

1.2 The characteristics of population density in insular endemic lizards

Maria Novosolov[1], Gordon Rodda[2], Anat Feldman[1], Amy Kadison[1], Roi Dor[1], Shai Meiri[1]
[1] Department of Zoology, Tel Aviv University, 6997801, Tel Aviv, Israel
[2] US Geological Survey, Fort Collins Science Center, Fort Collins, Colorado 80526 USA
Contact: marianovosolov@gmail.com

Islands have few species. This includes few predator and competitors for island species, which is thought to select for high population densities. We hypothesize that insular lizards have denser populations than mainland species and that density is negatively correlated with competitor and predator richness. We collected population density for 65 insular endemic lizard species, 36 insular populations of non-endemic species and 160 mainland species. We controlled for phylogenetic affinities, body mass and study area, which are strongly correlated with population density. Insular species (both endemic and non-endemic) have denser populations than mainland species and endemic populations are denser than insular populations of non-endemics. However, correcting for lizard and predator richness this difference disappeared. Lizard and predator richness affects population density, but we cannot determine whether the higher population densities in insular species evolved as an adaptation to the island environment or if mainland animals from dense populations had a better chance of successfully colonizing islands.
Keywords: Evolution, density compensation, island biogeography, island endemism, lizards

1.3 Havre Pumice Rafts: A unique test of the theory of Island Biogeography

Eleanor Velasquez[1], Jennifer Firn[1], Scott Bryan[1]
[1] Queensland University of Technology
Contact: em.velasquez@student.qut.edu.au

The Theory of Island Biogeography (TIB) was first proposed in 1963 and posits that more species will assemble in larger islands (or habitats) as a result of species turnover resulting in a dynamic equilibrium. A unique natural phenomenon which can be used to perform tests of TIB is that of pumice rafting. Pumice rafts formed from the eruption of submarine volcanoes produce trillions of individual pumice stones at the same time and place with similar underlying structure and chemistry. Preliminary results from 403 pumice clasts collected from 13 sites have corroborated the central principal of

TIB, with larger pumice clasts having more species. In addition, the effect of age is also significantly correlated with numbers of individuals and species richness. As TIB has been used extensively for understanding impacts on remnant habitats, this study has the potential to assist in the protection of shallow marine reserves.

Keywords: marine biodiversity, island biogeography, pumice rafting, ecology,

1.4 Species-specific responses to island connectivity cycles: refining the 'Pleistocene Aggregate Island Complex' (PAIC) model of diversification.

Anna Papadopoulou[1], L. Lacey Knowles[1]
[1] EEB Department, University of Michigan
Contact: apapadop@umich.edu

The contribution of Pleistocene sea-level fluctuations to biodiversity patterns, and specifically whether the repeated cycles of island connectivity and isolation acted as a 'species pump' is debated. Studying the divergence process in flightless insects across 'Pleistocene Aggregate Island Complexes' (PAICs), we show that this controversy is partly due to disregarding topographic characteristics and taxon-specific traits, which affect population persistence and gene flow among islands. Using bathymetric maps and ecological traits we generate predictions about a PAICs propensity to promote or inhibit diversification. We test these predictions through a series of hierarchical Approximate Bayesian Computation analyses that identify how simultaneous divergence in a Mediterranean PAIC is generally restricted to ecologically equivalent taxa, where the spatial scale for observed concordance is informed by bathymetric data. In a Caribbean PAIC, we demonstrate the power of genome-wide SNP data for inferring population history in such dynamic systems and thus refining further the role of PAICs as drivers of divergence across island archipelagos.

Keywords: Pleistocene sea-level change, island connections, comparative phylogeography, bathymetry, habitat persistence, Cyclades, Virgin Islands

1.5 Diversification of Sulawesi's murid rodent fauna

Jacob Esselstyn[1], Anang Achmadi[2], Kevin Rowe[3]
[1] Museum of Natural Science, Louisiana State University
[2] Museum Zoologicum Bogoriense
[3] Museum Victoria
Contact: esselstyn@lsu.edu

The rodent fauna of Sulawesi Island, Indonesia is entirely endemic and contains a wide range of morphological and apparently ecological diversity. Thirty-eight species are currently known in 15 genera, but recent fieldwork demonstrates that the fauna is dramatically undersampled, with several species and genera discovered in the last few years. Phylogenetic analyses of DNA sequence data reveal that this oceanic-island fauna is derived from at least eight independent colonization events, each of which led to an apparently idiosyncratic number of descendent species. We hypothesized that the clades descendant from the first lineages that colonized the island would be the most species rich and contain the greatest morphological or ecological disparity. However, current evidence indicates that time of colonization does not predict species-level diversity, which suggests that speciation rates and/or extinction rates have been idiosyncratic in this group of mammals. Ancestral state reconstruction of diet on a species-level phylogeny further shows that transitions between herbivory and carnivory occurred in both directions, further indicating the idiosyncratic nature of the diversification process.

Keywords: diversification, island biogeography, mammal, phylogenetics

1.6 Bioclimatic origins of the Hawaiian flora: niche conservatism or adaptive free-for-all?

Jonathan Price[1], Warren L. Wagner[2]
[1] Geography and Environmental Studies, University of Hawaii at Hilo, USA
[2] National Museum of Natural History, Smithsonian Institution, USA
Contact: jpprice@hawaii.edu

Globally, major adaptive shifts in the temperature tolerance of plants occur comparatively rarely, indicating a prevalence of niche conservatism, with tropical taxa typically developing cold-tolerance. However ecological opportunities on oceanic islands potentially represent exceptions to this rule. Numerous phylogenies and abundant ecological data for the Hawaiian flora permit comparison of the temperature tolerances of evolutionary lineages of temperate and tropical origin. While temperate lineages have higher elevational midpoints, they also have broader elevational ranges. Moreover, there are comparatively many species of temperate origin occupying tropical lowland habitats, whereas the converse is far less frequent. The net result is that many temperate lineages have shifted into tropical habitats, possibly stemming from greater lability and abundant open niche space. Tropical lineages, however, may be limited by niche conservatism whereby frost tolerance evolves comparatively rarely. The recent shift in habitat preference may put lowland species of temperate origin at a pronounced competitive disadvantage against tropical invasive species.

Keywords: niche conservatism, adaptation, tropical, temperate, Hawaiian Islands

1.7 Functional island biogeography: from isolated trees to oceanic islands

Robert Whittaker[1], Thomas Matthews[1], Eden Cottee-Jones[1]
[1] School of Geography and the Environment, University of Oxford
Contact: robert.whittaker@ouce.ox.ac.uk

Island biogeographical analyses of species incidence, nestedness and diversity have traditionally focussed on species as the unit of analysis. Recently developed analytical tools enable complementary analyses of functional diversity (FD) patterns based on analyses of species traits. Here, we examine FD patterns in: (i) isolated trees, (ii) habitat islands and (iii) oceanic islands. First we show an important role played by isolated fig trees in maintaining FD of bird assemblages in countryside landscapes. Second we use data comprising 1000 bird species and 19 forest-habitat-island studies in a first synthetic analysis of nestedness from a functional perspective, suggesting that fragmentation results in an ordered pattern of loss of species in relation to their traits. Third, we report analyses of emergent patterns of FD for oceanic (Azorean) island arthropods showing that FD scales with island species richness, which in turn scales with island area.

Keywords: functional diversity,functional traits, habitat islands, island biogeography, macroecology, nestedness

1.8 Community dimensions of island biogeography

Rosemary Gillespie[1], Andrew Rominger[1], Fernanda Valdavinos[1], Kari Goodman[1], Jun Ying Lim[1], Michael Brewer[2], Darko Cotoras[1], Curtis Ewing[1], Kerry Shaw[3], John Harte[1], Neo Martinez[4], Diana Percy[5], George Roderick[1], Daniel Gruner[6]
[1] University of California Berkeley
[2] East Carolina University, Greenville
[3] Cornell University, Ithaca
[4] University of Arizona, Tucson
[5] Natural History Museum, London
[6] University of Maryland, College Park
Contact: gillespie@berkeley.edu

Understanding how ecological and evolutionary processes synergistically determine biodiversity patterns remains a central goal in biology. In highly isolated archipelagoes such as the Hawaiian Islands, beyond the reach of equilibrium colonization dynamics, rapid in situ diversification and speciation have the potential to keep pace with ecological dynamics. Using multiple arthropod lineages across the Hawaiian model system, we explore how complex communities emerge from ecological (dispersal, trophic interactions) and evolutionary (genetic structuring, adaptation, speciation, extinction) processes. We combine micro-evolutionary and macro-ecological perspectives to show how patterns of divergence differ between lineages depending on trophic group, with communities as a whole showing trends of higher food web specialization over time. Our results are providing insights into how assembly by immigration and short time scale ecological processes give way to evolutionary processes in the assembly of these complex Hawaiian communities. These findings also provide motivation to expand ecological theory to better incorporate dynamic evolutionary processes.

Keywords: island biogeography macroecology speciation equilibrium

Contributed talks 2: Climate-change biogeography
Convener: Jessica Blois

2.1 The importance of population variability to the accurate detection of climate change responses

Christy McCain[1], Timothy Szewczyk[1], Kevin Bracy Knight[1]
[1] Dept. of Ecology & Evolutionary Biology, University of Colorado
Contact: christy.mccain@colorado.edu

The rush to assess species' responses to anthropogenic climate change (CC) has overlooked the importance of inter-annual population variability (PV). Researchers have assumed sampling rigor alone will lead to an accurate detection of change. Here we show using population simulations (discrete-time Ricker models) across an empirical range of PV that medium to high PV can lead to opposite and biased conclusions of CC response. Between pre- and post-CC sampling bouts, there is (1) a 50% probability of erroneously detecting the opposite trend in population abundance change and nearly zero probability of detecting no change; and (2) up to 50% probability of detecting a population extirpation when the species is present, but in low or undetectable, natural abundances. (3) Across multiple years of sampling it is almost impossible to accurately detect any directional shift in population sizes. (4) Under scenarios of medium to high PV across a species' range or at the range edges, there is a bias towards erroneous detection of range shifts or contractions. Such species (many small animals) may be inaccurate 'canaries in the coal mine' for CC. For CC, PV urgently needs more consideration.
Keywords: abundance, bias, climate change, extirpation, inter-annual population variability, population dynamics, range shifts

2.2 Testing the "space-for-time" substitution in biodiversity modeling and projection

Morgane Barbet-Massin[1], Frank La Sorte[2], Walter Jetz[3]
[1] National Museum of Natural History
[2] Cornell University
[3] Yale University
Contact: barbet@mnhn.fr

In a global change context, "space-for-time" substitution is widely used in biodiversity modeling when model parameters derived from spatial patterns are used to predict past or future temporal trends. In the case of species abundance, it however assumes that putative drivers of current spatial patterns will similarly predict temporal changes – an assumption that has rarely been tested. Here, we use a hierarchical Bayesian modeling framework and abundance data from the US Breeding Bird Survey for 31 species to test whether "space-for-time" substitution based on species' climatic associations could be used to predict species abundance changes over time. For most species, "space-for-time" substitution performed very poorly (mean R^2=0.015) despite climate explaining an important part of species abundance spatial variability (mean R^2=0.548) and part of species abundance temporal variability (mean R^2=0.142). Results highly depend on the species, with "space-for-time" predictions showing similar levels of accuracy for some species. However, for most species "space-for-time" substitution was unable to successfully predict the potential impacts of climate change on species abundance.
Keywords: model transferability, abundance data, bird species, climate change, Bayesian hierarchical modeling

2.3 Did montane refugia in peninsular India allow the persistence of mesic forest biota through Miocene climate change?

Ishan Agarwal[1], Praveen Karanth[1]
[1] Indian Institute of Science
Contact: ishan.agarwal@gmail.com

Tropical, range-restricted taxa are predicted to face high extinction risk from global warming. Here, we study how past climate change impacted mesic forest biota of peninsular India (PI), providing insights into potential future effects. We reconstruct the temporal history of an endemic radiation of ground-dwelling forest geckos (*Geckoella*) using multi-locus sequence data from 112 individuals and 89 localities across PI. *Geckoella* began diversifying 42–32 million years ago (mya), with increased extinction rates between 21–13 mya, and concurrent rapid diversification in

3 of 4 lineages into over 40 species across PI from 15–8 mya. Increased extinctions overlap with the Mid-Miocene climatic optimum (17–15 mya, MMCO), when the earth was 2–6° C warmer; rapid cladogenesis begins when cooler conditions return. Niche models projected onto conditions mimicking the MMCO show severe range contractions of two species complexes in the mesic zone, with high suitability only at elevations >800 m. Warming during the MMCO is likely to have caused widespread extinctions of terrestrial, cold-adapted taxa in the mesic zone of PI; with suitable conditions for persistence only at high elevations.

Keywords: Global warming; mid-miocene climatic optimum; niche modelling; palaeoclimate; lizards; Gekkonidae;

2.4 Branches of the tree of life weakened under climate change

Carlos E. González-Orozco[1], Laura J Pollock[2], Nunzio Knerr[3], Brent D. Mishler[4], Joseph T. Miller[3], Shawn W Laffan[5], Andrew H Thornhill[6], Dan F. Rosauer[7], Daniel P. Faith[8], David A. Nipperess[9], Heini Kujala[2], Nathalie Butt[2], Simon Linke[10], Bernd Gruber[1]
[1] Institute for Applied Ecology and Collaborative Research Network for Murray-Darling Basin Futures, University of Canberra
[2] The University of Melbourne
[3] Centre for Australian National Biodiversity Research, CSIRO
[4] University of California, Berkeley
[5] University of New South Wales
[6] Australian Tropical Herbarium, James Cook University
[7] Australian National University
[8] The Australian Museum
[9] Macquarie University
[10] Griffith University
Contact: carlos.gonzalez-orozco@canberra.edu.au

The consequences of climate change on species distributions have been shown to be overwhelmingly negative. By contrast, little is known about how climate change can alter the spatial distribution of phylogenetic diversity and endemism. Here we show that climate change re-distributes phylogenetic diversity and phylogenetic endemism using the eucalypts, the most dominant native forest plant group across the Australian continent. These effects can potentially cause shifts of branches over landscapes affecting concentrations of unique evolutionary heritage in important global hotspots such as south-west Australia. Even more critically, we found that climate change will cause loss of areas of paleo-endemism. Further work is needed to understand how climate change affects evolutionary heritage and allow effective conservation planning under future climate change.

2.5 Determining the evolutionary impact of biogeographic characters under climate change using simulation studies

Corinne Myers[1], Huijie Qiao[2], Erin Saupe[3], A. Townsend Peterson[4], Jorge Soberon[4]
[1] Dept. of Organismic & Evolutionary Biology, Harvard University
[2] Inst. of Zoology, Chinese Academy of Sciences
[3] Dept. of Geology and Geophysics, Yale University
[4] Dept. of Ecology and Evolutionary Biology and Biodiversity Institute, University of Kansas
Contact: cmyers@fas.harvard.edu

Abiotic niche and dispersal constraints are important biogeographic characteristics impacting evolution. We applied simulation studies to isolate the evolutionary impact and feedbacks between these characters and climate change. We tested whether: 1) species with narrow niche breadths have higher speciation and extinction rates; 2) species with large dispersal ability have reduced rates; and 3) faster climate change reduces rates. Niche breadths (defined by temperature and precipitation) were chosen from a diverse group of extant plant taxa with known physiological climate tolerances. Dispersal was defined as maximum search distance, and climate fluctuated between warm (mid-Holocene) and cold (LGM) conditions in Eurasia. Rate and periodicity of climate change were varied to produce fast, medium, and slow scenarios. Speciation and extinction was counted in virtual phylogenies. Results suggest dispersal as a primary control on evolution: narrowly dispersing taxa show elevated rates of speciation and extinction under all climate scenarios. Among strong dispersers, niche breadth has a secondary impact, where speciation and extinction are damped in taxa with large niche breadths.

Keywords: niche breadth, dispersal, climate change, speciation, extinction, simulation

2.6 Global patterns and attributions of non-analogous climate for terrestrial plants in the past and future

Xiaojun Kou[1], Qin Li[2], Carl Beierkuhnlein[3], Shirong Liu[4]
[1] College of Life Sciences, Beijing Normal University
[2] Department of Botany, University of British Columbia
[3] Department of Biogeography, BayCEER, University of Bayreuth
[4] Institute of Forest Environment and Ecology, Chinese Academy of Forestry
Contact: xj_kou@bnu.edu.cn

Non-analogous climate (NAC) plays a preeminent role in ecology, biogeography and conservation. However, quantitative analyses from organisms' perspective are scarce. Here we present a global overview of NACs of essential bioclimatic factors for terrestrial plants in the past and future. We identified major patterns of NAC based on a novel method (probability density function based). Then we calculated the relative contributions of thermal and hydraulic factors. Three time periods (21kBP, 6kBP, and 2100AD) were analyzed based on data derived from seven general circulation models (GCMs). The consistency in localities of NACs among GCMs was also estimated. Results show that: there are 50.5% of global land areas experience NAC in at least one time period (34.4% by thermal factor and 24.0% by hydraulic one). More NAC will occur in the future than occurred in the past. Thermal NACs highly concentrate in tropical areas in the future, while have been aggregated in high latitudes in 21kBP. The consistency of NACs is significantly higher for thermal factors than for hydraulic factors, and higher in the future than in the past. These findings in NAC patterns may have broad implications.

Keywords: Non-analogous climate (NAC) Bioclimatic factors General circulation model (GCM) Global pattern Attribution Terrestrial plants.

2.7 Including ecological constraints of pathogen and vector in modelling vector-borne diseases: Risk assessment for *Aedes albopictus* and Dengue

Anja Jaeschke[1], Stephanie Thomas[1], Nils Tjaden[1], Carl Beierkuhnlein[1]
[1] Department of Biogeography, BayCEER, University of Bayreuth
Contact: anja.jaeschke@uni-bayreuth.de

Current developments in the global spread of mosquitoes as vectors of pathogens emphasize the importance and urgency of well-informed projections concerning the expectable future development. To identify current and future areas at risk of diseases the combination of ecological knowledge and statistical species distribution models is required. We developed global current and future risk maps for *Aedes albopictus* – vector for Dengue – with special focus on the cold tolerance of the vector and the extrinsic incubation period (EIP) of the pathogen. Modelling was performed with R and the implemented package biomod2, which allows the use of an ensemble of different modelling algorithms. The distribution of *Ae. albopictus* is projected to increase with the statistical model. However, temperature-induced reproductive constraints as well as the temperature-dependence of the virus amplification affect the projected increase. We illustrate that assessing the risk of a spread of diseases requires the combination of projections for vector and pathogen as well as the inclusion of ecological constraints to yield a more realistic estimation.

2.8 From climate change to ecosystem response: cross-scale interaction and the chain of uncertainties

Antonello Provenzale[1], Elisa Palazzi[1]
[1] Institute of Atmospheric Sciences and Climate, National Research Council of Italy
Contact: antonello.provenzale@cnr.it

Global change is expected to affect ecosystem functioning and species distribution, with potential loss of ecosystem services. In order to develop appropriate adaptation and management strategies, it is important to obtain estimates of the expected ecosystem changes generated by climate and environmental variations. This goal, however, can be made difficult by the wide spectrum of interacting spatial and temporal scales active in climate and ecosystem dynamics. To complicate the picture, significant uncertainties affect climate projections at regional scale and propagate through the modelling chain, disturbing the assessment of ecosystem response. These two aspects lead to the general problem of estimating ecological processes in different global change scenarios under uncertain conditions. Here we discuss (1) the issue of cross-scale interactions and scale mismatch between climate projections and ecosystem response, and the associated downscaling/ upscaling techniques developed to cope with it; and (2) some of the most evident sources of uncertainty in the estimate of ecosystem and species dynamics response.

Keywords: Impacts of climate change Cross-scale interactions Future ecosystem projections

Contributed talks 3: Gradients, range limits, and beta diversity
Convener: Carl Beierkuhnlein

3.1 β-diversity is like a Siren's song: Conceptually beautiful but operationally deadly

Jonathan M. Chase[1]
[1] German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig Germany / Department of Computer Science, Martin Luther University Halle-Wittenberg, Halle Germany
Contact: jonathan.chase@idiv.de

In the 1960's, R.H. Whittaker conceptualized b -diversity to quantify diversity differences among local communities. Use of the concept has skyrocketed with the recognition of the key role of spatial process and pattern, and has been extended to include temporal b-diversity, functional b-diversity, and phylogenetic b-diversity. Unfortunately, the b-diversity concept has a largely unrecognized but fundamental flaw that even 'true' diversity conversions cannot fix. b -diversity is a linear approximation of an inherently non-linear scaling function, rendering comparisons of b-diversity across taxa, scales and biogeographic regions confounded by sampling grain and extent. I illustrate this using numerical simulations and real data from ponds and grasslands, as well as from draught beer diversity comparisons among German and the U.S. pubs. I advocate a less ambiguous approach that disentangles the degree to which intraspecific clumping contributes to biodiversity scaling. I show how this captures the essence of Whittaker's intended b-diversity concept, while explicitly eliminating the ambiguities that have plagued estimates and comparisons of b-diversity in practice.

3.2 Putting evolutionary history on the map: finding the unique phylogenetic contribution to spatial patterns of biodiversity

David Nipperess[1]
[1] Department of Biological Sciences, Macquarie University
Contact: david.nipperess@mq.edu.au

Phylogenetic measures of biodiversity have become increasingly popular in biogeography and ecology in recent years. In particular, Phylogenetic Diversity (PD) has been widely used, and has become the basis for a whole class of biodiversity measures derived from the simple premise that diversity can be represented as the sum of branch lengths on a phylogenetic tree. However, PD has a strong monotonic relationship with species richness, meaning that maps showing the spatial distribution of PD may simply be reflecting patterns of species richness. To determine the unique contribution of phylogeny to spatial patterns of diversity, it is necessary to correct for this relationship. I propose using the recently derived formula for rarefaction of PD as the basis for finding this unique contribution. By modelling the exact relationship between species richness and PD, it is possible to standardise all spatial units to a common standard or derive a simple measure (phylogenetic dispersion) directly from the initial slope of the rarefaction curve. I demonstrate the application of this methodology to exploring and explaining continental-scale patterns of diversity for Australian vertebrates.

Keywords: Phylogenetic Diversity Rarefaction Phylogenetic Dispersion Spatial Analysis Biodiversity

3.3 Which spatial patterns of species diversity overthrow Diamond's reserve-design rules? – Predicting outcomes of the SLOSS question by combining species-area curves at landscape and geographic scales

Even Tjørve[1]
[1] Lillehammer University College
Contact: even.tjorve@hil.no

The rules of reserve design, given by Jarred Diamond already in 1975, were born out of the MacArthur and Wilson's equilibrium theory and the species-area relationship (SAR). The discussions following, bridging ecology and biogeography into conservation biology, soon derived into the Single Large or Several Small (SLOSS) debate. Despite huge efforts and a tremendous literature, it soon became evident that there was no simple answer to the SLOSS

question. Yet, no systematic approach followed. Neither the equilibrium theory nor SARs were seen unsuited to resolve the issue. Not so, because by combining two or more SARs, I get models that will generate principles for how various spatial patterns of species diversity affect reserve-design rules and the SLOSS question. Model predictions drivers are species overlap between areas (as realised by β-diversity, nestedness, co-occurrence, and turnover), abundance or occupancy distribution, spatial aggregation of individuals, isolation, and at fine scales minimum areas. The principles generated serve as extensions to Diamond's reserve-design rules, with important implications for conservational strategies at both landscape and geographic scales.

Keywords: Keywords: conservation biogeography, reserve-design rules, SLOSS, species-area relationship

3.4 A novel null biogeographical model to study ecological speciation

Laura Nunes[1], Richard Pearson[1]
[1] Centre for Biodiversity and Environment Research, Department of Genetics, Evolution and Environment, University College London
Contact: laura.nunes.13@ucl.ac.uk

Niche conservatism is the retention of niche-related ecological traits between closely related species. Niche conservatism is often expected among allopatric pairs of closely related species, but niches would not be conserved if speciation occurred due to ecological divergence. We begin by outlining some limitations of current methods for quantifying niche conservatism. Next, we describe a proposed new technique for testing multidimensional niche similarity between species pairs, and a novel null bio-geographical model for testing the significance of the observed similarity. Finally, we test the performance of this approach using case scenarios concerned with ecological speciation among closely related species that have current parapatric or allopatric distributions. The findings often agree with the expected types of ecological speciation both theoretically or explicitly tested using other techniques. This new approach holds potential for testing associations between speciation mechanisms and ecological niche conservatism when applied to large phylogenies.

Keywords: evolutionary biogeography ecological speciation phylogenetic niche conservatism species distribution modelling

3.5 Biogeography is the major determinant of plant diversity in European forests

Alessandro Chiarucci[1], Giandiego Campetella[2], Stefano Chelli[2], Daniele Giorgini[3], Sara Landi[3], Roberto Canullo[2]
[1] Department of Biological, Geological and Environmental Sciences, University of Bologna, Italy
[2] School of Biosciences and Veterinary Medicine, University of Camerino
[3] Department of Life Sciences, University of Siena, Italy
Contact: alessandro.chiarucci@unibo.it

Europe forests are the result of biogeography, ecology and human transformation. This study compares the effects of biogeography and ecology to determine the plant diversity of European forests using a representative sample of 3100 plots all over Europe (BIOSOIL project). The general aim is to compare the effects of ecology and management with respect to biogeography. Total plant diversity was divided into different spatial components: plot, site, forest type (a proxy for ecological factors) and biogeographical region. Three hypotheses were tested: H1: The diversity accounted by the biogeographical region is higher that the diversity accounted by the lower scale components; H2: Beta nestedness is higher within than across biogeographical regions, while Beta complementarity is lower within than across biogeographical regions (after correction for extent). H3: Distance decay rate across biogeographical regions is higher than distance decay rate within biogeographical regions (after correction for extent). The results are used to understand how the different factors contribute to determine the forest plant diversity patterns and to get indication for future forest management.

Keywords: forests, Europe, species richness, species diversity, biogeography

3.6 Unifying species pools in ecology and biogeography

Dirk N. Karger[1], Anna F. Cord[2], Michael Kessler[3], Holger Kreft[4], Ingolf Kühn[5], Sven Pompe[2], Brody Sandel[6], Juliano Sarmento Cabral[4], Adam B. Smith[7], Jens-Christian Svenning[6], Hanna Tuomisto[1], Patrick Weigelt[4], Karsten Wesche[8]
[1] University of Turku
[2] Helmholtz Centre for Environmental Research – UFZ
[3] University of Zurich
[4] University of Goettingen
[5] German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
[6] University of Aarhus
[7] Missouri Botanical Garden
[8] Senckenberg Museum of Natural History Görlitz
Contact: dirk.karger@utu.fi

Species pools are central to many questions in biogeography. They however, require hard decisions on which species belong to the pool and which do not, resulting in often binary, arbitrary, and non-replicable outcomes. We propose to amend such concepts with a probabilistic framework that retains information about the mechanistic links between species pools and local communities. We illustrate how such pools can be calculated, and how different delineations affect inferences which can be derived from the species pool. We show that probabilities are consistent with actual events, present species pools using different dispersal and environmental constraints, and compare how different delineations affect species pool size, as well as compositional similarity between species pools and realized occurrences of species. We argue that the application of such probabilistic species pools results in biologically meaningful patterns and can be used as a valuable tool in biogeography, as it provides more nuances than previous concepts, and considers species membership in a pool as a continuous variable that takes into account relevant biological processes.

Keywords: species pools, biogeography, probabilistic concepts, community assembly, community composition, biogeographic tools

3.7 How are regional species pools used in community ecology?

Howard Cornell[1]
[1] Environmental Science and Policy, University of California, Davis
Contact: hvcornell@ucdavis.edu

A regional species pool comprises all species available to colonize a focal site. The pool concept allows ecologists to examine large-scale effects---including geographic area, evolutionary age, and immigration and diversification---on the diversity, composition, and phylogenetic structure of local communities. Both theory and evidence show that pool influences are greatest when local communities are not strongly and predictably structured by species interactions (e.g., under frequent disturbance or if many species are rare). Practical and conceptual issues to consider when delineating species pools include choosing an appropriate spatial scale, whether to account for environmental filtering, whether to include the species within a fixed geographic area versus those whose geographic ranges overlap with a site, or whether to use databases or geographic data sources. Each issue is discussed in the context of 63 studies using the species pool approach. Future studies must compare pool characteristics with community structure across multiple regions for a more complete understanding of community assembly.

Keywords: community assembly, environmental filtering, local diversity, phylogeny, regional diversity, species interactions

3.8 Principal factors controlling biodiversity: water, energy and their interaction

Ole R. Vetaas[1], Morten Christensen[2], Keshav P. Paudel[1]
[1] Department of Geography, University of Bergen
[2] Morten Christensen Consult
Contact: ole.vetaas@global.uib.no

Broad-scale variation in diversity is a well-documented spatial pattern in biogeography, but a mechanistic climate-based theory of diversity is lacking. Several energy-related theories infer similar diversity patterns, but two theories predict contrasting patterns: the Metabolic Theory of Ecology (MTE) links environmental energy to the metabolic rate of organisms, which may cause a log-linear increase in diversity of ectotherm taxa; and Water Energy Dynamics (WED) links energy to the control of available liquid water and predicts a nonlinear (parabolic) response to energy. These two models were evaluated using Akaike Information Criteria (AIC) on eleven broadly defined ectotherm taxa within animals, plants, and fungi. Diversity was based on range overlap along the central Himalayan elevation-gradient. All taxa have nonlinear relationships with energy, except fish. WED performed best, and is superior for 6 taxa, and for 7 taxa when diversity was invariant to net primary production. Including length of growing season in the model improves AIC for 8 taxa. WED incorporates water limitation caused by high and low energy at a macro-scale; hence WED is better and more general than MTE.

Keywords: Metabolic theory for ecology, Water–energy dynamics, Elevation–temperature, Gradient, Net primary production, Length of growing season, Himalayas

Contributed talks 4: Historical and paleo-biogeography
Convener: Corinne Myers

4.1 Cenozoic palaeofloristic regionalization – dispersal barriers rather than global climates as drivers of global regionalization

Hans Peter Linder[1], Yaowu Xing[1]
[1] Systematic Botany, University of Zurich
Contact: peter.linder@systbot.uzh.ch

We reconstructed the global phytogeographical patterns for each epoch in the Cenozoic, using the largest occurrence angiosperm fossil database assembled to date. Patterns of similarity between the continents and epochs were calculated based on shared families and shared genera. Consistent with the hypothesis that the regionalization of the angiosperm flora dates to the Cretaceous, we found no increase in the divergence among the continental floras during the Cenozoic. The global patterns are consistent with the hypothesis that the regionalization reflects barriers to dispersal. The deepest division is linked to the Tethys, separating the Northern and Southern Hemisphere floras. Within the Northern Hemisphere, we detect the impact of the Turgai Sea and its final Oligocene closure in the shifting similarities between the North American, Asian and European floras. The Southern Hemisphere floras are, consistent with the age and size of the southern oceans, much less closely related than the Nothern Hemisphere flora. Two regions can be detected: and Afro-Indian flora, and a Gondwanan flora.

Keywords: Cenozoic Floristic Kingdoms Dispersal Fossil angiosperm flora global regionalization

4.2 Born in the mountains: dominance of geological processes in the diversification of bush frogs in the Western Ghats Escarpment

S P Vijayakumar[1], Shanker Kartik[2]
[1] National Centre for Biological Sciences
[2] Indian Institute of Science
Contact: vijay_rhaco@yahoo.com

The historical processes behind high diversity in tropical biodiversity hotspots like the Western Ghats of Peninsular India remain poorly understood. Using a large clade of bush frogs, we tested the relative importance of Quaternary glaciations, ecological gradients and geological processes on the spatial patterns of lineage and sub-cladal diversification in a mountain setting. Our analyses reveal that a majority of recently diverged bush frog sister - lineages were characterized by non-overlapping geographical ranges, and were isolated on adjacent massifs, suggesting allopatric speciation events. Ancestral reconstruction of the elevation supported an independent highland origin among the bush frog sister clades. Independent transitions along elevational gradients among sub-clades during the Miocene lend support for diversification mediated by the uplift of the escarpment. In-situ diversification in the montane zone of the two highest massifs shows the effect of past-climate mediated forest-grassland dynamics, but divergence times lend less support for the role of Quaternary glaciations.

Keywords: Non-adaptive radiation, ecological gradients, Quaternary glaciations, allopatric speciation

4.3 Bayesian stochastic mapping for estimating biogeographic history on phylogenies

Nicholas Matzke[1]
[1] NIMBioS, Univ. of Tennessee
Contact: matzke@nimbios.org

Traditional likelihood methods in historical biogeography estimate the probability of each geographic range at each node. Usually the most-probable range at each node is plotted, and this is taken to be the approximate history. This is not technically accurate and might be badly misleading in some cases. A solution is stochastic mapping of possible histories on the phylogeny. This has been widely applied in phylogenetics for sequence data and discrete characters, but these character models are inappropriate in historical biogeography, where the state space is much more complex, and geographic range changes through both anagenetic and cladogenetic events. I present a novel algorithm that enables stochastic mapping on any biogeographic model available in BioGeoBEARS, as well as graphical display and statistical summary of the timing and frequency of dispersal and vicariance events. An animation of realizations of possible histories under the DEC and DEC+J models is demonstrated for Hawaiian Psychotria shrubs. R functions and

an example script performing stochastic mapping are available at http://phylo.wikidot.com/biogeobears. The functions build upon on the R package BioGeoBEARS, available for all platforms at CRAN.

Keywords: BioGeoBEARS, historical biogeography, biogeographical stochastic mapping, ancestral state inference

4.4 Historical-biogeographical and evolutionary hypotheses for diversity-environment correlations among microbes

Jason Pither[1]
[1] Biology, University of British Columbia
Contact: jason.pither@ubc.ca

Correlations between microbial diversity and pH are common, but their ultimate origins remain unclear. Evolutionary and historical-biogeographical hypotheses have shed new light on correlative biodiversity patterns among macroorganisms, but have rarely been applied to microorganisms. Here I consider freshwater diatom diversity and niche patterns along the pH gradient from a historical/evolutionary perspective. Acidic surface waters have been rare and unstable through evolutionary time, especially when compared to the alkaline surface waters of the ocean (the putative ancestral habitat of the diatoms), which have remained above pH 7.8 since the Mesozoic. These observations yield several testable predictions, including a decline in generic diversity from alkaline to acidic conditions, and a concomitant increase in pH niche breadth. I document empirical support for these predictions using regional and global datasets, and highlight some key implications my findings have for the use of diatoms in paleo-environmental research.

Keywords: niche evolution, historical biogeography, pH tolerance, diatoms, paleolimnology

4.5 Late Cenozoic climate change and the phylogenetic structure of conifer assemblages worldwide

Jens-Christian Svenning[1], Wolf L. Eiserhardt[2], Finn Borchsenius[3], Brody Sandel[1], W. Daniel Kissling[4], Alejandro Ordonez[1]
[1] Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University
[2] Royal Botanic Gardens, Kew
[3] Science Museums, Aarhus University
[4] Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam
Contact: svenning@biology.au.dk

Forests have been dramatically impacted by the cooling and drying trends over the last 30 million years. It is, however, poorly understood if and how current tree assemblages are shaped by these long-term climate changes. Using conifers as a model system, we combine data on current species distribution and past extinctions with a time-calibrated phylogeny and spatial climate data from different geological epochs to test if paleoclimate shapes phylogenetic assemblage structure. Current and past climate show similar relationships to conifer phylogenetic Net Relatedness Index (NRI) worldwide, suggesting that relations to current climate may reflect deep-time processes. Beyond these relations, conifer NRI is also related to Quaternary climate oscillations and gradual late-Neogene climate trends. Furthermore, known late-Neogene extinctions have had major impacts on conifer NRI. Present-day conifer phylogenetic assemblages patterns are strongly shaped by the dynamic Cenozoic climate, with effects linked to climate-driven extinctions as well as adaptive radiation into the expanding dry environments.

Keywords: climate change paleoecology community phylogenetic structure plant diversity extinction

4.6 The red island and the seven dwarfs: body size reduction in Cheirogaleidae

Judith Masters[1], Fabien Genin[1], Adrian Lister[2], Daniele Silvestro[3], Massimiliano DelPero[4]
[1] African Primate Initiative for Ecology & Speciation, University of Fort Hare, Alice, South Africa
[2] Earth Sciences Department, Natural History Museum, London, UK
[3] Department of Plant and Environmental Sciences, University of Gothenburg, Sweden
[4] Dipartimento di Scienze della Vita e Biologia dei Sistemi, Universita degli Studi di Torino, Torino, Italy
Contact: jdthmasters@gmail.com

Madagascar’s dwarf and mouse lemurs (Cheirogaleidae) are often viewed as model primate ancestors or 'basal primates'. We investigated body size evolution in this family and in its sister-taxon, the Lepilemuridae, from phylogenetic, ontogenetic and adaptive perspectives. Our results indicated that small body size is derived in this clade: cheirogaleids experienced at least four dwarfing events from an ancestor as large as living Lepilemuridae, probably by means of progenesis. Our interpretation is supported by the paedomorphic appearance and parallel ontogenetic trajectories of the dwarf taxa, as well as their very short gestation periods and increased fecundity. Dwarfing is likely to have been a response to Madagascar's high environmental unpredictability. Although the capacity to use hypothermy is related to small body size, this advantage is unlikely to have driven cheirogaleid body size reduction. Gummmivory/exudativory co-evolved with dwarfism in this clade, probably from a folivorous ancestral state. The evolution of small body size in cheirogaleids occurred under very different environmental conditions from those that witnessed the emergence of ancient primates, questioning their suitability as model ancestral primates.

Keywords: Ancestor reconstruction, body size evolution, dwarfism, hypervariability, island rule, lemurs, Lepilemuridae, Madagascar, ontogeny, progenesis.

4.7 No longer relying just on oldest fossils forced to specific nodes: The fossilized birth-death process illustrated in the worldwide fern family Osmundaceae

Susanne Renner[1], Guido Grimm
[1] Systematic Botany and Mycology, University of Munich
Contact: renner@lmu.de

For the past 50 years, molecular clocks have usually been calibrated with “oldest” fossils applied to one or more deep nodes in a tree. The FBD approach of T. Heath, J. Huelsenbeck, and T. Stadler (PNAS 2014) finally permits using all of a group’s fossils without having to force them to specific nodes. We applied the new method in the fern family Osmundaceae, which has more fossils than living species. The 11 extant species in four genera in the Northern Hemisphere, South Africa, and Australasia have a fossil record of ~150 species in ~17 genera and three families. In the FBD approach, many fossils can be assigned to the same clade regardless of their age. For comparison, we also used just the five oldest fossils for standard node dating in BEAST as well as Bayesian total evidence dating in MrBayes. Subsamples of 10%, 25%, and 50% of the fossils were used to assess model sensitivity. The new approach yielded older ages than BEAST for the deep nodes, and it also inferred a root age older than the oldest fossil. The inferred speciation and extinction rates, however, were similar to rates inferred with TreePar (Stadler PNAS 2011).

4.8 Establishing a paleobiogeographic framework for European Neogene freshwater systems

Thomas A. Neubauer[1], Mathias Harzhauser[1], Andreas Kroh[1], Elisavet Georgopoulou[1], Oleg Mandic[1]
[1] Geological-Paleontological Department, Natural History Museum Vienna
Contact: thomas.neubauer@nhm-wien.ac.at

Here we present the very first outline of a paleobiogeographic framework for European Neogene freshwater systems, based on the distribution records of 2,226 species-group taxa of freshwater gastropods from over 2,700 Miocene and Pliocene localities, grouped into paleo-freshwater systems. Cluster analyses were performed on separate datasets for the Early Miocene, Middle Miocene, Late Miocene, and Pliocene. The generally high degree of provincialism for the Neogene freshwater systems promoted the distinction of biogeographic units. The delimitations are based on the results of the cluster analyses, the degree of endemicity, and geographical coherence. One key factor for the presented proposition of the biogeographic units and faunal differences in general is the varied existence of large, long-lived systems. Because of their prolonged duration they immensely influenced the community composition on the family level, differences of the relative species richnesses per biogeographic region, and the rising rate of endemicity. This pattern is reflected in the continuing continentalization of Europe triggered by the Alpidic Orogenesis and the simultaneous retreat of the Paratethys Sea.

Keywords: Palaeobiogeography; Biogeographic regions; Endemism; Biodiversity; Freshwater gastropods; Miocene; Pliocene

CT5 Conservation biogeography

Contributed talks 5: Conservation biogeography
Convener: Jan Axmacher

5.1 Spatial insurance of fish functional diversity across coral reefs

Sebastien Villeger[1], Valeriano Parravicini[2], David Mouillot[3]
[1] ECOSYM, Centre National de la Recherche Scientifique (CNRS)
[2] CRIOBE, Ecole Pratique des Hautes Etudes, Perpignan
[3] ECOSYM, Université Montpellier 2
Contact: sebastien.villeger@univ-montp2.fr

Coral reef fishes are very diverse with more than 6500 fish species but some of their functions were shown to be highly vulnerable since supported by few species within assemblages. To insure the long-term persistence of the whole set of functions performed by fish on coral reefs, the level of functional beta-diversity across space is pivotal since it determines whether close faunas are able to provide, by dispersal, species performing the functions that would experience local decline. Using a worldwide database of coral reef fish occurrences and a database of their functional traits, we assessed two complementary indices of spatial insurance, functional dissimilarity and functional turnover across fish assemblages. These indices were also computed considering only the vulnerable functional entities (i.e. combinations of traits values represented by a single species within an assemblage). Functional dissimilarity and turnover were higher in the Atlantic realm than in the Indo-Pacific realm, especially when considering only vulnerable functional entities. These results will complement the taxonomy-based indices considered in conservation planning.

Keywords: functional diversity, fish, coral reefs,

5.2 The interplay of competition and habitat selection determines the colonisation pattern of bird communities in small forest fragments of East Africa

Werner Ulrich[1], Jan Christian Habel[2], Martin Husemann[3], Luc Lens[4], Julia J. Day[5]
[1] Chair of Ecology and Biogeography, Nicolaus Copernicus University
[2] Terrestrial Ecology, Technical University München
[3] Institute of Biology/Zoology, Universität Halle
[4] Department of Biology, Ghent University
[5] Department of Genetics, Evolution and Environment, University College London
Contact: ulrichw@umk.pl

Rapid transformation of large habitat blocks into fragmented and degraded habitat remnants is of major concern in the conservation of global biodiversity. Populations in small and highly isolated habitat patches are prone to demographic stochasticity and local extinction. Based on data from twelve forest remnants of the highly fragmented Taita Hills of SE Kenya, I present the potential effects of interspecific competition, habitat structures, and species´ traits on the assembly of bird communities (17,626 individuals from 75 species). The decline in species richness and abundance with decreasing patch area was less than expected from a neutral model. Fragment quality was a stronger predictor of species richness than fragment area. In 53 species local abundances were negatively correlated with fragment size. Species assemblages were neither significantly segregated nor nested. Competitive interactions were moderate and decreased with fragment size. The results indicate a shift from competition-dominated community structure in larger fragments to colonisation-driven assemblages in smaller ones. Such changes in community structure may stabilise diversity under severe habitat loss.

Keywords: Aves, competitive hierarchies, feeding guild, species associations, species turnover

5.3 Global patterns of agricultural land use intensity and biodiversity

Laura Kehoe[1], Tobias Kuemmerle[1], Cornelius Senf[1], Carsten Meyer[2], Christian Levers[1], Tomáš Václavík[3], Katharina Gerstner[3], Holger Kreft[2]
[1] Geography Department, Humboldt-University Berlin, Germany
[2] Free Floater Research Group Biodiversity, Macroecology & Conservation Biogeography, Georg August-University of Göttingen, Germany
[3] Department of Computational Landscape Ecology, UFZ – Helmholtz Centre for Environmental Research, Germany
Contact: laura.kehoe@geo.hu-berlin.de

Agricultural expansion and intensification are among the main drivers of the ongoing biodiversity crisis. The effects of agricultural expansion have received much attention, but where and how intensification threatens biodiversity remains unclear. We explored the nexus of land use intensity and biodiversity in two ways. First, we overlaid an array of agricultural intensity metrics with endemism richness, a range size-weighted species richness indicator, for mammals, birds and amphibians. We found that individual land-use intensity metrics highlight different regions suggesting that the choice of metric is crucial when considering conservation threat and thus, we recommend that conservation research adopts a multidimensional view when investigating biodiversity threat due to intensification. Second, we developed a species-area model that incorporates the area and intensity of land-use, as well as biomes and species traits for terrestrial mammals. We show that predictions of global species richness are improved by considering spatial variation and species traits. Our research confronts the knowledge gap of how different aspects of land-use intensity relate to biodiversity.

Keywords: Biodiversity conservation, land-use change, global agriculture, sustainable intensification, endemism richness, land-use intensity, species traits, species-area relationships, conservation biogeography,

5.4 How far can they go? Tracking climate across a fragmented landscape using climate corridors

Jenny McGuire[1], Joshua Lawler[2], Brad McRae[3], Tristan Nuñez[4]
[1] School of Biology, Georgia Institute of Technology
[2] School of Environmental & Forest Sciences, University of Washington
[3] The Nature Conservancy
[4] Department of Environmental Science, Policy, & Management, University of California- Berkeley
Contact: jmcguire@gatech.edu

Today's landscape is fragmented by roads, cities and farms. However, within the US, these disturbed areas transect millions of acres of natural habitats where plants and animals thrive. As climate changes, organisms living within these natural patches must move if their climate thresholds are exceeded. We examine to what extent fragmented landscapes prevent organisms living in natural patches from moving across the US. We ask how cool of a temperature an organism living in any given natural patch could reach by moving through adjacent natural patches. Given current levels of fragmentation, organisms living in approximately 70% of natural patches would be unable to move enough to stay at uniform mean annual temperatures over the next 85 years as projected under an ensemble A2 emission scenario. We then examined how well they could track their current temperatures if allowed to move freely. We created a nationwide connectivity map using climate corridor models. The presence of corridors allows organisms in 28% additional natural landscape patches to be able to track their preferred climates. Corridors most facilitate movement in the east and along the periphery of the plains and coasts.

Keywords: Fragmentation, corridors, climate change, climate corridor modelling, conservation biology

5.5 Habitat fragmentation and the species–area relationship

Thomas Matthews[1], Eden Cottee-Jones[1], Robert Whittaker[1]
[1] University of Oxford
Contact: txm676@gmail.com

We present meta-analyses of the form of the species–area relationship (SAR) focussed on a large number of datasets for habitat islands sourced from the literature. We test the fit of alternative models of varying complexity to determine the shape of the SAR, and the frequency of break-points in the relationship. In addition, we demonstrate variations in the parameters of the power model for habitat specialist vs generalist species for a subset of 23 bird-habitat island datasets from across the globe. We evaluate the implications for conservation of these analyses. For example, the results of the latter analysis indicate that studies that have used total richness when using the SAR to predict extinctions may be underestimating the impact of habitat loss on the loss of specialist species, which are likely to be those of greatest conservation concern.

Keywords: Habitat fragmentation Habitat islands Species-area relationship

5.6 Habitat amount determines species' extinction risk threshold

Ricardo Dobrovolski[1], Moreno Di Marco[2], Rafael Loyola[3], Marcel Cardillo[4], José Alexandre Felizola Diniz-Filho[3]
[1] Departamento de Zoologia, Universidade Federal da Bahia
[2] Global Mammal Assessment program, Dept Biology and Biotechnology, Sapienza University of Rome, Italy
[3] Departamento de Ecologia, ICB, Universidade Federal de Goiás, Goiânia, GO, Brasil
[4] Macroevolution and Macroecology Group, Research School of Biology, The Australian National University, Canberra, Australia
Contact: rdobrovolski@gmail.com

Species' extinction risk is determined by intrinsic and extrinsic factors. Among extrinsic factors, habitat destruction is the main threat to biodiversity. Here we combined information on habitat amount and intrinsic extinction risk of terrestrial mammal species to predict their threat status. We calculated the amount of natural habitat by overlaying the species' geographic distribution with a global land cover map. Intrinsic extinction risk was calculated from species' functional traits and phylogenetic information. We found that intrinsic extinction risk was able to predict threatened species with 60% of accuracy. When we included habitat amount information this value was raised up to 100%, following a threshold between 15% and 30%. The value of this threshold is higher for species with higher intrinsic extinction risk. This finding reinforces the effect of habitat destruction as central mechanism extirpating biodiversity in our planet. Also, our approach has a potential application for calculating the extinction risk of data deficient species and for predicting the future dimension of the global biodiversity crisis from scenarios of land cover change.

Keywords: extinction risk, habitat destruction, land cover change

Contributed talks 6: Modelling species and ecosystems
Convener: Francisco Rodriguez-Sánchez

6.1 Modelling the coupled dynamics of large grazers, vegetation and fire across Africa

Thomas Hickler[1], Pachzelt Adrian[1]
[1] Biodiversity and Climate Research Centre, Senckenberg Research Institutes and Natural History Museum
Contact: Thomas.Hickler@senckenberg.de

Large herbivores have been a fundamental component of savannah ecosystems since the Miocene. In spite of their potential importance for ecosystem dynamics, Dynamic Global Vegetation Models (DGVMs) do not include large herbivores. For the first time, we implemented a generalized physiological grazer module within a DGVM (LPJ-GUESS). The coupled model reproduces observed variations in grazer densities across African nature reserves and along environmental gradients. According to the model, grazer densities are mainly constrained by grass Net Primary Productivity (NPP) and the length of the drought season. Continental-scale simulations of the effects of large grazers on biome distribution, vegetation structure, carbon storage and fire dynamics suggest that natural grazers can consume up to 50 percent of grass biomass, but the strongest effects occurred via changes in fuel availability and fire. The simulated biome distribution, however, was similar with and without grazers. We conclude that natural populations of large grazers most probably have had a non-negligible effect on ecosystem structure and functioning in savannahs, but that they have not been shaping them.

Keywords: Africa, large grazers, vegetation dynamics, biome distribution, fire disturbance, carbon storage, dynamic global vegetation model

6.2 New insights on the implementation of the SESAM framework

Manuela D'Amen[1], Anne Dubuis[1], Mirko Di Febbraro[2], Antoine Guisan[3]
[1] Department of Ecology and Evolution, University of Lausanne, Biophore building, 1015 Lausanne, Switzerland
[2] Department of Biosciences and Territory, University of Molise, 86090 Pesche, Italy
[3] Department of Ecology and Evolution, University of Lausanne, Biophore building, 1015 Lausanne, Switzerland; Faculty of Geoscience and the Environment, University of Lausanne, 1015 Lausanne, Switzerland
Contact: manuela.damen@unil.ch

Integrating all parameters potentially affecting community assembly into a single modelling framework might be achieved by combining pre-existing approaches to biodiversity prediction, such as proposed by Guisan and Rahbek (SESAM, spatially explicit species assemblage modeling, 2011). Here we present results obtained from different implementations of the SESAM framework, tested on a variety of case studies (insects, plants, birds in different habitats, scales, and resolutions), applied with the aim of estimating both species richness and composition. Specifically, we explored how to improve the estimation of the macroecological control on the community and the effect of thresholding on the single species' models when reconstructing community composition. Moreover, we test diverse ecological assembly rules to decide which species can enter the community. These rules are based either on probabilities calculated from species distribution models (SDMs), on traits data, or on co-occurrence patterns. We add all these components (macroecological models, species distribution models, and ecological assembly rules) in the SESAM framework to propose novel solutions at community modelling.

6.3 Using phylogeny to improve single species distribution models

Ignacio Morales-Castilla[1], Pedro Peres-Neto[2], Jonathan Davies[2]
[1] Department of Biology, McGill University
[2] Département des sciences biologiques, Université du Québec à Montréal
Contact: ignacio.morales-castilla@mcgill.ca

Models of species distributions have proven valuable for understanding biodiversity gradients and for making predictions of future species' responses to changing environment. Although species distribution models are becoming increasingly sophisticated and can include factors other than climate (i.e. traits, biotic interactions, etc.), they rarely take into consideration the evolutionary relationships among species. Given that evolution occurs within a geographic context, phylogenies should contain at least some signal of the environments under which species evolved. Phylogenies can also serve as a useful surrogate when trait data are missing or hard to obtain. Here we propose a novel quantitative framework that incorporates phylogenetic information into models of both species and community distributions. We first evaluate this framework through simulations and then test its predictions using empirical data on terrestrial carnivores. We suggest that phylogenetic relationships can enhance the performance of species distribution models. Our approach has the potential to reconcile the apparent conflict between current versus historical factors as main drivers of biodiversity patterns.

Keywords: Niche modelling Unmeasured trait Metacommunity phylogenetics Stochastic simulation Community assembly

6.4 Multi-scale models for biogeography

Petr Keil[1], Adam Wilson[2], Hugh Sturrock[3], Bob O'Hara[4], Walter Jetz[2]
[1] Charles University in Prague
[2] Yale University
[3] University of California, San Francisco
[4] Biodiversity and Climate Research Centre
Contact: pkeil@seznam.cz

During the last four years we have developed a new class of statistical models for biogeographical data; these models operate at multiple spatial scales (grains, resolutions) simultaneously. The models were successfully used to map species distributions, species richness and risk of a disease infection, and have been especially useful for downscaling purposes, i. e. for predicting high-resolution maps based on coarse-resolution data only. The building blocks of these models are variants of generalized linear and generalized additive models (e. g. binomial or Poisson regression), with spatial scaling relationships linking these building blocks across grains. I will go through the basic idea of the multi-scale models, I will summarize the potential advantages and pitfalls of using such models in mapping of biodiversity and species distributions, and I will outline potentially fruitful directions for future improvements, such as integration of our models with point process models, and with the concepts of geostatistics.

Keywords: downscaling, species distribution models, beta diversity, epidemiology, species richness

6.5 From geographical distributions to ecological niches and back

Babak Naimi[1], Thomas Groen[2], Nicholas Hamm[2], Andrew Skidmore[2], Miguel Araújo[1]
[1] Department of Life Science, Imperial College London
[2] Natural Resources, University of Twente
Contact: b.naimi@utwente.nl

Appeals to have robust species distribution models (SDMs) led to the developing of many models in the direction of more complicated approaches. Several studies compared the performance of SDMs in order to identify the best method(s) but usually count on a global measure (*i.e.*, a single summary statistic for the entire area) to understand how well a model performs. Relying on a single statistic to assess model performance may lead to misleading conclusions, and would not be enough to understand the behaviour of a model. Moreover, the model-based uncertainty is also important but cannot be determined by the accuracy measures. In this study, we simulated a series of synthetic data (10 species) and compared 12 SDMs together with ensemble approaches using a comprehensive set of evaluation tools that assess the models' behaviours globally and locally (at pixel level) in both geographic and niche space of species distribution. The results provide a base of knowledge on SDMs' performance and indicate that the ensemble-based model (even when presence-only data are available) strongly outperforms the other models either when accuracy or uncertainty in the predictions is a matter.

Keywords: species distribution modelling, ecological niches, evaluation, uncertainty

6.6 Benchmarking range dynamic models with virtual community data

Damaris Zurell[1], Signe Normand[2], Wilfried Thuiller[3], Tamara Münkemüller[3], Jörn Pagel[4], Juliano Cabral[5], Stefan Dullinger[6], Dominique Gravel[7], Katja Schiffers[8], Frank Schurr[4], Kara Moore[9], Cory Merow[10], Peter Pearman[11], Boris Schröder[12], Justin Travis[13], Raphael Wüest[3], Niklaus E. Zimmermann[1]
[1] Landscape Dynamics, Swiss Federal Research Institute WSL, Switzerland
[2] Aarhus University, Denmark
[3] LECA, Univ. Grenoble, France
[4] Univ. Hohenheim, Germany
[5] Univ. Göttingen, Germany
[6] Univ. Vienna, Austria
[7] Univ. Québec, Canada
[8] BiK-F, Germany
[9] Univ. California, USA
[10] Smithsonian Environmental Research Center, USA
[11] UPV/EHU Bilbao, Spain
[12] Univ. Braunschweig, Germany
[13] Univ. Aberdeen, UK
Contact: damaris.zurell@wsl.ch

Statistical species distribution models (SDM) are increasingly used to predict species response to environmental change, but essentially ignore demography and dispersal mediated transient dynamics. Several approaches of varying model complexity have been suggested to overcome these shortcomings, for example by coupling SDM output with dispersal kernels or with dynamic population models. Others completely avoid using SDMs and suggest to jointly estimate the environmental response of demographic rates, population dynamics and dispersal within a Bayesian framework. Here, we constructed an individual-based virtual community model for benchmarking these model types under controlled conditions. We test the effect of demographic processes (dispersal, source-sink dynamics) on model predictive performance, and complicating effects of biotic interactions assuming different community processes (species sorting , neutral dynamics). These scenarios result in distinct abundance patterns and climate-induced range dynamics. We discuss the relative strengths and weaknesses of the different model types and derive preliminary guidelines regarding necessary model complexity.

Keywords: virtual ecologist approach, range dynamics, climate change, forecasting, demography

Contributed talks 7: Phylogeography
Convener: Anna Papadopoulou

7.1 The poleward range expansion of European populations of the wasp spider *Argiope bruennichi* is associated with a recent genome-wide admixture of Eastern and Western Palearctic glacial lineages

Henrik Krehenwinkel[1], Maxene Graze[2], Gabriele Uhl[2], Diethard Tautz[1]
[1] Evolutionary Genetics, Max Planck Institute for Evolutionary Biology
[2] General and Systematic Zoology, University of Greifswald
Contact: krehenwinkel@evolbio.mpg.de

Poleward range expansions are commonly attributed to global change. However, recent research indicates that they might be facilitated by adaptation. An example is provided by *Argiope bruennichi*, a widely distributed Palearctic spider, which greatly expanded its European range in the past decades. The colonization of habitats in Northern Europe was apparently enabled by a climatic niche shift. In order to unravel the genetic origin of expansive spiders, we sequenced genomes of populations throughout the species' range. Our analysis identifies three genetic lineages in the Palearctic, an East Asian, a European and an Azorean. The Asian and European clades form a contact zone in Central Asia, from where Asian genetic variation enters the European genepool. An analysis of historical DNA indicates that this secondary contact is less than 100 years old. Interestingly, we find considerable introgression in the newly colonized invaded habitat of the species in Northern Europe, while introgression is barely affecting native populations. We speculate that an admixture of glacial lineages might have provided the variation for a rapid genetic and evolutionary divergence of spider populations.

Keywords: Phylogeography, Palearctic, range expansion, hybridization, adaptation, historical DNA, whole genome sequencing

7.2 Insights from the past into biodiversity responses to future climate change using bats as a model

Orly Razgour[1], Antton Alberdi[2], Irene Salicini[3], Ettore Randi[4], Carlos Ibanez[3], Javier Juste[3]
[1] Biological & Environmental Sciences, University of Stirling
[2] Department of Zoology and Animal Cell Biology, University of the Basque Country
[3] Estación Biológica de Doñana (CSIC)
[4] Laboratorio di Genetica, Istituto Superiore per la Protezione e Ricerca Ambientale
Contact: Orly.Razgour@gmail.com

A key challenge this century is to understand how biodiversity responds to global change so we can predict the effects of major conservation threats, like climate change. Understanding past responses to Quaternary climatic fluctuations and extent of niche conservatism in climatic tolerance can help predict future consequences. We combined predictive modelling with genetic data (microsatellites, mitochondrial DNA genes and whole genomes) and Approximate Bayesian Computation inference to study the genetic consequences of past and future climate changes on bats with different distributions and ecological requirements. We reveal how past climates shaped the evolutionary history of both endemic and widespread species, and show that geographical variations in Pleistocene climates and intensity of vicariance events produced different evolutionary histories between and within species. Evidence of niche conservatism, predicted shifts in suitable areas and barriers to migration suggest that future climate change may result in high losses of genetic diversity, especially as it threatens former glacial refugia. We address the role of climate versus habitat loss in population declines.

Keywords: Global Change, Species Distribution Modelling, Approximate Bayesian Computation, Molecular Ecology, Evolutionary History, Niche Conservatism

7.3 UCE-primed sequence capture and the resolution of shallow divergences in cryptic species complexes: empirical applications in gecko and monitor lizard radiations in a Southeast Asian island archipelago

Rafe Brown[1]
[1] Biodiversity Institute, University of Kansas
Contact: rafe@ku.edu

We investigated the utility of the ultraconserved elements (UCE) strategy of sequence capture for the resolution of shallow, phylogeographic relationships in closely related island lineages. Philippine gecko and monitor lizard radiations have both been the subject of numerous systematic studies aimed at resolving phylogenetic relationships and species boundaries. Approaches using traditional morphological characters, cytogenetics, and Sanger sequence datasets have produced conflicting results and have not yet resolved species boundaries within either group. We took a genomic approach and targeted ultraconserved elements, yielding datasets of 1,700–4,000 gene loci, with robust phylogeographic sampling from throughout the archipelago. Our results demonstrate similarities to conventional sequencing methods but also include notable differences with respect to branching pattern, numbers of putative taxa delimited, and the interpretation of population affinities near biogeographic turn-over zones. In this talk, we will discuss approaches to analysis of new phylogenomic datasets for understanding processes of diversification of land vertebrates in island archipelago systems.

Keywords: genomics, phylogeography, island archipelagos, diversification, cryptic species complexes

7.4 Molecular phylogeny and biogeography of Philippine *Ixora* L. (Rubiaceae)

Cecilia Banag[1], Arnaud Mouly[2], Grecebio Jonathan Alejandro[3], Ulrich Meve[4], Sigrid Liede-Schumann[4]
[1] Department of Biological Sciences, College of Science, University of Santo Tomas, Philippines
[2] UMR 6249 Chrono-environnement, University of Franche-Comté - CNRS, France
[3] Research Center for the Natural and Applied Sciences, University of Santo Tomas, Philippines
[4] Department of Plant Systematics, University of Bayreuth, Germany
Contact: ceciliabanag@gmail.com

The Philippine archipelago has emerged as one of the globally important model island archipelagoes for studying evolutionary processes of diversification. However, previous molecular studies on the pantropical genus *Ixora* have failed to include representative species from the Philippines due to lack of available genetic samples. Hence, the first molecular study on Philippine *Ixora* is here presented. Two chloroplast markers (rps16 and trnT–F) and two nuclear markers (ITS and ETS) were used, totalling in 4309 base pairs. The Philippine *Ixora* was found to be polyphyletic, with representatives from at least three independent lineages. In both the parsimony and Bayesian analyses, two main lineages of *Ixora* were recovered, an Asian-Pacific lineage and a widespread Asian-Afro-Neotropical one. The results of the Statistical Dispersal-Vicariance Analysis indicate a complex biogeographical history for *Ixora* with several dispersal and vicariance events that have led to its current distribution. Furthermore, Philippines are shown to constitute an overlay zone into which species from both major lineages of *Ixora*, the Pacific and the widespread one, have immigrated and subsequently radiated.

Keywords: biogeography, Huxley's line, Ixora, molecular systematics, Philippines, phylogeny, S-DIVA, Wallace's line

7.5 A step backwards to move forward: Footprints of climate change on genetic populations dynamics

Alexander Florez-Rodriguez[1], Katherine Ann Marsk[1], David Nogués-Bravo[1]
[1] Center for Macroecology, Evolution and Climate, Natural History Museum of Denmark
Contact: alexflorezr@gmail.com

Population and range size dynamics under climate change are of utmost importance to understand extinction and its effects in current and future biodiversity patterns. Advances in fossil dating, ancient DNA (aDNA) techniques, spatiotemporal resolution of palaeoclimate data and ecological and coalescent genetic models have improved our understanding of how single species responded to past climate change. However, a synthesis on past population responses to climate change across taxa and large environmental gradients is still lacking. We have compiled a large-scale dataset of palaeoclimatic reconstructions, modern and aDNA, dated fossil record and traits for twenty species of co-distributed Holarctic mammals, to test for single-specific versus concerted demographic trends in genetic parameters during the last 50,000 years under climate change. Past responses vary across taxa, suggesting complex responses to climate change. Our study provides a large-scale multi-taxa comparative framework to Late Quaternary population responses under environmental change and lays the foundations to improve forecasting of future extinctions based on past responses to climate change at genetic level.

Keywords: Climate change, ancient DNA, comparative phylogeography, population expansion.

7.6 Diversification of neotropical ferns: some do it in Amazonia, others outside

Hanna Tuomisto[1], Samuli Lehtonen[1], Glenda Cárdenas[1]
[1] Department of Biology, University of Turku
Contact: hanna.tuomisto@utu.fi

Speciation in Amazonia has been thought difficult due to lack of dispersal barriers, and the high species richness has been explained by factors such as the museum effect (survival of old lineages) and immigration of species from more active speciation centrums (such as the Andes). However, the geological history of Amazonia is complex and has resulted in high soil heterogeneity. Many Amazonian plants are edaphic specialists, so an obvious question is if their speciation was due to adaptive radiation to different soils. To test these ideas, we have compiled ecological information and produced phylogenetic hypotheses based on chloroplast DNA for three fern genera: Danaea, Lindsaea and Metaxya. Each one of these occurs both in Amazonia and in other neotropical rain forest areas. Interestingly, we encountered very different phylogeographic patterns in these three genera. Some clades were divided into an Amazonian and a non-Amazonian subclade, others showed more diversification within Amazonian lineages than outside Amazonia, and in some it was possible to trace the history of migration across the continent. Several Amazonian sister species pairs grow on different kinds of soil.

Keywords: phylogeography, plants, Amazonia, neotropics, edaphic specialisation, ferns

Contributed talks 8: Quaternary and cultural legacies
Convener: Daniel Gavin

8.1 Pleistocene oscillations and Anthropogene reduction of biome surface in the Andean and Indian Ocean tropics; implications for biodiversity

Suzette Flantua[1], Henry Hooghiemstra[1], Erik De Boer[1], Zaire González-C[1], César Velásquez-R[2]
[1] Inst. Biodiversity Ecosystem Dynamics, Univ. of Amsterdam
[2] Univ. Nacional de Colombia, Medellin
Contact: H.Hooghiemstra@uva.nl

We use digital elevation models of mountain topography and pollen-based reconstructions of past altitudinal changes of forest ecotones to assess dynamic biome connectivity in the northern Andes since the Last Glacial Maximum. We compare dynamics in the high-topography Andes (> 4500 m) with the low-topography island of Mauritius (< 800 m). The Andes shows evidence of altitudinal migration, temporary loss of the cold shrub biome due to different rates of change, and abundant no-analogue vegetation. Latest Pleistocene pollen records from mountain forests in Mauritius show no-analogue vegetation communities only, including a remarkable cascadic turnover of arboreal taxa making up the slope forests. We assume in Mauritius river bed locked gallery forest serves as a biodiversity reservoir supplying taxa to rapidly change slope forest composition, whereas in the Andes biodiversity seems mainly locked in the montane slope forest itself. We show evidence that natural as well as anthropogenic biome reduction up to below 5% of its Pleistocene maximum does not necessarily lead to biodiversity loss under certain conditions.

Keywords: oceanic islands, sky islands, rates of change, migration, area reduction

8.2 Geospatial analysis of human-megafaunal overlap in North America

Edward Davis[1], Meaghan Emery[1], Brianna McHorse[2]
[1] Department of Geological Sciences, University of Oregon
[2] Museum of Comparative Zoology and Concord Field Station, Organismic and Evolutionary Biology, Harvard
Contact: edavis@uoregon.edu

The role of humans in the late Pleistocene megafaunal extinction is an ongoing debate. Few sites preserve evidence of human-megafaunal coexistence, making trends difficult to detect. To address the lack of explicit overlap, we used kriging interpolation to examine local and continental trends in the overlap between megafaunal last appearance datums (LADs) and human first appearance datums (FADs). Humans occupied most of North America before the extinction. The highly localized patterns of our overlap models lend little support to either Blitzkrieg or illness hypotheses: no continent-wide trend exists. Overlap is regional in nature, varying between human arrival not significantly different from local extinction (Alaska, California) to significantly pre-dating it by over 1000 years (Midwest, Pacific Northwest, Northeast). Our models predict a younger extinction than previously estimated: the bulk of megafaunal LADs are 11 to 10.5 thousand calibrated years before present (k cal yr BP). Older regional extinctions may be more related to the Younger Dryas than human occupation. LADs in the Southwest were youngest (10 - 8 k cal yr BP), but still show 300-500 years of overlap.

Keywords: Extinction, Pleistocene, Holocene, Kriging, Megafauna, Paleobiogeography

8.3 The story of a rodent's Holocene extinction from the tropical Loltún cave, Yucatan, Mexico

Tania Gutiérrez-García[1], Ella Vázquez-Domínguez[1], Joaquín Arroyo-Cabrales[2], Hendrik N. Poinar[3]
[1] Ecología de la Biodiversidad, Universidad Nacional Autónoma de México
[2] Instituto Nacional de Antropología e Historia
[3] McMaster Ancient DNA Centre
Contact: evazquez@ecologia.unam.mx

Most genetic studies of Holocene fauna have been performed with ancient samples from dry and cold regions, in which preservation of fossils is facilitated and molecular damage is reduced. We analysed ancient DNA from rodent jawbones identified as *Ototylomys phyllotis*, found in Holocene and Late Pleistocene stratigraphic layers from Loltún, a humid tropical cave located in the Yucatan peninsula. We extracted DNA and amplified six short overlapping fragments of the cytochrome b gene, totalling 666 bp, which represents an unprecedented success considering tropical ancient DNA samples. We performed genetic, phylogenetic and divergence time analyses, combining sequences from ancient and modern *O. phyllotis*, in order to assess the ancestry of the Loltún samples. Results show that all ancient samples fall into a unique clade that diverged prior to the divergence of the modern *O. phyllotis*, supporting it as a distinct Pleistocene form of the *Ototylomys* genus. Hence, this rodent's story suggests that the sister group to modern *O. phyllotis* arose during the Miocene-Pliocene, diversified during the Pleistocene and went extinct in the Holocene.

Keywords: Quaternary mammals; Ancient DNA; Cricetidae

8.4 Beyond causation? The ecosystem consequences of the terminal Pleistocene Megafaunal Extinction

Felisa Smith[1], S. Kathleen Lyons[2], Scott Elliott[3], Emma A. Elliott Smith[1], Seth D. Newsome[1], Thomas W. Stafford[4], Catalina Tome[5]
[1] Biology Department, University of New Mexico
[2] Department Of Paleobiology, National Museum Of Natural History, Smithsonian Institution
[3] Climate, Ocean, Sea Ice Modeling Team, Los Alamos National Laboratory
[4] Department Of Physics & Astronomy, University Of Aarhus
[5] iology Department, University of New Mexico
Contact: fasmith@unm.edu

Recent studies connecting the decline of large predators and consumers with the 'unraveling' of ecosystems overlook that this natural experiment already occurred. As recently as 14 ka, millions of large-bodied mammals were widespread across the American continents. Within 1,000 years of the arrival of humans, ~80% were extinct including *all* species >600 kg. While the cause of the extinction remains contentious, what has been largely overlooked is the *consequence* of the loss of millions of large-bodied animals. Here, we examine the influence of the extinction at Hall's Cave in the great plains of Texas, which has unparalleled temporal resolution over the past 20ka, allowing characterization of the community before and after the extinction. This site experienced catastrophic loss of 80% of large-bodied herbivores and 20% of the apex predators in the ecosystem. Using a series of tightly constrained temporal windows spanning the full glacial to the modern and comprehensive faunal lists, we reconstruct mammal associations and body size distributions over time. Distribution and species association are examined using the statistical moments and the null model program PAIRS.

Keywords: megafauna, extinction, late Pleistocene, community structure, conservation paleoecology, paleoecology

8.5 Refugium of the Late Pleistocene biota in the mountains of southern Siberia

Milan Chytrý[1], Michal Horsák[1], Věra Pavelková Řičánková[2]
[1] Department of Botany and Zoology, Masaryk University, Brno, Czech Republic
[2] University of South Bohemia, České Budějovice, Czech Republic
Contact: chytry@sci.muni.cz

Our recent studies of modern flora and fauna in the Altai-Sayan Moutains of southern Siberia and their comparisons with fossil floras and faunas from Europe and other regions of Eurasia demonstrated that southern Siberia harbours probably the best preserved refugium of full-glacial biota in Eurasia. This finding was supported by a considerable similarity of modern pollen deposition in this area with fossil pollen spectra from the Late Pleistocene deposits in Central Europe, by the discovery of the whole community of terrestrial snails typical of the loess deposits from the coldest stages of the Pleistocene in the Russian Altai, and by revealing high similarity between recent mammal assemblages of the south-eastern Altai-Sayan Mountains and the Pleistocene faunas of several regions in northern Eurasia.

Keywords: Full-glacial, Late Pleistocene, Mammals, Modern analogue, Molluscs, Relict, Vascular plants

8.6 Floristic legacies of the Quaternary climate change: an example from European beech forests

Wolfgang Willner[1], Borja Jiménez-Alfaro[2], Milan Chytrý[2], the Braun-Blanquet project consortium
[1] Vienna Institute for Nature Conservation and Analysis (VINCA)
[2] Masaryk University Brno
Contact: wolfgang.willner@vinca.at

A biogeographical analysis of species having an optimum in European beech forests demonstrated that the distribution of many of these species is limited by post-glacial dispersal rather than by their environmental requirements. In the present study, we asked if this historic signal can also be detected when not only character species but the complete species composition of beech forests is taken into account. From the database of the Braun-Blanquet project (http://www.sci.muni.cz/botany/vegsci/braun_blanquet.php?lang=en), we selected all plots with a cover of *Fagus sylvatica* > 50%. This data set was classified using the TWINSPAN algorithm. The first division separated acidic and basiphilous beech forests. Within the latter, two groups with a distinct biogeographical character could be detected as most of their diagnostic species are linked to one of the two main glacial refuge areas of European beech (NW Balkan, S Italy). We conclude that phytosociological methods are a useful supplement to palaeobotanical and molecular studies, especially when the focus is not on single species but on a group of ecologically related species.

Keywords: dispersal limitation, phytosociology, post-glacial migration, refuge areas

Contributed talks 9: The Grand Subject
Convener: Larry Heaney

9.1 Mapping biogeographical ignorance

Joaquin Hortal[1], Geiziane Tessarolo[2], Richard J. Ladle[3]
[1] Dept. Biogeography & Global Change, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Spain
[2] Dept. Ecologia, Universidade Federal de Goiás, Goiânia, Brazil
[3] Institute of Biological and Health Sciences, Federal University of Alagoas, Brazil & School of Geography and the Environment, University of Oxford, UK
Contact: jhortal@mncn.csic.es

Biogeography aims to study the distribution of life across space and time at all scales of analysis. Describing such variations involves mapping the spatial distributions of species, communities and other biodiversity attributes such as traits or lineages. However, our knowledge on the distribution of biodiversity is scarce and unevenly distributed in space and time. This shortfall impedes describing spatial patterns and temporal dynamics directly from the data. Such biased and incomplete knowledge makes difficult to estimate and model the responses of populations, species and communities to environmental gradients, biotic interactions and global changes. This generates an unknown amount of spatial- and temporally explicit uncertainty in any estimate of the distribution of biodiversity. We propose a conceptual framework to estimate our degree of ignorance on biogeographical phenomena. We also provide several clues about the analytical approaches that could be used for mapping biogeographical ignorance.
Keywords: biodiversity data uncertainty bias Wallacean shortfall environmental coverage survey completeness

9.2 On hypothesis testing in macroecology

David J. Currie[1]
[1] Biology Dept., University of Ottawa, Canada
Contact: dcurrie@uottawa.ca

Macroecology addresses the statistical variability among systems in state variables such as diversity, species composition, metabolic activity, etc. The strength of this approach is that it permits statistical inference – predictions -- about natural systems. In contrast, experimental ecology in beakers or quadrats permits inference about statistical populations of beakers or quadrats. The clear drawback of macroecology is that controlled experiments to test causal hypotheses are usually impossible. It is nonetheless possible to test hypotheses rigorously, even mechanistic ones, by several macroecological means. However, the macroecological literature is rife with logically dubious hypothesis "tests", particularly inference by induction that particular correlations "support" a hypothesis. Rigorous hypothesis testing is critical, especially when weak effects are studied because surprisingly strong correlations may arise by chance when independent variables are strongly autocorrelated. I will illustrate these issues with literature concerning historical effects on contemporary species richness.
Keywords: Macroecology, Hypothesis testing, prediction, statistical inference

9.3 Deconstructing phylogenies: Phylogenetic scale in ecology and evolution

Catherine Graham[1], Machoc Antonin[1], Storch David[2]
[1] Stony Brook University
[2] Charles University
Contact: catherine.graham@stonybrook.edu

Both biological patterns, and the mechanisms influencing these patterns, vary across spatial and temporal scales. That spatial scale can influence biogeographic patterns is well-established in biogeography; however, phylogenetic scale is undeveloped even though many fundamental questions in biogeography are addressed using phylogeneties. Most research using phylogenies to understand patterns of diversity implicitly chose a scale which can then dictate the patterns observed and inferences made about mechanisms generating these patterns. For instance, the latitudinal diversity gradient is not universal and while it applies to most clades some, like penguins, show the opposite pattern than that of all birds. Given that this, and many other, fundamental questions depend on what clades are used we feel that the concept of phylogenenetic scale should be defined and explored. Here we use definitions and theory developed in spatial scaling as a guide to explicitly define phylogenetic scale. We show how explicitly considering phylogenetic scale, and potentially evaluating multiple phylogenetic scales, allows us to address outstanding controversies in biogeography.

Keywords: phylogenetic scale

9.4 The silence of biogeography

Mark V. Lomolino[1], Bryan C. Pijanowski[2]
[1] College of Environmental Science
[2] Department of Forestry and Natural Resources, and Center for Global Soundscapes, Purdue University, West Lafayette
Contact: island@esf.edu

Modern biogeography now encompasses an impressive diversity of patterns and phenomena of the geography of nature, providing insights fundamental to understanding the forces influencing the spatial and temporal dynamics of biological diversity. However, rather than praise our discipline for its great breadth of visions, our purpose here is to point out our glaring oversight of a potentially transformative frontier in the geography of nature.

Contributed talks 10: Invasions
Convener: Bethany Bradley

10.1 The global biogeography of alien plants in the Anthropocene: human legacy and future outlooks

Marten Winter[1], Hanno Seebens[2], Franz Essl[3], Wayne Dawson[4], Holger Kreft[5], Jan Pergl[6], Petr Pyšek[6], Patrick Weigelt[5], Mark van Kleunen[4]
[1] German Centre for Integrative Biodiversity Research (iDiv)
[2] University of Oldenburg
[3] University of Vienna, Environmental Agency
[4] University of Konstanz
[5] University of Göttingen
[6] Academy of Sciences of the Czech Republic
Contact: marten.winter@idiv.de

One of the main ecologically relevant features in the Anthropocene is the (un-)deliberate movement of species across biogeographical barriers and thus the enforcement of novel species communities with associated changes in functional and phylogenetic compositions. Here we present the most comprehensive global biogeographical analyses of established alien vascular plants. This unique and new database (GloNAF – Global Naturalized Alien Floras) that covers 828 terrestrial regions, including 272 islands. We present global patterns of taxonomic, functional and phylogenetic alpha and beta diversity of almost 11,700 species. We also discuss and reconstruct the historical and current global movement of alien plant species and predict based on global trade data and climate change scenarios, where and to which extent we expect future invasions.

Keywords: Alien species, database, global, functional, phylogenetic, diversity

10.2 Range expansions across ecoregions: interactions of climate change, physiology and genetic diversity

Marc Rius[1], Susana Clusella-Trullas[2], Christopher D. McQuaid[3], René A. Navarro[4], Charles L. Griffiths[5], Conrad A. Matthee[6], Sophie von der Heyden[6], Xavier Turon[7]
[1] Ocean and Earth Science, University of Southampton
[2] Department of Botany and Zoology, Centre for Invasion Biology, Stellenbosch University, South Africa
[3] Department of Zoology and Entomology, Rhodes University, South Africa
[4] Animal Demography Unit, Department of Biological Sciences, University of Cape Town, South Africa
[5] Department of Biological Sciences, Centre for Invasion Biology, University of Cape Town, South Africa
[6] Evolutionary Genomics Group, Department of Botany and Zoology, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa
[7] Centre for Advanced Studies of Blanes (CEAB-CSIC), Blanes, Spain
Contact: M.Rius@soton.ac.uk

Climate change is expected to drive range shifts among a wide array of organisms. Recent studies have indicated that climate change facilitates non-indigenous species (NIS) at local scales. However, the generality of these effects is unclear, as there is a dearth of comparative studies that assess how rapid environmental change affects species ranges across taxa and ecoregions. We obtained biogeographic and genetic data of coastal organisms along the South African coastline and compared these with global information for the same species. In addition, we conducted physiological experiments to assess how thermal tolerance (seawater temperature) was related to species distribution. This study provides empirical evidence that NIS, regardless of their thermal tolerance, range size and genetic variability, are expanding their ranges and increasing in abundance. This trend is uncorrelated with levels of human-mediated NIS transport but concurrent with changes in seawater temperature, which suggests that climate change fosters the spread and abundance of NIS across multiple spatial scales

10.3 Major drivers of invasion risks throughout the world

Céline Bellard[1], Boris Leroy[2], Wilfried Thuiller[3], J-F Rysman[4], Franck Courchamp[2]
[1] CBER, University College of London
[2] Ecologie, Systématique & Evolution, UMR CNRS 8079, Univ. Paris-Sud, France
[3] Univ. Grenoble Alpes, Laboratoire d'Écologie Alpine (LECA), France
[4] Laboratoire de Météorologie Dynamique (IPSL/CNRS), Ecole Polytechnique, Palaiseau, France.
Contact: celine.bellard@u-psud.fr

During the last few decades, the number of invasive alien species (IAS) has drastically increased. For these reasons, understanding the factors that are the most important drivers of invasions is of primary importance. In this paper, we investigate the main drivers due to habitat, human related activities, land-use and climate, which explain the current distributions of a large number of major IAS included in the "*100 of the world's worst invasive alien species*" from the *IUCN*. We predicted the areas of invasion risks and their major sources across the globe for those species. We found that climate and local species richness variables were primarily responsible for the distribution of these IAS. The propagule pressure (related to the *nearest distance to airports*, *seaports* and *human population density*) was also an important predictor. We showed that the areas at the highest risk of invasions are located in Western Europe, Eastern United States, Central America, and the eastern coast of Australia. Finally, this study provides strong evidence of the importance of considering both socio-economic factors and climate change for the current and future management of biological invasions.

Keywords: Biological invasions, biogeography, climate, .

10.4 Grasses and forbs respond similarly to eutrophication and vertebrate herbivory at sites home and away

Jennifer Firn[1], The Nutrient Network[2]
[1] Queensland University of Technology
[2] http://nutnet.umn.edu
Contact: jennifer.firn@qut.edu.au

European herbaceous species have naturalized in diverse habitats on every continent, being considered some of the world's highest impact invaders. Many drivers are proposed to explain this success, but few experiments are conduced at sites in both native and introduced ranges, and none have measured species responses to two of the most significant anthropogenic disturbances—eutrophication and altered vertebrate consumer pressure. At six randomly selected European and eight North American sites, we compare growth responses of 17 herbaceous species (8 grasses and 9 forbs) to three years of nutrient addition (all factorial combinations of nitrogen, phosphorus and potassium (NPK)) and vertebrate exclusion treatments. We find species responses sometimes differed between ranges but other times responses were similar. Responses were contingent on the type of treatment and life-form. Overall evidence suggests differences in biotic and abiotic processes in species' away ranges underlie naturalization and invasion not outright superiority in resource acquisition traits or release from herbivores.

Keywords: Nutrient Network (NutNet), enemy release hypothesis, resource fluctuation hypothesis, invasional meltdown, competition, nutrient limitation, nitrogen, phosphorus, potassium, herbivory, grazing, consumer pressure, biogeography, invasion

Contributed talks 11: Latitudinal biodiversity gradients
Convener: Roland Jansson

11.1 Into and out of the tropics: the generation of the latitudinal gradient among New World passerine birds

Jonathan Kennedy[1], Zhiheng Wang[1], Jason Weir[2], Carsten Rahbek[1], Jon Fjeldsa[1], Trevor Price[3]
[1] University of Copenhagen
[2] University of Toronto
[3] University of Chicago
Contact: jonathan.kennedy@bio.ku.dk

One prominent explanation for the latitudinal gradient proposes that its prime cause is the greater age and/or higher origination rates of tropical clades, and the infrequent/delayed dispersal of their component species into temperate regions. An alternative is that species' carrying capacities vary regionally, influencing rates of diversification via ecological opportunity. We contrast these hypotheses, to assess historical influences upon the gradient of New World passerine birds, comparing diversity patterns, climatic correlates, and the distribution of phylogenetically old and young species among the two suborders present (the oscines and suboscines), which are known to have had different origins within the region. While the colonization of new areas appears to stimulate diversification among the oscines (which continues for longer in those with greater carrying capacity), the suboscine distributions potentially reflect a large historical barrier to dispersal and niche conservatism of climatic tolerances. Although contemporary conditions can explain much of the passerine diversity patterns, history has had an important influence on the taxonomic composition of this gradient.

11.2 Topography-driven isolation, speciation and global plant biodiversity

Manuel Steinbauer[1], Richard Field[2], John-Arvid Grytnes[3], Panayiotis Trigas[4], Claudine Ah-Peng[5], Fabio Attorre[6], H. John B. Birks[3], Paulo A.V. Borges[7], Pedro Cardoso[7], Chang-Hung Chou[8], Michele De Sanctis[6], Miguel M. De Sequeira[9], Maria C. Duarte[10], Rui B. Elias[11], José-Maria Fernández-Palacios[12], Rosalina Gabriel[11], Roy E. Gereau[13], Rosemary G. Gillespie[14], Josef Greimler[15], David E. V. Harter[1], Tsurng-Juhn Huang[8], Severin D.H. Irl[1], Daniel Jeanmonod[16], Anke Jentsch[1], Alistair S. Jump[17], Christoph Kueffer[18], Sandra Nogué[19], Rüdiger Otto[12], Jonathan Price[20], Maria M. Romeiras[21], Dominique Strasberg[5], Tod Stuessy[22], Ole R. Vetaas[3], Carl Beierkuhnlein[1]
[1] University of Bayreuth
[2] University of Nottingham
[3] University of Bergen
[4] University of Athens
[5] Université de La Réunion
[6] University of Rome
[7] zorean Biodiversity Group
[8] China Medical University
[9] Universidade da Madeira
[10] University of Porto
[11] Azorean Biodiversity Group
[12] Universidad de La Laguna
[13] Missouri Botanical Garden
[14] University of California Berkeley
[15] University of Vienna
[16] Université de Genève
[17] University of Stirling
[18] ETH Zürich
[19] University of Oxford
[20] University of Hawai'i at Hilo
[21] University of Lisbon
[22] The Ohio State University
Contact: manuel.steinbauer@uni-bayreuth.de

Isolation is a fundamental driver of speciation, and thus biodiversity origination, yet is largely ignored when trying to explain the latitudinal diversity gradient. However, it has recently been suggested that topography may drive

speciation by increasing allopatric isolation, an effect that may be most pronounced in the tropics. Here we show a strong, globally consistent empirical relationship between elevation and endemism, indicating an effect of topography-driven isolation on speciation whose generality has hitherto been unrecognized. Isolation is locally more important than temperature, biotic interactions and area in influencing speciation rate, on both mountainous islands and continental mountains. We infer that isolation plays a more prominent role in generating the latitudinal diversity gradient than previously thought, an effect enhanced by glaciation reducing absolute elevation at high latitudes. This represents a mechanism to explain why there are so many terrestrial species overall, and also why they increase in number towards the equator.

Keywords: elevational gradients, speciation, latitudinal diversity gradient, isolation, metabolic theory of ecology

11.3 Climatic tolerances and geographical patterns in species richness

Véronique Boucher-Lalonde[1]
[1] Biology, University of Ottawa
Contact: veronique.boucher.lalonde@gmail.com

At broad spatial extents, variations in species richness of high-level taxa are highly correlated with climatic variables. Although this *strong* richness–climate relationship is nearly ubiquitous, the underlying mechanisms remain contentious. An intuitive explanation is that more species occur in warm and wet areas because more species are adapted to these conditions. And, indeed, lots of species can physiologically tolerate tropical-like conditions while fewer can tolerate increasingly cold or dry conditions. But, I argue that, although physiological tolerances do predict *a* positive richness–climate relationship, they fail to predict *the* observed richness–climate relationship. In fact, the relationship predicted by climatic tolerances is much steeper than what we observe empirically. Thus, the proportion of the species' pool (defined by climatic tolerances) that occurs in a fixed-size area is relatively large in cold areas, yet is increasingly small in warmer areas. Therefore, given species' climatic tolerances, the interesting question becomes: Why is the observed richness–climate relationship so *weak*? I propose testable mechanisms that could explain this relationship.

Keywords: Richness-climate patterns, Physiological tolerances, Thermal niche

11.4 Global patterns of mammalian coexistence: phylogenetic and morphological structure within species ranges

Fabricio Villalobos[1], Marcus Cianciaruso[1], Miguel Olalla-Tárraga[2], Thiago Rangel[1], José Alexandre Diniz-Filho[1]
[1] Universidade Federal de Goiás
[2] Rey Juan Carlos University
Contact: fabricio.villalobos@gmail.com

Geographic biodiversity patterns result from the overlap of species' ranges, which depends on species relatedness, habitat requirements and biotic interactions. Such causes act at distinct scales and linking them remains elusive. Integrating information on species' phylogeny and ecology may help assess the relative importance of historical vs. ecological processes in determining species co-occurrence. We evaluate the coexistence among the world's mammals considering the phylogenetic structure and body size distribution of species co-occurrence within individual ranges, under the novel framework of phylogenetic fields. Mammalian coexistence reveals the imprint of historical origins and dispersal of mammalian lineages, showing structuring within specific regions. Phylogenetic structure within mammalian ranges is driven by the distinct histories among and within biogeographic realms whereas the morphological structure within those ranges shows a weaker influence of such patterning. Integrating species' distributional, phylogenetic, and morphological information show promise for linking evolutionary and ecological approaches to understand geographic patterns of biodiversity.

Keywords: phylogenetic fields, geographic co-occurrence, morphological structure

Contributed talks 12: Biodiversity hotspots
Convener: Jürgen Dengler

12.1 Island and continental biogeography dynamics in the assembly of the Western Ghats (India) avifauna

Sushma Reddy[1], V V Robin[2], C K Vishnudas[2], Pooja Gupta[2], Uma Ramakrishnan[2]
[1] Biology, Loyola University Chicago
[2] National Centre for Biological Sciences, India
Contact: sreddy6@luc.edu

The Indian subcontinent is a biogeographic enigma with high species richness yet low endemism despite a history of isolation before reaching its current geographic position. The Western Ghats, an isolated montane region in peninsular India, is a biodiversity hotspot with a diverse range of endemic species. The origins of this species has been a mystery and the prevailing hypothesis is that species in the Western Ghats colonized from the Himalayas when peninsular India was covered in moist forest and were later isolated when India dried up. We analyzed phylogenetic relationships of all 35 endemic species and conducted ancestral area reconstruction to examine their origins of these taxa. We found substantial evidence for colonization of the Indian subcontinent from the Indian Ocean. Endemic species colonized the Western Ghats from all five possible source directions and at different times, supporting the idea that the biogeography of the Indian subcontinent is driven as much by island dynamics as vicariance events.

Keywords: Birds, tropics, montane, phylogenetics

12.2 Temporal stability of Eastern Afromontane forests: evidence from Amphibians and Reptiles

Simon Loader[1]
[1] Biogeography Research Group, University of Basel
Contact: simon.loader@unibas.ch

The persistence and stability of habitats through time are considered predictors of high levels of biodiversity in some environments. Based on sparse phylogenetic and palaeoenvironmental data, it has been suggested that long-term habitat persistence and stability may explain the species-rich, endemic fauna and flora of the Eastern Afromontane Biodiversity Region (EABR). Using complementary phylogenetic and biogeographic approaches I will outline results on a studies examining evolutionary patterns in EABR amphibians and reptiles. Using these data I test whether amphibian history reflects patterns of long-term persistence and/or stability across the fragmented mountains of the EABR.

Keywords: Eastern Afromontane, Stability, Amphibians

12.3 Diverging diversity patterns in species-rich taxa – Implications for biodiversity conservation

Jan Axmacher[1]
[1] UCL Department of Geography, University College London
Contact: j.axmacher@ucl.ac.uk

Priority areas for biodiversity conservation are commonly identified based on higher plant and vertebrate species - groups that represent only a small fraction of the global species pool. This is based on the assumption that plant diversity in particular is a strong indicator of overall species richness, since plants form the basis of food-chains, strongly influence habitat structure and often govern microclimatic conditions. Nonetheless, comparisons of spatial diversity patterns in vascular plants, macro-moths and ground beetles across a wide range of temperate and tropical ecosystems indicate that the species richness of highly diverse insect taxa is only weakly related to plant diversity and vegetation structure. While different insect taxa also display widely independent diversity patterns, climatic conditions form a key common driver of changes in their diversity. This indicates that plant-based conservation

priority areas like Biodiversity Hotspots are potentially poorly suited to safeguard overall biodiversity and that we have potentially strongly underestimate the threat climate change presents for the global species pool.

Keywords: Biodiversity indicators, climate change, insects, vegetation

12.4 Geodiversity, a novel predictor for biodiversity?

Harry Seijmonsbergen[1], Rudy Otto[2], Rachel Chambers[1], Kenneth Rijsdijk[1], Jose Maria Fernandez-Palacios[2], Gerard Oostermeijer[1], Daniel Kissling[1]
[1] Institute for biodiversity and ecosystem dynamics, University of Amsterdam
[2] Island Ecology and Biogeography Research Group, La Laguna University
Contact: k.f.rijsdijk@uva.nl

Geodiversity is the variation of the abiotic landscape, in particular the number, range and relative frequency of soil, geological and geomorphological units, supplemented with the variation of selected land surface parameters (LSPs), such as slope and aspect. Our proposed Geodiversity Index (GDI) is a combined result of the weighted units and LSPs. The GDI quantifies the variability of these landscape parameters across space and as such characterizes the spatial landscape diversity. We evaluate whether a GDI is a meaningful predictor of biodiversity and whether high GDI values are spatially congruent with biodiversity hotspots. We test two GDIs for the island of Tenerife (2034 km^2) for 500m^2 grid cells based on LSPs derived from a 5m resolution Digital Elevation Model (DEM), and from existing data from geological and soil maps. We correlate the high values of the gridded GDI maps with a endemic plant species richness map at 500 m^2 grid cells. The results suggest further avenues for GDI research, including automated mapping of GDIs based on expert knowledge, introduction of LiDAR DEMs and remotely sensed imagery, in order to use the GDIs as a predictor of biodiversity hotspots on islands and between islands.

Keywords: Geodiversity, Biodiversity, Islands, Endemic Species

Posters

⚡ - Posters presented in the Lightning Talk Sessions at rooms H21, H22, H24 and H25

Posters from Plenary Symposium 2: Tracking changes from space: Advances of remote sensing in biogeography

PS2.1 glUV: a global UV-B radiation data set for macroecological studies

Michael Beckmann[1], Tom V[1], Ameur Manceur[1], Henrik von Wehrden[2], Erik Welk[3], Anna Cord[1]
[1] Department of Computational Landscape Ecology, Helmholtz Centre for Environmental Research - UFZ
[2] Institute of Ecology/Faculty of Sustainability, Leuphana University Lüneburg
[3] Institute of Biology/Geobotany and Botanical Garden,Martin Luther University Halle Wittenberg
Contact: anna.cord@ufz.de

Global-scale biogeography has prospered in recent years due to the wide array of climatic data which has become available for research. However, important environmental variables are still missing, including data on UV-B radiation, an increasingly recognized driver of ecological processes. We developed a set of global UV-B surfaces (glUV), which is suitable to match common spatial scales in macroecology, based on remotely sensed records from NASA's Ozone Monitoring Instrument. Following a similar approach as for the WorldClim/CliMond data, we processed daily UV-B measurements into bioclimatic variables. UV-B data showed distinct seasonal variance at a global scale, while UV-B intensity decreased towards higher latitudes and was modified by topographic and climatic heterogeneity. UV-B surfaces were correlated with global mean temperature and radiation data, but exhibited variable spatial associations across the globe and were otherwise widely independent of existing bioclimatic surfaces. As UV-B is a known driver of numerous biological processes, our data set offers the potential to generate a better understanding of these dynamics in biogeography, global change research and beyond.

Keywords: Aura-OMI, Bioclim, climatology, CliMond, global data, macroecology, species distribution modelling, UV-B radiation, WorldClim

PS2.2 ⚡ (Semi-) Natural grasslands monitoring from multi-seasonal Very High Resolution Earth Observation data (WorldView2): achievements of the FP7 BIO_SOS project

Palma Blonda[1], Maria Adamo[1], Cristina Tarantino[1], Richard Lucas[2], Valeria Tomaselli[3], Antonio Sigismondi[4], Paola Mairota[5]
[1] Institute of Intelligent Systems for Automation (ISSIA), CNR-Italy
[2] University of New South Wales. Australia
[3] nstitute of Biosciences and BioResources (IBBR), CNR, Bari-Italy
[4] Regione Puglia, Ufficio Parchi, Bari-Italy
[5] Dipartimento di Scienze agro-ambientali e territoriali, UNIBA, Bari-Italy
Contact: blonda@ba.issia.cnr.it

The FP7 BIO_SOS project developed al system, named EO Data for Habitat Monitoring (EODHaM), for automatic monitoring of NATURA 2000 sites. The system can map (semi-)natural grassland and is based on the elicitation of expert rules concerning phenology, spatial features and agricultural practices rules. The study area is located in Italy within the Natura 2000 "Murgia Alta" site (SCI/SPA IT9120007). Four multi-seasonal Very High Resolution images (e.g., Worldview2) were used to map natural grasslands. EHODaM provided two classified maps corresponding to small and large objects in the scene. The Small Object (SO) map can detect single trees and small patches in the grasslands. This layer is useful for encroachment studies. The Large Object (LO) map was produced by aggregating the small objects in the previous map according to a dominance rule. The Overall Accuracy (OA) of the SO map was 91% with 0.13% error tolerance. The OA of the LO map was 88% with 0.13 error tolerance. Plant height measurements from LIDAR data were integrated with spectral indices to discriminate vegetation types.

Keywords: earth observation; very high resolution; grasslands monitoring; grassland enchroachment; automatic change detection

Continued next page

PS2.3 ⚡ Using time series of remotely sensed imagery to understand the dispersal dynamics of invasive species

Caroline Curtis[1], Bethany Bradley[1]
[1] University of Massachusetts
Contact: cacurtis@cns.umass.edu

Dispersal away from sites of initial establishment is a critical stage of invasion, with patterns likely influenced by spatial and temporal environmental factors. Yet, dispersal is understudied geographically; most studies focus on local dispersal over short time scales. We aim to understand how geography influences patterns of invasive plant dispersal using non-native pine (*Pinus radiata* and *Pinus contorta*) invasion in southern Chile as a case study. *P. radiata* and *P. contorta* were first introduced to this region ca. 40 years ago and spread away from plantation edges is already evident in imagery. In Argentina, pine saplings began establishing outside of plantations within only 12 years, suggesting that widespread invasion in Chile might be imminent. We used a time series of Landsat imagery (1984-2014) to model percent cover of new pine invasions stemming from plantations. Aerial photographs were used to validate Landsat estimates. Our results demonstrate that remotely sensed imagery can be used to model historical invasion patterns. These data will improve our understanding of the spatial and temporal processes influencing invasive plant dispersal on the landscape.

Keywords: Invasive plant, dispersal, remote sensing

PS2.4 ⚡ Artifacts in WORLDCLIM precipitation fields

Michael Douglas[1], Rahama Beida[1]
[1] Cooperative Institute for Mesoscale Meteorological Studies, University of Oklahoma
Contact: douglasnoaa@gmail.com

WORLDCLIM provides high spatial resolution gridded data of the most important climatological quantities controlling the distribution of biota and is thus widely used in niche modeling studies. This talk describes some widespread artifacts that can limit the effectiveness of WORLDCLIM precipitation fields for niche modeling. By comparing satellite-estimated cloudiness climatologies from MODIS and other sources of meteorological measurements with the WORLDCLIM data we present examples from regions where such discrepancies exist. These WORLDCLIM artifacts are due in large part to the insufficient density of long-duration precipitation measurements in mountainous regions where precipitation gradients are largest. This lack of observations affects the WORLDCLIM procedure for extending information along terrain slopes and leads to unrealistic precipitation patterns around isolated peaks and along some mountain ranges. This is important because these regions of varied topography are usually regions of great biodiversity. We suggest some procedures that might reduce such artifacts and suggest that an major effort is needed for developing an updated version of WORLDCLIM.

Keywords: WORLDCLIM, MODIS, climatology, precipitation, biodiversity, cloudiness

PS2.5 Assessing avian species richness in the eastern Tibetian Plateau with multi-scale remote sensing data

Fabian Fassnacht[1], Li Li[2], Andreas Fritz[3]
[1] Institute for Geography and Geoecology, Kalsruhe Institute of Technology (KIT)
[2] Wildlife Ecology and Management, University of Freiburg
[3] Remote Sensing and Landscape Information Systems
Contact: fabian.fassnacht@kit.edu

Species richness is supposed to be dependent upon habitat properties. Habitat properties for bird species in alpine environments are strongly connected to vegetation types and status. In the current project a set of optical remote sensing data including Unmanned Aerial Vehicle, high resolution (RapidEye) and medium resolution (Landsat) data was acquired. Along with the remote sensing data, field data which mainly consisted of bird counts was collected. Main objectives of the study is to examine the potential of multi-scale remote sensing data to estimate habitat conditions potentially related to bird species and thereby indirectly estimate species richness. Targeted variables include the vegetation classes as well as the degradation of grassland. Furthermore, as a second step, it is intended to temporally track grassland degradation processes and changes of vegetation composition over the last two decades and connect them to known political and demographic processes.

Keywords: avian species richness, alpine ecosystem, UAV, optical remote sensing, vegetation types, degradation

PS2.6 Vegetation types at large spatial scales. Can we predict where they meet?

Michelle Greve[1]
[1] Plant Science, University of Pretoria
Contact: michelle_greve@yahoo.com

Ecotones represent areas where vegetation types meet. Little is known about what determines the position and distribution of ecotones at large spatial scales, and particularly to what extent they correspond to sharp environmental gradients. Here I tested whether vegetation ecotones in Africa could be predicted by environmental factors. I specifically tested whether ecotones of physiognomic vegetation types classified using remote sensing data were better explained by the environment than ecotones of floristic vegetation types drawn by experts. Ecotonal areas for the two different types of vegetation were extracted and mapped. The magnitude of environmental change around ecotonal areas was compared to that of non-ecotonal areas using Maxent. Environmental gradients around ecotonal areas did not significantly differ from those of non-ecotonal areas. This may be due to factors other than those considered here, such as fire or vegetation history, having an influence on ecotonal zones.

Keywords: vegetation Africa ecotone biogeographic boundary

PS2.7 ⚡ Remote sensing to shape the next generation species distribution models

Kate He[1], Nathalie Pettorelli[2], Bethany Bradley[3], Anna Cord[4], Duccio Rocchini[5], Mao-Ning Tuanmu[6], Woody Turner[7], Martin Wegmann[8]
[1] Murray State University
[2] Zoological Society of London
[3] University of Massachusetts
[4] Helmholtz Centre for Environmental Research
[5] Fondazione Edmund Mach
[6] Yale University
[7] NASA
[8] University of Wurzburg
Contact: xhe@murraystate.edu

Current species distribution modeling (SDM) research calls for more realistic approaches that better integrate biotic interactions and a robust modelling framework flexible enough to accommodate multiple scales. One of the current limitations of SDMs relates to a lack of availability of ecologically and spatially explicit parameters to feed into the considered models. In this respect, we believe that novel remote sensing data provide a unique opportunity for biogeographers to progress from classical SDMs to a new generation of SDMs. We here propose a new class of modelling approach, the *next generation species distribution models* (NG-SDMs). We define NG-SDMs as across-scale predictive models that (1) sit on the mid-section of the correlative/mechanistic continuum incorporating the strengths of both modelling approaches that have been explored in previous SDM studies, (2) make use of new information to inform parameter selection, and that (3) explicitly consider biotic interactions with valid proxies and population dynamics. We demonstrate how modern remote sensing may revolutionize the way we model species distribution in both terrestrial and aquatic habitats.

PS2.8 Remote sensing approach for evaluating the invasion strategic of Mesquite (*Prosopis juliflora*) in Sub-Saharan Africa

Buho Hoshino[1], Kazuya Nishimura, Shunsuke Yabuki, Kiyotsugu Yoda, Hiroshi Yasuda, Hiroshi Nawata, Karamalla Abdelaziz, Suliman Mahgoub, Elgamri Mohamed
[1] Department of Environmental Symbiotic College of Agriculture, Food and Environment Sciences, Rakuno Gakuen University
Contact: aosier@rakuno.ac.jp

In the Sub-Saharan Africa, the problems of desertification, land degradation and dust storm are still serious. Because, the invasive species Mesquite has a high capacity to fix sand dunes, mesquite trees were introduced into Sudan in 1917 from South Africa and Egypt and planted in Khartoum and Eastern Sudan. However, the tree was invaded both natural and managed habitats, including watercourses, floodplains, highways, degraded abandoned land and irrigated areas. In this study, to monitor mesquite water use efficiency the concept of a NDII, which is defined as the ratio of actual to foliar water content, have been applied and compared with the ground measurements of stomatal conductance, field spectral, volumetric soil water content. As results, on the base of the PALSAR L-band microwave polarimetric backscatter coefficient, the soil moisture and surface roughness could be estimated with a good accuracy for bare-soil surfaces. The time series satellite imagery for the period 1985 to 2013 was used, to extract and classify the Mesquite trees expansion areas. The results showed that mesquite was expanded inside of the curves of the major rivers, within 500m from the river channel.

Keywords: invasive species Mesquite (Prosopis juliflora), Sub-Saharan Africa, change detection, Remote Sensing Approach

PS2.9 ⚡ Assimilation of Remote Sensing Data for Land Surface Models

Emily Lines[1], Jose Gomez-Dans[2], Philip Lewis[2]
[1] School of Geography, Queen Mary University of London
[2] Department of Geography, University College London
Contact: e.lines@qmul.ac.uk

Earth Observation (EO) data provide information about terrestrial ecosystems on longer temporal and higher spatial scales than is available from ground-based measurements. Using these data to drive terrestrial ecosystem models is therefore an attractive prospect, but linking EO data to vegetation properties of interest (i.e. leaf area and biochemistry) in a consistent way is not straightforward and requires the use of a radiative transfer (RT) model describing canopy structure. Realistic RT models are slow to run and have many parameters which are often poorly constrained, making the inversion problem impractical at large scales and over long timeframes. To overcome these issues we introduce a data assimilation scheme that uses statistical emulators (Gaussian processes) in place of the original model, providing significant calibration efficiencies. We present a method to further improve the inversion through constraints on phenology and leaf biochemistry using published data of leaf biochemical measurements. The speedup in retrieval using emulators is substantial compared to the original models, making this a very attractive approach for inverting large-scale and long-term data.

Keywords: Remote sensing Radiative transfer Data assimilation

PS2.10 ⚡ Species distribution modelling of a new invasive mosquito in North East Italy: A Bayesian approach

Matteo Marcantonio[1], Baldacchino Frederic[1], Metz Markus[1], Rosà Roberto[1], Arnoldi Daniele[1], Kleinschmit Birgit[2], Förster Michael[2], Bussola Francesca[1], Montarsi Fabrizio[3], Capelli Gioia[3], Neteler Markus[3], Rizzoli Annapaola[3]
[1] Fondazione Edmund Mach, San Michele all'Adige (TN), Italy
[2] Geoinformation in Environmental Planning Lab, Technische Universität Berlin, Germany
[3] Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (PD), Italy
Contact: matteo.marcantonio@fmach.it

Aedes koreicus is a highly invasive mosquito, recognised as zoonotic vector of infectious diseases. Native to East-Asia, it has recently become established in Europe. Only limited data is currently available on its ecology. Using data from LExEM, a project that aims to study *Ae. koreicu*s, we created a presence/absence dataset of *Ae. koreicu*s in Northeast Italy. We enriched this dataset with remotely sensed predictors (MODIS LST and NDWI), land use and topographic information to create a Bayesian SDM. Bayesian data analysis is particularly useful when distribution data of a species is sparse, as is often the case with new invasive species. It allows the inclusion of prior knowledge about the species, and thus provides more robust coefficient estimates. We used both mildly and strongly informed priors derived from the scientific literature. Data acquisition regarding the ecology of invasive species and the modelling of their potential distribution are critical in supporting public health policy. Indeed, the spread of new invasive mosquitoes is of increasing concern due to the risk of outbreaks of exotic vector-borne diseases that they can trigger.

Keywords: Invasive species, Public Health, Vector-borne diseases, Species Distribution Modelling, Bayesian inference.

PS2.11 Evaluating scale-dependence in species-environment relationships

Katherine Mertes[1], Walter Jetz[1]
[1] Yale University
Contact: katherine.mertes@yale.edu

Previous investigations of species distribution dynamics, hierarchical habitat selection, and perceptual capacities indicate that vertebrate species likely respond to environmental conditions differently at different spatial scales. Wiens (1989) introduced the concept "domains of scale" to describe regions along a theoretical axis of spatial grain where species responses to environmental conditions are relatively similar, separated by transition zones where species responses may abruptly take different forms. A key challenge in ecology is to develop reliable methods to identify scale domains for species or broader groups, in order to select grains and extents of analysis that enable accurate inferences on ecological relationships and distribution predictions. Here, we use a multi-grain modeling framework to describe scale-dependence in species-environment relationships for select East African bird species. We use remotely sensed data at six relatively fine spatial grains (10–1000m) to represent biologically meaningful environmental conditions, and fuse observational and movement data to capture intraspecific variation in habitat preferences.

Keywords: scale, grain, species-environment relationships remote sensing

PS2.12 ⚡ Using remotely sensed predictors for SDMs to explain distribution of canopy tree species of Miombo woodlands

Rasmus Revermann[1], Manfred Finckh[1], Marion Stellmes[2], Jens Oldeland[1]
[1] Biodiversity, Ecology and Evolution of Plants, University of Hamburg, Germany
[2] Remote Sensing and Geoinformatics, University of Trier, Germany
Contact: rasmus.revermann@uni-hamburg.de

The Miombo woodlands of southern and central Africa have been identified as one of the global tipping points where drastic loss of biodiversity and decline of ecosystem services are likely to occur in the near future; at the same time, this region is largely understudied. Based on two scales, plot and basin scale, we investigate the realized distribution of canopy tree species and their environmental habitat requirements within the Okavango Basin. Presence / absence data of the species is derived from a vegetation database with over 300 vegetation plots. On the plot scale results from soil samples and topographic attributes calculated from the SRTM DEM serve as predictor variables. On the basin scale the distributional range of the canopy tree species is analyzed. Phenological metrics derived from a MODIS time series analysis spanning 12 years as well as bioclimatic variables resulting from downscaled reanalysis of a regional climate model serve as input. SDMs are calculated in the BIOMOD framework and predictions are based on ensemble forecasting. The results show a clear separation of Miombo woodlands sensu strictu from the drier *Baikiaea plurijurga* / *Burkea africana* dominated woodlands of the lower basin.

Keywords: Angola; Miombo; MODIS; Okavango; realized distribution; SDM; time-series; woodlands;

PS2.13 ⚡ Predictive mapping of dwarf shrub vegetation in an arid high mountain ecosystem using remote sensing and random forests

Kim André Vanselow[1], Cyrus Samimi[2]
[1] Institute of Geography, FAU Erlangen-Nürnberg
[2] Department of Geography, University of Bayreuth
Contact: kim.vanselow@fau.de

In many arid mountains, dwarf shrubs represent the most important fodder and firewood resources; therefore, they are intensely used. For the Eastern Pamirs (Tajikistan), they are assumed to be overused. However, empirical evidence on this issue is lacking. We used random forest models based on remote sensing data and 359 plots to predictively map total vegetative cover and the distribution of the most important firewood plants, *K. ceratoides* and *A. leucotricha*. These species were mapped as present in 33.8% of the study area (accuracy 90.6%). The total cover of the dwarf shrub communities ranged from 0.5% to 51%. Areas with very low cover were limited to the vicinity of roads and settlements. The model could

explain 80.2% of the total variance. We conclude that the combination of statistical models and remote sensing data worked well to map vegetation in an arid mountainous environment. With this approach, we were able to provide tangible data on dwarf shrub resources in the Eastern Pamirs and to relativize previous reports about their extensive depletion.

PS2.14 ⚡ High-resolution global cloud dynamics for ecosystem and biodiversity monitoring

Adam Wilson[1], Walter Jetz[1]
[1] Ecology & Evolutionary Biology, Yale University
Contact: adam.wilson@yale.edu

Clouds are a key component of the global climate system, affecting energy balance, latent heat flux, radiation flux, and moisture transport and can vary drastically over fine spatial grains (<2km) due to topography and land cover. Consequently, cloud cover critically drives many ecological processes, such as drought stress, tree growth, available photosynthetically active radiation, eco-physiology, and animal behavior. Despite this relevance and the need to capture biodiversity-habitat ("microhabitat") associations and to globally monitor their dynamics at the appropriate resolution, the understanding of detailed spatial and seasonal cloud variation has remained remarkably limited. We will introduce ≈1km resolution monthly cloud climatologies derived from over a decade of global satellite observations that capture highly heterogeneous spatiotemporal variation in cloud cover not otherwise available. The newly developed layers provide a new lens through which to understand spatial and seasonal variability of global cloud cover and associated biodiversity and ecosystem dynamics in unprecedented detail.

Keywords: Cloud, climate, species distribution model, biogeography, remote sensing

PS4.1 Seasonal differences in growth and leaf physiology between lianas and trees. A test of the dry season growth advantage hypothesis.

Leonor Alvarez-Cansino[1], Stefan Schnitzer[2]
[1] Plant Ecology, BayCEER, University of Bayreuth
[2] University of Wisconsin-Milwaukee and Smithsonian Tropical Research Insitute
Contact: leonor.alvarez-cansino@uni-bayreuth.de

Determining the factors that control large-scale patterns of species distributions is a key goal in ecology, yet the mechanisms responsible for the number of lianas and trees through the tropics with annual rainfall have received little attention. Lianas are key components of most tropical forest and they peak in abundance in seasonally dry tropical forests. The dry season growth advantage hypothesis propose that lianas are more abundant in seasonally dry forest because they may avoid physiological stress by remaining active and growing during dry periods. We tested the dry season growth advantage hypothesis for liana and trees along a steep rainfall gradient across the Isthmus of Panama. We measured liana and tree growth and seasonal physiological responses and leaf traits in co-occurring lianas and trees in a dry, moist, and wet forest. Lianas had stronger stomatal control and higher water use efficiency than trees in the drier forest, but not the wet forest. Greater leaf-level seasonal resource use strategies and growth during the dry season supports the dry season growth advantage hypothesis and may explain why lianas peak in abundance in seasonally dry tropical forests.

PS4.2 ⚡ Functional relationships between interacting species across scales - from species interactions to regional patterns

Matthias Dehling[1], Katrin Böhning-Gaese[1], Matthias Schleuning[1]
[1] Biodiversity and Climate Research Centre (BiK-F)
Contact: matthias.dehling@senckenberg.de

Relationships between interacting species groups on large spatial scales have mostly been assessed via the comparison of species richness patterns which do not account for co-adaptations between species. Here, we assessed the co-adaptations between two interacting species groups (frugivorous birds and fleshy-fruited plants) across scales, from species interactions to regional patterns of functional diversity. Using data from species interaction networks, we identified functional traits that influence which species interact. We then studied whether co-adaptations between species lead to a correspondence of functional roles in bird and plant assemblages, and, ultimately, to co-variation in the functional diversities of birds and plants. We identified close functional relationships between frugivorous birds and fleshy-fruited plants, from trait matching in species interactions and congruency in their morphologies to co-variation in functional diversity on large spatial scales. Our results imply that the consideration of co-adaptations in functional traits is indispensable for the investigation of the relationships between interacting species groups on large spatial scales.

PS4.3 ⚡ A tale of bees and flowers – mapping pollination traits with imaging spectroscopy

Hannes Feilhauer[1]
[1] Geography, Friedrich Alexander Universität Erlangen-Nuremberg
Contact: hannes.feilhauer@fau.de

Remote sensing is increasingly used to map and monitor functional ecosystem properties. In particular leaf traits such as the specific leaf area, leaf biochemistry, or structural properties of the canopy are frequently targeted. In contrast, our current knowledge on remote sensing of flowering and pollination traits is very limited. This study thus addresses the following questions for an extensively used mosaic of grasslands and mires in Bavaria, Germany: How are pollination traits distributed across the occurring vegetation types? Are pollination traits in the study site related to optical traits that account for a characteristic spectral signature? Can we map spatial patterns of pollination traits with remote sensing? To answer these questions, 100 vegetation records were sampled across the study site. Pollination traits of the occurring species were extracted from trait data bases. Simultaneously, imaging spectroscopy data were acquired with the airborne

sensor AISA Dual. The data sets were analyzed using statistical models. The results show that relations between optical and pollination traits exists and enable a detailed and accurate mapping of the related patterns.
Keywords: functional traits, grassland, mire, pollination, remote sensing, vegetation mapping

PS4.4 Global geographic patterns of sexual size dimorphism in birds and their climatic correlates

Nicholas Friedman[1], Vladimir Remes[1]
[1] Department of Zoology, Palacky University
Contact: vladimir.remes@upol.cz

Sexual size dimorphism (SSD) is widespread among animals, and is a common indication of differential selection among males and females. Sexual selection theory predicts that SSD should increase as one sex competes more fiercely for access to mates, but it is unclear what effect spatial variation in ecology may have on this behavioral process. To address this, we mapped the global distribution of SSD in body size across 2581 species of birds. We examined correlations between SSD and nine predictor variables representing physical geography, climate, and climate variability. Our results show guarded support for a latitudinal trend in SSD, with a strong prevalence of species with low or female-biased SSD in the far North. However, this trend and several others were not supported consistently among zoogeographical regions or methods of analysis. Moreover, uneven global distribution of major clades of birds might have contributed to the latitudinal pattern without environmental factors having any effect. These results broadly agree with studies of SSD in other groups, and suggest that SSD is linked to behavioral dynamics that may be largely independent of environmental conditions.
Keywords: sexual dimorphism, sexual selection, climate, spatial analyses, global, birds

PS4.5 The importance of local dynamics and species' dispersal for species' potential to spread in landscape

Lucie Hemrova[1], James Bullock[2], Danny Hooftman[2], Steven White[2], Zuzana Münzbergová[1]
[1] Institute of Botany, Academy of Sciences of the Czech Republic
[2] Centre for Ecology and Hydrology, Wallingford, UK
Contact: lucie.hemrova@ibot.cas.cz

We estimated the potential to spread in the landscape in seventeen dry grassland species of the Czech Republic using analytical wavespeed model. This model combines a demographic matrix model with integrodifference equations describing dispersal. Then we investigated to what extent the potential to spread in landscape is affected by local population dynamics (i.e. by rate of increase, net reproductive rate or life span) and by species' dispersal (i.e. by dispersal distance, terminal velocity, seed release height or wind speed). We found that local population dynamics is more important for species' potential to spread. Species with higher rate of increase, net reproductive rate and shorter life span had better potential to spread. However, higher potential to spread was also found for species with better dispersal ability, specifically those with longer dispersal distances and bigger seed release height. When demographic matrices were changed to have comparable rates of increase, dispersal ability (lower terminal velocity and bigger seed release height in particular) was the crucial factor for final spread potential.
Keywords: dispersal, landscape-level dynamics, population dynamics, species' spread

PS4.6 ⚡ Relative food limitation drives geographic clutch size variation in South African passerines: a large-scale test of Ashmole's seasonality hypothesis

David Hořák[1], Anna Tószögyová[1], David Storch[2]
[1] Department of Ecology, Charles University in Prague
[2] Center for Theoretical Study, Charles University and the Academy of Sciences of the Czech Republic, Prague
Contact: david.horak@natur.cuni.cz

We separated the effect of overall resource level from the effect of seasonality on avian clutch size and tested Ashmole's hypothesis that birds have larger clutches in seasonal environments due to high *per capita* food availability during the breeding season. We used a large-scale environmental gradient in South Africa and

investigated effects of normalized difference vegetation index on clutch size variation among local passerine assemblages (25 x 25 km grid cells). The importance of the resource level and seasonality was distinguished by using General Additive Models and subsetting the data so that variation in one of the parameters was minimized. Assemblage mean clutch size showed a hump-shaped relationship with maximum resource availability but an increase with seasonality. When the variation in maximum resource availability was fixed, clutch size increased with increasing seasonality, but it decreased with increasing maximum resource availability when we fixed the variation in seasonality. Results hold for all feeding guilds except granivores, for which we found opposite patterns. Our analyses indicate that the spatial trends are mostly driven by variation between families.

Keywords: avian assemblages, David Lack, biogeographical approach, normalized difference vegetation index, number of eggs, Philip Nelson Asmole

PS4.7 ⚡ TRY – a global database of plant traits

Jens Kattge[1], Sandra Diaz[2], Sandra Lavorel[3], Paul Leadley[4], Colin Prentice[5], Gerhard Boenisch[1], Christian Wirth[6]
[1] Max Planck Institute for Biogeochemistry, Jena, Germany
[2] Instituto Multidisciplinario de Biología Vegetal, Universidad Nacionalde Córdoba, Argentina
[3] Laboratoire d'Ecologie Alpine (LECA), CNRS, Grenoble, France
[4] Laboratoire d'Ecologie, Systématique et Evolution (ESE), Université Paris-Sud, France
[5] Grantham Institute, and Division of Biology, Imperial College, Silwood Park, Ascot, London, UK
[6] Institute for Special Botany and Functional Biodiversity, University of Leipzig, Germany
Contact: jkattge@bgc-jena.mpg.de

The characteristics of plants - plant traits - are highly heterogeneous, exhibit a low degree of standardization and are linked and interdependent at various levels of biological organization. In addition plant traits reside in a multitude of small databases, with little consolidation across datasets and are often not available for reuse. To overcome this situation the TRY initiative (try-db.org) has developed a framework of intellectual property guidelines, data curation workflow and services to compile, consolidate and share public (open access) and non-public plant trait data. The framework respects the high efforts of trait measurements, while at the same time providing attractive incentives for data sharing: access to additional trait data, the opportunity of collaborations and co-authorship, and being cited if trait data are re-used via TRY. So far the TRY initiative has successfully facilitated the compilation and consolidation of several hundred plant trait datasets, providing an unprecedented coverage of 5.6 million trait records, and has served about 300 scientific projects by provision of customized trait datasets.

Keywords: plant traits, global database

PS4.8 Functional resilience towards climate-driven extinction - the trait signature of the European and North American tree floras.

Mario Liebergesell[1], Christian Wirth[1], Björn Reu[1], Martin Freiberg[1], Erik Welk[2], Ulrike Stahl[3], Jens Kattge[3]
[1] Systematic Botany and Functional Biodiversity, University of Leipzig
[2] Geobotany Department, Halle University
[3] Max-Planck-Institute for Biogeochemistry, Jena
Contact: cwirth@uni-leipzig.de

During glacial periods, harsher climatic conditions in Europe have led to higher extinction rates of tree species compared to North America, which resulted in a depauperate European tree flora. As a consequence, we hypothesized that not only species number, but also European tree functional diversity is reduced compared to the North American. Functional diversity was quantified based on a matrix of 27 functional traits for 154 and 66 species in North America and Europe, respectively, and grid-based co-occurrence of species derived from distribution maps. Our hypothesis holds true for gymnosperms: Standardized for species richness, functional richness and functional dispersion are similar in Europe and North America, but due to the higher species numbers in North America, functional richness of the total pool is higher. We reject the hypothesis for angiosperms. European angiosperm floras show a higher standardized functional richness and functional dispersion than North American angiosperm floras. We conclude, that strong climate-driven extinction events may not necessarily decrease functional diversity, thus pointing to a high functional resilience of continental floras.

Keywords: functional diversity, glacial extinction, resilience

PS4.9 ⚡ Multi-million year climate change legacies in global mammal functional diversity patterns

Marco Girardello[1], Jens-Christian Svenning[1]
[1] Section for Ecoinformatics and Biodiversity, Department of Bioscience-Ecoinformatics and Biodiversity, Aarhus, University of Aarhus
Contact: marco.girardello@bios.au.dk

Understanding how current and historical climatic conditions affect geographical patterns of diversity is a fundamental question in biogeography. Deep-time climatic changes have caused extinction, speciation, and range dynamics. However, the influence of multimillion-year paleoclimatic changes on of present-day patterns in functional diversity patterns remains virtually unexplored. Using climate reconstructions from the Miocene, Pliocene and the Last Glacial, we quantified the relative importance of current environment and past climatic changes for global patterns in mammal functional diversity. We found that current functional diversity is partially linked to precipitation changes since the Miocene, with weaker, but also important links to Quaternary glacial-interglacial climatic oscillations. Furthermore, a large fraction of the explained variation is shared between contemporary drivers and paleoclimatic changes. Overall, the results indicate that past climate changes have left multimillion-year disequilibrium legacies in contemporary mammal functional diversity, supplementing strong relations to current environment that may themselves include a long-term cumulative component.

PS4.10 ⚡ Cold vegetarians live longer - on longevity and biogeography of reptiles

Shai Meiri[1], Inon Scharf[1], Uri Roll[2], Anat Feldman[1], Maria Novosolov[1], Daniel Pincheira-Donoso[3], Yuval Itescu[1]
[1] Zoology, Tel Aviv University
[2] Geography and the Environment , Oxford University
[3] Life Sciences, University of Lincoln
Contact: uncshai@post.tau.ac.il

Longevity is an important life-history trait, directly linked to fitness. We examined which biogeographic feature affect reptile maximum longevity using a global dataset of literature & museum data on the maximum longevity of 1171 species. Correcting for body size, turtles live 55% longer than snakes, which live 20% longer than lizards. Herbivorous & omnivorous reptiles live ~40% longer than carnivorous ones. Nocturnal reptiles live ~35% longer than diurnal ones, presumably as a consequence of having lower metabolic rates. There is also a clear geographic signal in longevity: tropical reptiles lead the shortest lives, Holarctic reptiles live ~25% longer, while reptiles in Australia and Oceania live longest, perhaps because of reduced extrinsic mortality. Above and beyond that, longevity further increases with latitude and decreases weakly with NPP and temperature. Biome and precipitation have little effect on longevity. We conclude that lower metabolic rates and shorter activity seasons, together with poor diets and reduced extrinsic mortality select for long lives.

Keywords: longevity, lifespan, temperature, season length, natural history, life history, reptiles, mortality, NPP, latitude, Realms, turtles, lizards, snakes

PS4.11 ⚡ Do community-mean trait values reflect optimal strategies? Insights from niche models of Puerto Rican trees.

Robert Muscarella[1], María Uriarte[1]
[1] Ecology, Evolution, Environmental Biology, Columbia University
Contact: bob.muscarella@gmail.com

Trait-environment relationships provide a physiological basis for understanding species distributions and community variation along abiotic gradients. Theory predicts that community-weighted mean trait values (CWMs) reflect optimal strategies in particular abiotic conditions. However, the high amount of trait variation among co-occurring species challenges the predictive ability of this theory. We tested the hypothesis that species-specific habitat suitability is negatively related to a species' deviation from the local CWM for 230 species of trees in Puerto Rico. We measured three key functional traits (wood density, leaf mass per area, and maximum height) and characterized

CWM in plots located across the island's broad precipitation gradient. We related the trait data to species-specific models of habitat suitability. Negative relationships between estimated habitat suitability and deviation from the local CWM offer support our hypothesis. However, deviation from the CWM was not related to local abundance. Our study demonstrates how viewing plant functional traits from a biogeographic perspective can help elucidate the processes that govern local community composition.

Keywords: functional traits, ecological niche models, tropical trees, Puerto Rico

PS4.12 ⚡ sPlot – the new global vegetation-plot database for addressing trait-environment relationships across the world's biomes

Oliver Purschke[1], Jürgen Dengler[2], Helge Bruelheide[3], Milan Chytrý[4], Florian Jansen[5], Stephan M. Hennekens[6], Ute Jandt[3], Borja Jiménez-Alfaro[4], Jens Kattge[7], Valério De Patta Pillar[8], Brody Sandel[9], Marten Winter[1], The sPlot Consortium
[1] German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany
[2] Disturbance Ecology, BayCEER, University of Bayreuth, Germany
[3] Geobotany and Botanical Garden, Institute of Biology, Martin Luther University Halle Wittenberg, Halle (Saale), Germany
[4] Department of Botany and Zoology, Masaryk University, Brno, Czech Republic
[5] Institute of Botany and Landscape Ecology, University of Greifswald, Greifswald, Germany
[6] Centre for Ecosystem Studies, Wageningen University and Research, Alterra, Wageningen, The Netherlands
[7] Max-Planck-Institute for Biogeochemistry, Jena, Germany
[8] Department of Ecology, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil
[9] Department of Bioscience, Aarhus University, Ny Munkegade, Aarhus, Denmark
Contact: oliver.purschke@idiv.de

The trait composition of plant communities is determined by abiotic, biotic and historical factors, but the importance of macro-climatic factors in explaining trait-environment relationships at the local scale remains unclear. Such knowledge is crucial for biogeographical and ecological theory but also relevant to devise management measures to mitigate the negative effects of climate change. To address these questions, an iDiv Working Group has established the first global vegetation-plot database (sPlot). sPlot currently contains ~ 600,000 plots from over 50 countries and all biomes, and is steadily growing. Approx. 70% of the most frequent species are represented by at least one trait in the global trait database TRY and gap-filled data will become available for the most common traits. In our talk, we will give an overview about the structure and present content of sPlot in terms of spatial distribution, data properties and trait coverage. We will explain next steps and perspectives, present first cross-biome analyses of community-weighed mean traits and trait variability, and highlight some ecological questions that can be addressed with sPlot.

PS4.13 ⚡ Species physiological tolerances and ecological niche processes jointly shape regional-scale biodiversity gradients

Björn Reu[1], Ulrike Stahl[2], Christian Wirth[1]
[1] Institute of Biology, University of Leipzig
[2] Max-Planck-Institute for Biogeochemistry, Jena
Contact: bjoern.reu@uni-leipzig.de

The physiological tolerance hypothesis states that species richness (SR) is highest in warm and humid climates because more functional strategies can survive under these conditions. However, it ignores that species have to interact with each other while competing for the same set of limiting resources. Here, we show how both processes shape regional-scale diversity gradients analyzing the dispersion and packing of 250 tree species in multivariate trait space across North America. To consider different niche dimensions, we grouped 24 traits into 4 different syndromes: leaf-level carbon gain, tree architecture, demography and biotic interactions. The leaf and demography traits exhibit a functional convergence towards high SR and climatically favorable environments, whereas species packing in architecture traits exhibits a significant functional divergence. This is caused by plant maximum height and geographically related to patterns in AET. Our results not only suggest the occurrence of limits in similarity and resource acquisition at the regional scale, but also demonstrate that a functional convergence in one niche dimension can be compensated by niche differentiation in another.

Keywords: Functional diversity, functional convergence, functional divergence, plant traits, physiological tolerance hypothesis, limiting similarity, environmental filtering, latitudinal diversity gradient, functional biogeography, plant functional type

PS4.14 ⚡ Biodiversity turnover along environmental and spatial gradients in Europe

Bianca Saladin[1], Wilfried Thuiller[2], Sébastien Lavergne[2], Luigi Maiorano[3], Nicolas Salamin[4], Niklaus E. Zimmermann[1]
[1] Swiss Federal Research Institute WSL, Birmensdorf
[2] Laboratoire d'Ecologie Alpine, University of Grenoble
[3] Department of Biology and Biotechnologies, University of Rome
[4] Department of Ecology and Evolution, University of Lausanne
Contact: bianca.saladin@wsl.ch

Biodiversity turnover can be analyzed for taxonomic-, functional- and phylogenetic beta diversity. Phylogenetic- and functional diversity both give interesting insights into underlying evolutionary processes of diversification. For example, phylogenetic turnover along environmental gradients can reveal where - in ecological space - radiations have occurred and functional innovations during evolution to new environmental conditions were required. Little is known about the structure of phylogenetic beta diversity in environmental space in Europe. Here, we investigated in a broad and taxonomically comprehensive assessment, using terrestrial vertebrates in Europe and Turkey, the structure of phylogenetic turnover along two major environmental gradients (precipitation and temperature). With this study, we aim at analyzing (1) the pattern of phylogenetic and taxonomic turnover in geographic space, (2) how (phylogenetic and taxonomic) diversity changes along environmental gradients, and (3) how taxonomic and phylogenetic diversity differ in geographic and environmental space. Our results contribute to general beta biodiversity theories and can serve as a basis for conservation management.

Keywords: betadiversity, taxonomic turnover, phylogenetic turnover, tetrapods, Europe, environmental gradients, phylobeta

PS4.15 ⚡ Plant functional diversity effects on ecosystem resilience – linking traits and ecosystem functioning at the continental scale

Franziska Schrodt[1], Miguel D. Mahecha[2], Fabian Gans[2], Sophia Ratcliffe[3], Mario Liebergesell[3], Erik Welk[4], Martin Jung[2], Matthias Forkel[2], Jens Kattge[2], Ingolf Kühn[5]
[1] German Centre for Integrative Biodiversity Research (iDiv) Halle - Jena - Leipzig, Max Planck Institute for Biogeochemistry
[2] Max Planck Institute for Biogeochemistry
[3] University of Leipzig
[4] University of Halle
[5] Helmholtz Centre for Environmental Research UFZ
Contact: f.i.schrodt@gmail.com

Classical biogeography supports the notion that functional diversity (FD) is tightly linked to ecosystem functioning (EF). However, limited availability of large-scale data as well as unclear guidelines on the measures of FD resulted in many unanswered questions. Amongst them are large-scale spatial patterns of FD, the relative effect of FD on EF and to what extent FD influences an ecosystem's resilience to climatic extreme events. In this study we capitalize on an extensive database of plant functional traits (TRY) in tandem with species distribution and satellite remote sensing data in order to derive a consistent map of FD across European trees and answer some of these questions. We present FD maps of 18 foliar and woody traits of trees across Europe, using distribution maps for 168 tree species derived from an ensemble of species distribution models which we validated using European Vegetation Archive (EVA) and GBif data. By applying 9 different FD indices, we explore the overall variability of FD, as well as how spatial patterns of FD are related to EF in European Eco-regions and draw conclusions on the effect FD may have on ecosystem resilience to climatic extreme events.

Keywords: plant traits, biodiversity, ecosystem functioning, climatic extremes, large-scale, upscaling

PS4.16 Functional traits and global productivity gradient: can we predict ecosystem processes using plant assemblage composition?

Irena Šímová[1], Brody Sandel[2], Cyrille Violle[3], Jens-Christian Svenning[2], John C. Donoghue II[4], Brad Boyle[5], Naia Morueta-Holme[6], Nathan J.B. Kraft[7], Brian J. McGill[8], Brian J. Enquist[4]
[1] Center for Theoretical Study, Charles University in Prague
[2] Section for Ecoinformatics and Biodiversity, Department of Bioscience, Aarhus University, Denmark
[3] Centre d'Ecologie Fonctionnelle et Evolutive, CNRS, Montpellier, France
[4] Department of Ecology and Evolutionary Biology, University of Arizona, USA
[5] The iPlant Collaborative, Thomas W. Keating Bioresearch Building, USA
[6] Dept. Integrative Biology Berkeley, USA
[7] Department of Biology, University of Maryland, College Park, MD, 20742 USA
[8] School of Biology and Ecology / Sustainability Solutions Initiative, University of Maine, Orono, USA
Contact: office@cts.cuni.cz

Understanding the links between functional traits and ecosystem processes is the ‘Holy Grail’ of plant functional ecology. Here we aimed to predict large-scale variation in ecosystem processes, such as net and gross biomass production and canopy height, using information about species occurrences and their functional traits. We hypothesized that these relationships would differ for tropical vs. temperate assemblages. We used the recently developed BIEN database of species occurrences and functional traits covering the entire New World. As expected, mean and maximum assemblage height and mean seed mass corresponded to remotely sensed canopy height. Net and gross primary production strongly increased with increasing assemblage height and specific leaf area and decreased with increasing leaf nitrogen and leaf phosphorus content. While these relationships were consistent across the New World, they often varied in strength between tropical and temperate assemblages. Functional traits can significantly improve the vegetation components of global dynamic vegetation models, although regional differences in their performance should be considered and further explored.

PS4.17 Cross-function congruence of functional diversity patterns

Mariana Tsianou[1], Athanasios Kallimanis[1]
[1] Department of Environmental and Natural Resources, University of Patras
Contact: mtsianou@upatras.gr

Recent research has focused on functional diversity patterns. However, it remains unclear if different functional traits or group of traits (FTG) show congruent functional diversity patterns and if one FTG could act as a surrogate for another FTG. We quantified the functional diversity of amphibians of Europe and examined six metrics of ecological function (FD, FRic, FEve, FDis, FDiv, RaoQ) in each community. Each metric was calculated firstly based on 41 functional traits encompassing morphological (M), reproductive (R) and habitat-related (H) traits and secondly only for each FTG (M, R, H), or for combinations of FTG (MH, MR, RH), quantitative and qualitative FTG separately. Congruence between FTG was higher for MH FTG while it was markedly lower for R FTG and all the others. The cross-function congruence between quantitative and qualitative FTG varied according to the different metrics. Our results indicate that for metrics which reflect range of functional space any FTG could be used as surrogate for other components while for functional evenness this is less feasible.

Keywords: functional trait group, surrogacy, amphibians, functional diversity indices

PS4.18 Processes entangling plant-hummingbird networks across space: how widespread is the importance of forbidden links in detriment of abundances?

Jeferson Vizentin-Bugoni[1], Maruyama Pietro K[1], Rui Ana M[2], Dalsgaard Bo[3], Sazima Marlies[1]
[1] Universidade Estadual de Campinas
[2] Universidade Federal de Pelotas
[3] University of Copenhagen
Contact: jbugoni@yahoo.com.br

Despite the increasing consensus on the importance of species abundance defining interactions in communities, recent studies on plant-hummingbird networks have pointed to higher importance of forbidden links in detriment of species abundances. However, how general these finding are across plant-hummingbird networks remains elusive. Here we used null models, associated to likelihood analysis and models selection to investigate the relative importance of forbidden links (FL) *vs.* abundances on the structure of six plant-hummingbird networks from three biomes in Brazil: Atlantic Rainforest, Cerrado and Pampas. The frequencies of interactions were better predicted by FLs than by abundances in all networks, except Pampas. The discrepancy found for Pampas could be explained by the high similarity of traits, both for hummingbirds and plant species (which results in low specialization), as well as by the high dominance of a single hummingbird. Ours findings show that, more than abundances, ecological and evolutionary processes acting on species traits produces spatio-temporal and morphological mismatches, which create FLs and define network structure across plant-hummingbird networks.

Keywords: Plant-pollinator networks, plant-hummingbird interactions, pollination, South America, macroecology

P1 Island biogeography

1.1 Age and distribution patterns of *Melicope* (Rutaceae) in the Pacific

Marc S. Appelhans[1], Jun Wen[2], Warren L. Wagner[2]
[1] Department of Systematic Botany, University of Goettingen, Germany
[2] Smithsonian Institution, Washington/DC, USA
Contact: marc.appelhans@biologie.uni-goettingen.de

With about 235 species, *Melicope* is the largest genus of the Citrus family (Rutaceae). It is mainly distributed in SE Asia, Malesia, Australasia and the Pacific, and also shows a disjunct distribution in Madagascar and the Mascarene Islands. The genus is subdivided into four sections, all of which are present on several Pacific archipelagos. *Melicope* colonized most Pacific islands groups; and the most isolated archipelagos on which the genus can be found are the Hawaiian Islands in the Northeast and the Austral and Marquesas Islands in the Southeast. Species from all archipelagos have been sampled in our molecular phylogenetic and dating analyses, thus allowing the reconstruction of dispersal routes and age estimations. The most noteworthy insights are that (1) the geographic origin of the species from the Marquesas Islands are the Hawaiian Islands instead of the much less remote Society Islands; (2) two independent colonization events from Hawaii brought *Melicope* to the Marquesas Islands; and (3) the occurrence on the isolated Austral Islands is the result of two independent colonization events, with one lineage derived from Vanuatu/Fiji and the other one from New Zealand.
Keywords: Island Biogeography; Melicope; Molecular dating; Pacific Islands; Rutaceae

1.2 ⚡ Species abundance distributions (SADs) in different trophic groups accross archipelagos

Paulo Borges[1]
[1] Azorean Biodiversity Group, University of the Azores
Contact: pborges@uac.pt

The observation that ecological systems contain a small number of very abundant species and numerous relatively rare species is often described as one of only a few universal ecological laws. In this contribution we use standardized arthropod and vascular plant datasets from the Azores, Madeira, Canary Islands and La Reunion to investigate the impact island characteristics in species abundance distributions (SADs). We found that in Azores a large number of communities are bimodal, comprising very rare species (i.e. with low abundances) and relatively common species. Satellite taxa, introduced species and species that are more adapted to anthropogenic land surrounding the native forest tend to be found in lower abundances. More generally for all the archipelagos, we also found that SADs change as a function of species rarity and island age. In this respect, island identity is more important than trophic group in the properties of SADs. The consistent observed differences in the shape and parameters of island SAD models demonstrate that the study of relative species abundances is potentially useful in island biogeography
Keywords: SADs; community assembly; Macroecology;Azores, Canary Islands, La Reunion

1.3 ⚡ Species sorting in metacommunities of endorheic shallow lakes

Andreu Castillo-Escrivà[1], Luis Valls[1], María Belenguer[1], Máximo Florín[2], José Antonio Gil-Delgado[1], Rafael U. Gosálvez[3], Celia Laguna[2], Antonio Picazo[1], Carlos Rochera[1], Ángel Velasco[4], Xavier Armengol[1], Antonio Camacho[1], Francesc Mesquita-Joanes[1]
[1] Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia
[2] Grupo de Investigación en Hidroecología, Universidad de Castilla-La Mancha
[3] Departmento de Geografía y Ordenación del Territorio, Universidad de Castilla-La Mancha
[4] Departmento de Ciencias Ambientales, Universidad de Castilla-La Mancha
Contact: mezquita@uv.es

The metacommunity concept suggests that local communities are linked by dispersal of component species. Ecologists have recently investigated the potential importance of environmental and spatial processes in structuring metacommunities, observing differences between types of ecosystems and taxa. In this framework, the important role of organism traits such as body size and dispersal mode, have been highlighted. This study aims to determine the relative influence of environmental and spatial effects on bacterioplankton, branchiopod and ostracod metacommunities in endorheic shallow lakes of the Iberian Peninsula. Variation partitioning analysis allowed separating pure environmental and spatial (MEMs) components. Our results reveals the dominance of the environmental factors in all the taxa studied. In contrast with previous studies, space was not found significant, and the percentage of variance

explained by environmental components was lower in bacteria than branchiopods and ostracods. Studies with different taxa and large environmental gradients should be considered to understand the mechanisms underlaying the assembly of metacommunities. This work was supported by the project ECOLAKE (CGL2012-38909).

Keywords: Metacommunities, , dispersal, endorheic lakes, Bacteria, Ostracoda, Branchiopoda

1.4 Diversity, differentiation, and zonation of marine lake communities

Michael Dawson[1], Lauren Schiebelhut[1]
[1] School of Natural Sciences, University of California, Merced
Contact: mdawson@ucmerced.edu

Marine lakes are 'islands' — bodies of seawater entirely surrounded by land — that come in a great variety of shapes, sizes, distances from the 'mainland' sea, environmental characteristics, and species complements. We are exploring the factors that shape patterns of genetic, taxonomic, and functional diversity geographically and through time in marine lakes. Here, we use point-intercept transect surveys of macro-invertebrates and macrophytes to describe patterns in the genetic and taxonomic components of diversity, differentiation, and zonation of communities inhabiting a subset of 6 marine lakes in Palau, Micronesia. Preliminary analyses suggest (1) genetic and species diversity are related to the isolation and size of a lake, (2) that the degree of differentiation among lakes is driven by environmental factors, and (3) strong vertical zonation is present when lakes are stratified strongly by temperature, salinity, and light. In these respects, marine lakes show patterns similar to those in many other island assemblages suggesting that general ecological and dynamic models may be informative for a wide diversity of island types.

Keywords: marine biogeography, island biogeography, biodiversity, invertebrates, algae, Pacific

1.5 ⚡ Wasted seed dispersal by Galapagos tortoises?

Diego Ellis Soto[1], Stephen Blake[2], Stefan Lötters[1]
[1] Biogeography, Universität Trier
[2] Max Planck Institut for Ornithology, Vogelwarte Radolzfell
Contact: Diego.Ellis-Soto@uni-konstanz.de

We compared the abundance and distribution of vascular plant species found in tortoise (*Chelonoidis nigra*) dung piles and in living plants. A total of 225 dung piles and 60 vegetation plots with 50 m^2 cover were sampled along an altitudinal gradient of 0-400m covering three vegetation zones of Santa Cruz Island, Galapagos. Vegetation community differs greatly between living plant and seed data. Our vegetation plots show a more homogeneous distribution of plant species along altitude than the distribution of plant species in dung piles and none of the most common plant species found in dung was commonly present as living plant. Potential range extension through long distance dispersal was found in all common vascular plant species dispersed by tortoises. Additionally, each the current and future climatic suitability of two invasive and one native plant species dispersed by tortoises was modeled with Maxent. Results suggest a suitability decrease and a potential range shift under climate change in all three species, resulting into an increased overlap and hypothetical seedling competition of the invasive passion fruit (*Passiflora edulis*) and the native cat´s claw (*Zanthoxylum fagara*).

Keywords: Invasive species ,Galápagos tortoises, seed dispersal, species distribution modeling

1.6 Abundance-area relationships in passerines on Mt Cameroon: montane forest species compensate for less space available

Michal Ferenc[1], Jon Fjeldså[2], Ondřej Sedláček[1], Francis Njie Motombi[3], Eric Djomo Nana[1], Karolína Mudrová[1], David Hořák[1]
[1] Department of Ecology, Charles University in Prague, Czech Republic
[2] Center for Macroecology, Evolution, and Climate, Zoological Museum, University of Copenhagen, Denmark
[3] Botanic Garden, Limbe, Cameroon
Contact: ferenc.michal85@gmail.com

One of the most pervasive patterns in ecology - the positive interspecific abundance-range size relationship (ARSR) - appears to be distorted in tropical mountains. We aimed at describing this relationship for passerine bird communities along a tropical elevational gradient of Mt Cameroon. Abundance estimates of birds based on 16 point counts at six different elevations were related to their range sizes and total area occupied on the mountain. In

contrast with theory, we revealed a negative ARSR for the entire passerine community. However, this relationship seems to be a compound of different patterns, as for within-elevation communities the slope of ARSR changed from a positive one in the lowland to a negative and zero slope at higher altitudes. The negative ARSR therefore seems to be driven by high abundances of montane species possibly caused by high degree of specialisation and/or competitive release in species poor montane communities. The pattern might be further reinforced by an extinction filter removing less widespread species with low abundances and our data indeed suggest that montane birds compensate for smaller area occupied locally by having higher local abundances.

Keywords: abundance-range size; density compensation; extinction filter; specialization; tropical elevational gradient

1.7 ⚡ Biogeographic ranges not predicted by niche theory in radiating Canary Island plant genera

Richard Field[1], Manuel Steinbauer[2], José-Maria Fernández-Palacios[3], Rüdiger Otto[3], Carl Beierkuhnlein[2]
[1] School of Geography, University of Nottingham, UK
[2] Department of Biogeography, Bayreuth Center of Ecology and Environmental Research BayCEER, University of Bayreuth, Germany
[3] Departamento de Ecología, Facultad de Biología, Universidad de La Laguna, Spain
Contact: richard.field@nottingham.ac.uk

The competitive displacement hypothesis holds that closely related co-occurring species should diverge, while niche conservatism suggests they should have similar niches. If these are key structuring forces, they should be detectable for endemic species in radiating genera in oceanic archipelagos, where closely related species exist in both sympatry and allopatry and the entire species' ranges are known. We tested whether the climatic niche relationships predicted by the two hypotheses are found for the plant genera *Aeonium, Argyranthemum, Descurainia, Echium* and *Sonchus* in the Canary Islands. We used a new, high-resolution dataset to compare patterns between sympatric and allopatric species, and where possible within species pairs: comparing climatic niches for sympatric and allopatric populations. Phylogenetic distance–climatic niche differentiation relationships were weak and mostly non-significant. Niche differentiation was greater in allopatry in the relatively few significant comparisons. Thus we found little signal of niche conservatism in the biogeographic ranges of species in Canarian plant radiations and the opposite of the competitive displacement hypothesis predictions.

Keywords: competition, niche conservatism, ecological character displacement, adaptive radiation, climate, endemic plants, sister clades, speciation, divergence, ghost of competition past

1.8 ⚡ Spatial and environmental drivers of vascular plant richness across the islets of Sardinia

Mauro Fois[1], Giuseppe Fenu[1], Gianluigi Bacchetta[1]
[1] Centro Conservazione Biodiversità, University of Cagliari
Contact: mau.fois1@studenti.unica.it

Islands have often been considered as "natural laboratories" for studies on the biology, ecology, and genetics of plant species. Although, distribution patterns of vascular flora of Sardinia (second largest island of Mediterranean Basin), and its 261 circum-Sardinian islets, have been poorly investigated. We focused our research on distribution of the vascular flora in all the islets around Sardinia; besides all common island species–area relationship (ISAR; including choros) functions, the correlation between total vascular flora/endemic richness and geographic, topographic, climatic and anthropic drivers have been analyzed. A total of 81 islets hosted endemic plants; all ISAR functions showed significant correlations but the responses of endemic richness were higher influenced by elevation, distance from the main island and human disturbances than total richness. Our study provided new insights into the small Mediterranean island biogeography, useful for future conservation activities.

Keywords: Island biogeography, Sardinia, endemic vascular flora, Mediterranean Basin

Continued next page

1.9 Biogeography of the high-spired planorbids (Gastropoda: Planorbidae) in Wallacea

Pauline Gauffre Autelin[1], Christian Albrecht[1], Thomas von Rintelen[2]
[1] Department of Animal Ecology & Systematics, Justus Liebig Universität, Giessen
[2] Museum für Naturkunde, Leibniz-Institut für Evolutions- und Biodiversitätsforschung, Berlin
Contact: pauline.gauffre@hotmail.fr

Wallacea is a geologically and tectonically complex region that is considered as a biodiversity hotspot and a model region for studying island biogeography. While the biogeography of its largest island, Sulawesi, has been extensively investigated, few studies exist for the adjacent regions (Moluccas archipelago and Papua New Guinea (PNG)). Freshwater molluscs with limited dispersal capabilities should be good candidates to test biogeographic hypotheses across wide geographic and geological time scales, particularly in an insular setting. High-spired planorbid gastropods occur in Australia, PNG, Sulawesi and other parts of Indonesia. We performed a Bayesian divergence time estimation based on a fragment of the mitochondrial *Cox* I gene. The phylogenetic relationships reveal three island-specific clades within Wallacea and two clades within PNG. The divergence time estimates indicate rather recent dispersal events in the early Pliocene to late Pleistocene. Given the estimated age and geological history of each island, the biogeographical pattern of this group in Wallacea and PNG is likely the result of passive dispersal events, although Australia-PNG vicariance cannot be excluded.

Keywords: Island Biogeography, Wallacea, freshwater gastropods

1.10 ⚡ Biodiversity patterns of freshwater snails in European lakes

Elisavet Georgopoulou[1], Thomas A. Neubauer[1], Mathias Harzhauser[1], Andreas Kroh[1], Oleg Mandic[1]
[1] Geological-Paleontological, Natural History Museum of Vienna
Contact: elisavet.georgopoulou@nhm-wien.ac.at

We investigate the biogeography of freshwater gastropods of European lakes. For the first time, we compiled occurrence records for more than 200 snail species, as well as data on the limnological and geographical parameters (e.g. latitude, longitude, altitude and shoreline) for more than a 1000 lakes across Europe. Our goals are to identify biogeographical regions, document the patterns of freshwater gastropod species richness and reveal possible causes of their distribution. To identify the regions, cluster analyses were conducted in order to estimate the similarity of lake faunas. Moreover, regression models were applied to explore the relationships between species richness and lake parameters. Preliminary results show that species richness is increasing in south- and north-eastern Europe. An increase of endemic species is observed in southern Europe, while, central and north European lake faunas are rather homogenous with a clear absence of endemic species. Dendrograms reveal well-defined units for central and northeastern European lake groups. Among the main factors explaining species richness is lake size.

Keywords: European lakes, freshwater gastropods, species richness, faunal patterns, biogeography

1.11 ⚡ Scale-dependent species–area relationships in a uniform habitat in fragmented Mediterranean grasslands.

Itamar Giladi[1], Yaron Ziv[2]
[1] Mitrani Department of Desert Ecology, Ben Gurion University
[2] Department of Life Science, Ben-Gurion University of the Negev
Contact: itushgi@bgu.ac.il

The species-area relationship (SAR) is a frequently used tool for biodiversity conservation in fragmented landscapes. However, the pattern that relates species density with fragment area (D-SAR) is much less explored, even though it can also inform conservation decisions. In plants, DSAR is an elusive pattern whose detection and significance are grain-size dependent. Using hierarchal sampling to sample plant species density and species richness we constructed SAR and grain-dependent D-SARs for fragments of a relatively uniform habitat within a semi-arid agro-ecosystem. We found a significant SAR, but insignificant D-SARs. These results contrast those from a previous study, where significant DSARs were found for heterogeneous fragments, indicating that habitat heterogeneity may have a significant contribution to the generation of D-SARs. The comparison of grain size-dependent analyses in sites with different habitat complexity shed light on the mechanisms that generate the relationships between species richness or species density and fragment area. This should also have implications for practical considerations involving conservation decisions.

Keywords: SAR, Scale-dependent patterns, agro-ecosysetm, Plants

1.12 ⚡ What drives range size differences of endemic plant species on an oceanic island?

Severin D.H. Irl[1], David E.V. Harter[1], Anke Jentsch[2], Carl Beierkuhnlein[1]
[1] Biogeography, BayCEER, University of Bayreuth
[2] Disturbance Ecology, BayCEER, University of Bayreuth
Contact: severin.irl@uni-bayreuth.de

Oceanic islands harbor a wide range of endemic species. However, within each island endemics can have strongly varying range sizes, some being highly range-restricted 'specialists' and others widespread 'generalists'. In addition, specific traits (e.g. growth form, dispersal mode, N-fixing and succulence), which are connected to specific environmental conditions, might determine the range size of endemics. Also, it is not clear if small-ranged specialists or an agglomeration of generalists create hotspots of endemic richness (ER). Single-island endemics (SIEs), which evolved in situ under island conditions, will likely have different range sizes than archipelago endemics (AEs). We hypothesize the following: i) Environmental conditions and specific ecological traits determine the range size of endemics, ii) hotspots of ER result from the agglomeration of generalist species, and iii) SIEs have smaller ranges and are therefore more specialized than AEs. To test this, we use a spatially highly resolved dataset of endemic vascular plants and environmental data in 890 plots on La Palma, Canary Islands to relate various range size metrics to ER and environmental variables.

Keywords: Plant traits; range size rarity; island biogeography; spatial ecology; endemics

1.13 ⚡ Body size evolution across insular populations of two Mediterranean lizards – playing by the rules?

Yuval Itescu[1], Colin Donihue[2], Alex Slavenko[1], Johannes Foufopoulos[3], Panyiotis Pafilis[4], Shai Meiri[1]
[1] Department of Zoology, Tel Aviv University, Israel
[2] School of Forestry and Environmental Studies, Yale University, New Haven, USA
[3] School of Natural Resources and Environment University of Michigan, Ann Arbor, Ann Arbor, USA
[4] Section of Zoology and Marine Biology, Department of Biology, University of Athens, Greece
Contact: yuvitescu@gmail.com

Island animals often differ in size from mainland relatives. Theory and some data suggest this is affected by biotic and abiotic characteristics of islands. To test the effect of island characteristics, we measured snout-vent lengths of the lacertid *Podarcis erhardii* (2821 specimens, 48 islands) and the gecko *Mediodactylus kotschyi* (808 specimens, 32 islands) from the Aegean Sea, in the field and in museums. We tested how size is affected by island area, isolation, predator presence and richness, competitor presence and richness, and presence of sea-bird nesting colonies (enabling marine subsidies). The size of *P. erhardii* is unaffected by any predictor. The size of *M. kotschyi* is negatively correlated with competitor richness, but is not affected by the other predictors. We conclude that either the factors thought to drive size evolution have little effect or that common indices for these forces do not adequately measure selection intensity. Insular environments are more complex than is usually thought and insular animals therefore don't necessarily 'play by the rules'. We suggest that such 'mis-behavior' may be a rule in itself.

Keywords: Biogeography, Body size, Islands, Lizards

1.14 ⚡ Habitat history in subtropical oceanic island summit ecosystems, with special reference to the Canarian flora

José María Fernández-Palacios[1], Rüdiger Otto[1], Cristophe Thebaud[2], Jonathan Price[3]
[1] University of La Laguna
[2] CNRS/Paul Sabatier University
[3] Hawai'i University at Hilo
Contact: jmferpal@gmail.com

Summit ecosystems of oceanic islands constitute one of the most ephemeral and isolated ecosystems existing, harbouring specific features that confer their biota an outstanding singularity. Summits are ephemeral, being the last ecosystems to be constructed during the growth of the new oceanic island, and the first to vanished due either to island subsidence, island erosion, or both of them. Whereas their geological emergence/disappearance is controlled by the volcanic/erosion activity, the Pleistocene glaciations, forcing in the last million years the altitudinal shift of the

timberline, have also created or destroyed summit ecosystems, enabling the appearance of alpine ecosystems in glaciation maxima where they were not present in interglacial periods and vice versa. On the other hand, summit ecosystems constitute islands within islands, being more isolated from similar ecosystems than the coastal lines of the islands containing them. Thus summit biota, frequently displaying a high endemicity, may originate either through dispersal from other close summit ecosystems during peak periods, or from the colonization of the summits and later evolution to the new conditions from mid-altitude species of the same island.

Keywords: Subtropical oceanic islands geological summit emergence summit flora climatic summit emergence

1.15 ⚡ Historical Biogeography of selected Macaronesian Laurel forest species

Paulina Kondraskov[1], Nicole Schütz[1], Christina Schuessler[1], Mike Thiv[1]
[1] Stuttgart State Museum of Natural History
Contact: paulina.kondraskov@smns-bw.de

Macaronesia has been traditionally recognized as a distinct biogeographic unit consisting of five Atlantic volcanic archipelagos: Azores, Madeira, Salvage Islands, Canary Islands, and Cape Verde Islands. Unique climate and geological conditions on these islands are essential for survival of highly specialized vegetation types, like the Macaronesian laurel forests (MLF). We studied the biogeography of the MLF, which occur on the Azores, Madeira and the Canary Islands using phylogenetic, molecular dating and biogeographic analysis of 18 representative forest taxa. Our preliminary results indicate a heterogeneous biogeographical pattern of the MLF within and across the archipelagos. Most of the MLF taxa colonized Macaronesia from Europe in a relatively recent single event, while for some taxa independent colonizations of these archipelagos have been detected. Radiation of the MLF taxa within and across the Macaronsian islands appears to be rare. Furthermore speciation and distribution histories of the taxa seem not to correlate with the geological island histories.

Keywords: island biogeography, dispersal, laurel forest, radiation, geological island history

1.16 Assessing peculiarities of island biota: A global analysis of taxonomic and functional disharmony in vascular plants

Christian König[1], Patrick Weigelt[1], Holger Kreft[1]
[1] Biodiversity, Macroecology & Conservation Biogeography Group, University of Goettingen
Contact: chr.koenig@hotmail.de

Disharmony describes the compositional imbalance of island biota compared to mainland source regions. It may arise from taxon-specific differences in the ability to disperse to and to survive and diversify on islands and thus involves key biogeographical processes. Here, we present a global quantitative analysis of island disharmony, based on vascular plant floras of 315 islands and 43 mainland units. Species were assigned to a consistent taxonomy and supplemented with information on growth form (tree, shrub, herb), woodiness and epiphytism from literature resources. We quantified taxonomic and functional disharmony by calculating the mean Bray-Curtis dissimilarity between the relative family and trait level proportions of an island and 100 samples randomly drawn from the most probable mainland source regions in the dataset. Islands were more variable in their compositional structure than mainlands and showed an overrepresentation of ferns and epiphytes. Isolation, island size and bioclimatic conditions had significant effects on functional and taxonomic disharmony, highlighting the crucial roles of dispersal abilities and ecological constraints for global species distributions.

Keywords: Disharmony, Island Biogeography, Vascular plants, Compositional patterns

1.17 ⚡ Island biogeography: moving beyond species numbers

Christoph Kueffer[1], Jialin Zhang[1]
[1] ETH Zurich
Contact: kueffer@env.ethz.ch

The island biogeography theory of McArthur and Wilson (1967) is the most influential theory in biogeography. It is a powerful way to explain and predict the number of species present in an isolated land area as a consequence of immigration and extinction. However, the theory does not address patterns of phylogenetic or functional diversity.

Thanks to the rapidly growing availability of phylogenetic and ecological data from oceanic islands, it becomes increasingly possible to address such dimensions of island biodiversity. In this talk I will give an overview of research on the phylogenetic and functional diversity of island floras at local to global scales that we do in my research group and in collaboration with partners from around the world. We have recently compiled a global database of floristic data from c. 120 island archipelagos that allows us to investigate what determines phylogenetic diversity and drives plant radiations on islands. In the Seychelles (Western Indian Ocean) and Canary Islands (Macaronesia) we combine such information on speciation patterns with comprehensive data on plant functional traits collected in the field.

Keywords: island biogeography, speciation, adaptive radiation, oceanic island, functional diversity, phylogenetic diversity, plants, global

1.18 The general dynamic model of island biogeography revisited on the level of major plant families

Bernd Lenzner[1], Manuel Steinbauer[1], Patrick Weigelt[2], Holger Kreft[2], Carl Beierkuhnlein[1]
[1] Department of Biogeography, BayCEER, University of Bayreuth
[2] Biodiversity, Macroecology & Conservation Biogeography Group, University of Göttingen
Contact: bernd_lenzner@gmx.de

The “general dynamic model of island biogeography” (GDM), by Whittaker et al. (*J. Biogeogr.* 2008) serves to explain general biotic patterns of oceanic archipelagos for major taxonomic groups in relation to the ontogeny of oceanic islands. Here, we explore, if the model predictions can successfully be applied when overall species richness is deconstructed into different major plant families. We investigate species richness and endemism patterns for the ten most common vascular plant families on 17 oceanic archipelagos worldwide. Our results yield contrasting patterns for individual family richness and endemism with area being consistently more important than age. The pattern of single families differed among each other and from the pattern that all of them show combined. Consequently, we find that the GDM has proven to be very successful in providing a theoretical framework with broad generality. Nevertheless, our results indicate that general patterns for vascular plants are driven by a few large families and thus are strongly biased towards them.

Keywords: general dynamic model of island biogeography, species richness, endemism, vascular plants

1.19 ⚡ Island ontogeny and the macroevolutionary dynamics of clades on oceanic islands: testing hypothesized diversity under and overshoots in Hawaii

Jun Ying Lim[1], Tiago Quental[2], Charles Marshall[3]
[1] Integrative Biology, University of California, Berkeley
[2] Universidade de São Paulo, São Paulo, SP, Brazil
[3] Integrative Biology, UC Berkeley
Contact: junyinglim@berkeley.edu

MacArthur & Wilson’s Equilibrium Theory of Island Biogeography posits that the species richness of islands is an emergent equilibrium between immigration and extinction. For remote volcanic islands, however, immigration events may be so infrequent that in situ speciation becomes the dominant factor in generating species richness. In addition, most volcanic islands are not static entities, growing in size as they form, and gradually decreasing in area due to erosion or subsidence. Recent models attempt to account for these processes by considering the fact that the equilibrium species richness (the carrying capacity) can vary with time, but remain largely qualitative. Here, we develop a quantitative model that incorporates a model of island ontogeny to predict the temporal trajectories of species richness over the lifetime of an oceanic island. We test our model using published data of species richness across a variety of plant and animal clades across the Hawaiian archipelago, where islands effectively reflect different stages of island building and erosion, and show that different clades can exhibit different macroevolutionary dynamics relative to the changing physical landscape.

Keywords: macroevolution, island ontogeny, cladogenesis, Hawaii, extinction, equilibrium diversity

Continued next page

1.20 The relationships between local abundance, range size and niche breadth of woody plant species in a mountain context

Ye Liu[1], Zehao Shen[1], François Rigal[2], Zhiheng Wang[1], Kostas A. Triantis[2]
[1] Department of Ecology, Peking University
[2] Azorean Biodiversity Group, Universidade dos Açores
Contact: lye@pku.edu.cn

The abundance-range size relationship is a fundamental question in macroecology albeit it has been rarely studied in a mountain context. In this study, for 360 woody species in the forests of a subtropical mountain in China, we obtained two measures of abundances , and three range size measurements . We also introduced a niche breadth index using three descriptors of the local topography. We show a persistent positive and significant relationship between abundances, proportion of occupied sites, altitudinal extent and niche breadth. National range size was poorly correlated with most of the other variables. Controlling for sampling effect, the relation between the both abundances and niche breadth turned negative, highlighting the competition vs. adaptation trade-off of ecological strategy existed between the specialist and generalist species. Our results provide support to the metapopulation dynamics hypothesis but not to the niche breadth hypothesis, and stress the scale-dependence of the abundance-range size relationship.

1.21 ⚡ Endemic butterfly radiation on the Caribbean: insights from historical biogeography and phylogenetic diversification

Pavel Matos-Maravi[1]
[1] Institute of Entomology, Biology Center AS CR
Contact: pavelm14@gmail.com

Calisto is the largest butterfly genus in the West Indies whose crown age was estimated at the early Oligocene (31 Ma). We found that a single shift in phylogenetic diversification rate following a diversity-dependent speciation process was the best explanation for its present-day diversity distribution. Moreover, the ancestral geographical distribution of *Calisto* is in line with the paleogeographical model of Caribbean colonization, which favours island-to-island vicariance. However, long-distance dispersal was also invoked as the best explanation for the colonization of Jamaica and the Bahamas. The arrival of *Calisto* to the West Indies remains to be explained, although, given its age and historical biogeography, the hypothesized GAARlandia land bridge might have been a plausible introduction route from continental America. Intra-island radiation caused by ecological innovation and the abiotic creation of niche spaces was found to be the main force shaping *Calisto* diversity and island endemism in Hispaniola and Cuba. By understanding the evolution of *Calisto* butterflies, we attempted to identify the main processes acting on insular insect diversity and the causes of its origin.
Keywords: Caribbean; Ecological limits; Historical biogeography; Intra-island diversification; Island-island vicariance; Lepidoptera; Molecular phylogeny

1.22 ⚡ Origin, evolution, assembly and maintenance of biodiversity – local mechanisms and their effect on patterns of SE Asian plant diversity

Alexandra Muellner-Riehl[1], Melanie Grudinski[2], Caroline Pannell[3]
[1] University of Leipzig & German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany
[2] University of Leipzig & Biodiversity and Climate Research Centre (BiK-F)/Senckenberg and Goethe University, Frankfurt am Main, Germany
[3] University of Oxford, Department of Plant Sciences, Oxford, UK
Contact: muellner-riehl@uni-leipzig.de

Southeast Asia has one of the most diverse terrestrial biota on our planet. In contrast to continental Amazonia, megadiverse SE Asia is largely insular in nature. It comprises numerous archipelagos of thousands of mostly smaller oceanic and larger continental islands. This fragmented nature of SE Asia's geography is mirrored in the distribution of its extant terrestrial biota, characterized by a high degree of regional and local endemism. We review current knowledge on the interplay of local mechanisms (geological and climatic changes) with patterns of SE Asian flowering plant diversity. In addition, we present an updated and resolved phylogenetic tree for a widespread animal -dispersed woody angiosperm genus (*Aglaia*, Meliaceae), and shed light on its geographic origin and dispersal history. Our analyses (BEAST, S-DIVA, DEC), based on DNA sequences of 157 accessions representing 102 species and

all phylogenetic entities, shows that the directionality of dispersal events was predominantly eastwards, following the expansion of wet tropical forest across Wallace's Line and beyond. Most reconstructed areas and events temporally coincide with the known historical geological settings.

1.23 A framework and experimental approach for testing the role of plant dispersal on ecosystem function

Luka Negoita[1], Jason Fridley[1]
[1] Syracuse University
Contact: lnegoita@syr.edu

One of the central aims of ecology is to understand how biotic processes drive ecosystem function. For example, the movement of plant species, or their dispersal, may have important effects on local nitrogen and carbon dynamics. The role of dispersal on ecosystem function, however, remains largely understudied. This is surprising in light of the importance of dispersal in an increasingly fragmented world. I present a framework for linking plant dispersal with terrestrial ecosystem function and propose an experimental method for quantifying these effects. The framework follows a basic community assembly model in which the regional species pool is filtered into a local species pool by dispersal processes, and then those species interact to generate the realized community. The experimental method provides a way to quantify the functional composition of the local pool and realized community to test hypotheses about the role of dispersal on ecosystem function. I propose applying this experimental approach to old-field plant communities in eastern North America, and using my results to test predictions about the effect of dispersal across fragmented and insular landscapes.

Keywords: dispersal, ecosystem function, plants, community assembly, methods, island biogeography

1.24 Testing neutral vs. niche species assembly in the canopy arthropod communities of the Azorean native forests

Rui Nunes[1], Pedro Cardoso[2], António Soares[1], Brent Emerson[3], Paulo Borges[1]
[1] Azorean Biodiversity Group, University of the Azores
[2] Finnish Museum of Natural History, University of Helsinki
[3] Island Ecology and Evolution Research Group, Instituto de Productos Naturales y Agrobiología (IPNA-CSIC)
Contact: rui.mr.nunes@gmail.com

There is an on-going debate on the processes that structure ecological communities in which the neutral theory emphasizes the importance of stochastic processes and the niche-theory emphasizes mechanisms such as competitive interactions and local adaptations. In this contribution we implemented an arthropod sampling protocol at a plot scale in a native Laurisilva forest patch in Terceira Island (Azores Archipelago) consisting of a combination of year-round SLAM traps, sticky flight-intercept traps and fogging of the canopies, with the intent of answering the following questions: 1) what is the taxonomic and functional diversity of the arthropod communities present in the canopies of native Azorean trees, as well as the composition and structure of their trophic guilds? 2) what are the re-colonization processes that guide these communities. A comparison between fogging on one individual tree and beating on several Juniper trees seems to indicate low β-diversity amongst the arthropod community at small scales. Moreover, SADs show clear differences between herbivores that follow the assumptions of neutral theory and spiders that are more structured based on competitive interactions.

Keywords: neutral vs. niche theory; biodiversity; functional diversity; canopy arthropods; Azores; Laurisilva

1.25 ⚡ Factors affecting chasmophytic plant species diversity and endemism on the habitat islands of rocky limestone slopes and cliffs in Greece.

Maria Panitsa[1], Anna Kontopanou[1]
[1] University of Patras
Contact: mpanitsa@upatras.gr

The interior, mainly limestone, rocky formations with inclination of 65-90^{0}, are shelters for important, rare and sporadic plant species. Habitat type "Calcareous rocky slopes with chasmophytic vegetation" is included in Annex I to Directive 92/43 / EEC under the code 8210. A significant number of plant species in Annexes II, IV and V of that

Directive, several having a priority for protection due to their very limited geographical distribution, occur exclusively in this habitat type together with a large number of greek or local endemic plant species. For this study, a database has been prepared including plant taxa found exclusively, mainly or occasionally in such rocky ecosystems as also their protection status, their life form and their geographical distribution in the 13 different phytogeographical regions of Greece and in more than 70 rocky gorges or open rocky formations. Based on this database, an analysis of the diversity of chasmophytic plant species and of endangered, vulnerable or critically endangered plant taxa has been carried out as well as the study of the correlation of the chasmophytic plants diversity in the different phytogeographical regions of Greece and in different tocky formations.

Keywords: Endemism, habitat islands, rocky formations, cliffs, chasmophytic plant diversity

1.26 ⚡ Approximate Bayesian Computation reveals the crucial role of oceanic islands for the assembly of continental biodiversity

Jairo Patiño[1], Carine Mark[2], Mardulyn Patrick[3], Devos Nicolas[4], Mateo Rubén G.[1], González-Mancebo Juana M.[5], Shaw A. Jonathan[4], Vanderpoorten Alain[1]
[1] Department of Biology, Ecology and Evolution, University of Liege
[2] Department of Life Sciences, The Natural History Museum, London, UK
[3] Evolutionary Biology and Ecology, Free University of Brussels, Brussels, Belgium
[4] Department of Biology, Duke University, Durham, USA
[5] Department of Plant Biology, University of La Laguna, Tenerife, Spain
Contact: jpatino.llorente@gmail.com

In the oceanic island biogeography paradigm, volcanic islands are considered both engines of speciation and evolutionary dead-ends. We investigate whether such a paradigm holds for extremely mobile organisms, using bryophyte species that are disjunct between the mid-Atlantic Macaronesian archipelagos and Western Europe as a model. We compared the genetic structure and diversity observed in island and continental populations with those data simulated under three competing demographic scenarios, according to which: island populations derive from continental ones in agreement with classical island biogeography theory; gene flow from islands to continents and viceversa are recurrent and balanced, providing support to the hypothesis that islands have served as glacial refugia; and island populations are the source of colonists of continental landmasses *de novo*. Using an Approximate Bayesian Computation framework, we demonstrate that the patterns of genetic variation observed in the species examined are more compatible with a scenario in which continental populations have a Macaronesian origin. Our results therefore indicate that oceanic islands may be a key source of biodiversity for continental regions.

Keywords: approximate Bayesian computation; bryophytes; de novo colonization; island biogeography; last glacial maximum; long-distance dispersal

1.27 Using genetic variation to infer the comparative demographic history of avian populations in the West Indies

Maria Pil[1], Robert Ricklefs[1]
[1] Department of Biology, University of Missouri-St. Louis
Contact: ricklefs@umsl.edu

The sizes and distributions of populations vary over time, and episodes of population expansion and contraction create characteristic patterns of genetic variation that open a window onto demographic history. Here, we use indicators of population size change, including Tajima's D, Fu's FS, and mismatch distributions, based on mitochondrial genetic diversity, to infer demographic histories of three tanager-like bird species (*Coereba flaveola, Loxigilla noctis,* and *Tiaris bicolor*) across 19 islands in the West Indies. All three species showed evidence of dynamic, but independent, biogeographic and demographic histories, including phases of geographic expansion across the archipelago, heterogeneous phylogeographic affinities, and rapid expansion in several individual island populations. In several cases, genetic evidence suggests that recent population expansions extended across islands with older remnant populations.

Keywords: phylogeography, birds, West Indies

1.28 Global patterns of diversification on oceanic islands

François Rigal[1], Isabel R. Amorim[1], Ana M.C. Santos[2], Kostas A. Triantis[3], Robert J. Whittaker[4], Luis Borda-de-Água[5], Joaquin Hortal[2], Brent C. Emerson[6], Paulo A.V. Borges[1], Aristeidis Parmakelis[3]
[1] Azorean Biodiversity Group (CITA-A), and Portuguese Platform for Enhancing Ecological Research & Sustainability (PEERS), Departamento de Ciências Agárias, Universidade dos Açores, Portugal.
[2] Departamento de Biogeografía y Cambio Global, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain.
[3] Department of Ecology and Taxonomy, Faculty of Biology, National and Kapodistrian University of Athens, Greece.
[4] Conservation Biogeography and Macroecology Programme, Oxford University Centre for the Environment, UK.
[5] Centro de Biologia Ambiental, and Platform for Enhancing Ecological Research & Sustainability (PEERS), DBA/FCUL, Lisboa, Portugal
[6] Island Ecology and Evolution Research Group, IPNA-CSIC, La Laguna, Tenerife, Canary Islands, Spain
Contact: rigal@uac.pt

One of the central questions in oceanic island biodiversity studies concerns the tempo and the mode of evolutionary diversification among lineages and over time. Several empirical studies and recent theoretical developments (e.g. General Dynamic Model of insular biogeography) have emphasized the prevalent role played by both ecological, geographical and historical opportunities (e.g. isolation, area, topography of the island and geological age) in shaping diversification patterns in oceanic volcanic islands. However, no formal extensive analysis across groups of organisms and island systems has yet been performed, and to date, the factors causing variations in diversification patterns between islands and taxa remain poorly understood. We develop a meta-analysis approach in which diversification patterns of various island taxa originating from different oceanic archipelagos, will be investigated using a large set of molecular phylogenies retrieved from the literature and public sequence databases. Our ultimate goal is to identify whether diversification patterns and processes are shared both between the different oceanic archipelagos and the different taxa investigated.

1.29 ⚡ Macroevolutionary signals of insular adaptive radiations: Synthesizing across island systems with a novel statistical method

Andy Rominger[1], Rosemary Gillespie[1]
[1] University of California Berkeley
Contact: ajrominger@gmail.com

Recent advances in empirical and theoretical island biogeography have highlighted the importance of speciation, in addition to immigration and extinction, in driving patterns that seem to break MacArthur and Wilson's seminal predictions. One such example is higher diversity found on middle-aged and intermediately sized oceanic islands. Despite the importance of past macroevolutionary events in driving contemporary island diversity, we lack statistical methods to accurately estimate speciation and extinction from molecular phylogenies, often the only source of macroevolutionary information in insular systems. Here we develop a new method that utilizes the space-for-time information found in chronologically formed insular systems (such as hot spot oceanic islands and rift lakes) to estimate potentially complex models of waxing and waning diversification over the course of geological time. We apply this model to vertebrate, plant and arthropod adaptive radiations in Pacific islands and the East African Rift Lakes to search for generality in the accumulation of species through time and the trajectories of speciation, extinction and immigration in clades that achieve spectacular diversity.

Keywords: Adaptive radiation, island biogeography, phylogenetic inference

1.30 ⚡ Biogeography of Macaronesian-Mediterranean distributed Urticaceae

Christina Schüßler[1], Christian Bräuchler[2], Mike Thiv[1]
[1] Staatliches Museum für Naturkunde Stuttgart
[2] Ludwig-Maximilians-Universität München
Contact: christina.schuessler@smns-bw.de

Macaronesia harbors many endemics and is part of the Mediterranean Basin hotspot. Close biogeographic links between the Macaronesian and the Mediterranean flora have been proposed. Questions include the origin of island endemics, the time of colonization and possible shifts in ecological preferences. To address these problem we studied three Macaronesian endemics of Urticaceae, *Gesnouinia arborea* growing in the laurel forests and

Forsskaolea angustifolia and *F. procridifolia* occurring in dry habitats. Preliminary results from dated phylogenies based on *trnL-trnF* spacer and ITS sequences show that the closest relatives of both groups are species widely distributed in the Mediterranean region. The dry-adapted genus *Forsskaolea* is likely to have originated in Africa during Miocene when the global climate became more arid. Its spread into the Mediterranean and Macaronesia in Plio/Pleistocene correlates with the aridification in the Mediterranean. *Gesnouinia* dispersed to Macaronesia in the Pliocene. It shows a preference for shady and moist habitats like its Mediterranean relatives. Accordingly, *Forsskaolea* and *Gesnouinia* can be seen as examples for phylogenetic niche conservatism.

1.31 ⚡ Clutch size variability in an ostensibly fix-clutched lizard: effects of insularity on a Mediterranean gecko

Alex Slavenko[1], Yuval Itescu[1], Johannes Foufopoulos[2], Panayiotis Pafilis[3], Shai Meiri[1]
[1] Department of Zoology, Tel Aviv University
[2] School of Natural Resources and the Environment, University of Michigan
[3] Department of Zoology and Marine Biology, University of Athens
Contact: gluttony14@gmail.com

The island syndrome describes the evolution of life history traits in insular environments. Animals are thought to evolve slower life histories (e.g., smaller clutches of larger offspring) in insular environments, in response to release from predation pressure and interspecific competition. As islands grow larger and less isolated, they further resemble mainland environments. As such, life histories are expected to become slower with decreasing island area and increasing isolation. We present an intraspecific analysis of clutch sizes of 17 insular populations of *Mediodactylus kotschyi*, a small gecko, from the Cyclades archipelago, land-bridge islands in the Aegean Sea. Clutch size of *M. kotschyi* decreases with increasing island area, suggesting the evolution of faster life histories on smaller islands. However, there is no relationship between clutch size and either island age, maternal SVL, presence of competitors or snake richness. Larger clutch sizes on small islands could reflect increased resource abundance in the form of marine subsidies from nesting seabirds, as populations on islands with nesting seabirds have larger clutch sizes than on islands devoid of nesting seabirds.

Keywords: Cyclades, island biogeography, island syndrome, Kotschyi's gecko, life history, reproduction

1.32 ⚡ Aeolian Islands as an observatory for human-environment dynamics: resilience and reliance of prehistoric communities

Claudia Speciale[1], Girolamo Fiorentino[1]
[1] Laboratory of Archaeobotany and Paleoecology, University of Salento
Contact: claudiaspeciale@gmail.com

The Aeolian archipelago is a group of 7 little volcanic islands located off the northern coast of Sicily, emerged about 2 millions of years ago. The archipelago is very rich and heterogenic in terms of geomorphology and biodiversity and there are extremely different biotopes, including several endemic plants. Aim of this Poster is to analyze the delicate balance of human islanders communities during Prehistory (V-I millennium BC), dependent mainly on the environmental changes and the knowledge and use of the territory and its natural resources, to evaluate if the archipelago could be independent from the coast and self-sufficient. Internal relations, such as the occupation, abandonment and re-occupation of the single islands during the millennia will be considered, as well as the relation between inland and coast and between all the ecological landforms; furthermore, cultural exchanges and short/long distance contacts will be analyzed to identify their influence on supply systems. Vegetal macroremains from the archaeological sites were used in carbon stable isotope analysis to establish the paleoclimate trend and compare it with the cultural dynamics and the paleodemographic and socioeconomical data.

Keywords: Prehistory, Aeolian Islands, Sicily, Resilience, Paleodemography, Carbon Stable Isotope Analysis, Human-Environment Dynamics

1.33 ⚡ Patterns of colonization and diversification in the Western Indian

Ocean: creating a phylogeographic synthesis

Joeri Sergej Strijk[1], Timothée Le Péchon[2]
[1] Plant Ecophysiology and Evolution Group, Guangxi University, College of Forestry
[2] School of Life Sciences, University of KwaZulu-Natal, South Africa
Contact: jsstrijk@hotmail.com

The vast Western Indian Ocean region is interspersed by a large number of differentially isolated islands and island systems that are dissimilar in their mode of origination, geological age and palaeogeographical history. Although comparatively small in surface area, they are home to many endemic lineages, making them ideal models to study plant evolution and diversification in isolation through both space and time. The islands share unique floral assemblages, consisting of descendents of ancestral lineages that dispersed across oceanic barriers, rafted for extensive periods on continental fragments or intermittently resided on currently submerged oceanic banks. Colonizers arrived at different points in time, via different routes and dispersal agents, with many diversifying in-situ, adapting to each island's unique combination of age, topography and resident biota. The number of phylogeographic studies in the region incorporating biogeographical and molecular dating analyses has been steadily increasing. With major patterns becoming visible, we can commence the construction of a phylogeographic synthesis of the evolution and diversification of the Western Indian Ocean flora.

Keywords: Phylogeography, Diversification, Madagascar, Islands, Indian Ocean

1.34 Morphological and taxonomical diversity patterns of oceanic archipelagos

Kostas Triantis[1], Francois Rigal[2], Christine E. Parent[3], Robert A. D. Cameron[4], Bernd Lenzner[5], Aris Parmakelis[1], Norine W. Yeungh[6], Miguel Ibáñez[7], António M. de Frias Martins[8], Dinarte N.F. Teixeira[9], Kenneth A. Hayes[10], María R. Alonso[7], Owen L. Griffiths[11], Richard C. Preece[12], Robert H. Cowie[6]
[1] Department of Ecology and Taxonomy, Faculty of Biology, National and Kapodistrian University of Athens, Greece
[2] Azorean Biodiversity Group, University of Azores, Terceira, Azores, Portugal
[3] Department of Biological Sciences, University of Idaho, Moscow USA
[4] Department of Zoology, The Natural History Museum, London, UK
[5] Department of Biogeography, BayCEER, University of Bayreuth, Germany
[6] Pacific Biosciences Research Center, University of Hawaii, Honolulu, USA
[7] Departamento de Biología Animal, Universidad de La Laguna, Tenerife. Canaries, Spain
[8] CIBIO-Açores, Department of Biology, University of the Azores, Portugal
[9] Secretaria Regional do Ambiente e dos Recursos Naturais – Direcção Regional do Ambiente , Madeira, Portugal
[10] Department of Biology, Howard University, Washington DC, USA
[11] Biodiversity Conservation Madagascar (BCM) Ltd. Rivière des Anguilles, Mauritius
[12] Department of Zoology, University of Cambridge, UK.
Contact: island.biogeography@gmail.com

Macroecological and macroevolutionary patterns are revealed mainly by the two most intuitive measures of biological diversity: taxonomic diversity and morphological disparity. We collated taxonomic, morphological and biogeographical data for the indigenous, endemic and native, terrestrial snails of 10 major oceanic archipelagos to answer the following questions: (i) Is morphological diversity of each archipelagic fauna related to taxonomic richness? (ii) Is morphological and taxonomic diversity respond to biogeographic variables such as total archipelagic area, elevation, isolation and geological age, and do they respond to these variables in a similar fashion? We find that morphological diversity among archipelagos is strongly related to the number of genera but not with species richness. Additionally, available ecological space, measured as the total archipelagic land area, explains a significant portion of the variation in taxonomic richness but none of the morphological variation observed

1.35 ⚡ A novel phylogenetic method for exploring the dynamics of island

Continued next page

community assembly

Luis Valente[1], Albert Phillimore[2], Rampal Etienne[3]
[1] University Potsdam
[2] University of Edinburgh
[3] University of Groningen
Contact: valente@uni-potsdam.de

Do islands tend towards an equilibrium number of species over evolutionary time scales? In order to address this outstanding question we have developed DAISIE (Dynamic Assembly of Island biotas through Speciation, Immigration and Extinction), a likelihood-based phylogenetic method that allows biogeographers to estimate island-wide rates of colonisation and diversification. We applied DAISIE to molecular estimates of colonisation and speciation times of the terrestrial avifauna of the Galápagos islands - including Darwin's finches. We found that total bird species diversity of the Galápagos is in an ascending phase and has not achieved an equilibrium steady state even after several million years of existence of the archipelago. We discovered that two distinct macroevolutionary dynamics operate in the Galápagos. One applies to Darwin's finches, which evolve through a coalescent process where rapid speciation is offset by rapid extinction. The other applies to the remainder of the terrestrial bird species and is typified by an absence of diversity controls. Our results suggest that avian species richness may be on the rise and challenge the current equilibrium biodiversity paradigm.

Keywords: Island biogeography, phylogeny, diversification, Galápagos

1.36 Island scale spatial and ecological differentiation within two species of a radiating genus on the Canary archipelago

Alfons Weig[1], David Harter[1], Mike Thiv[2], Anke Jentsch[1], Carl Beierkuhnlein[1]
[1] BayCEER, University of Bayreuth
[2] Stuttgart State Museum of Natural History
Contact: david.harter@uni-bayreuth.de

Population differentiation may be a first step towards divergence and potential speciation. The Crassulacean genus *Aeonium* on the Canary archipelago is a popular example for rapid species radiation on islands. However, while allopatric speciation among islands is well studied, the role of intra-island speciation by topography-driven or ecological differentiation among populations is still unclear. We studied population genetic patterns (ISSR variation) within two island-endemic *Aeonium* taxa of La Palma (one widespread generalist and one narrow specialist species) to identify potential spatial and/or ecological drivers of population differentiation and possible differences in species evolutionary potentials. Although only low spatial population structures were detected for both species, some clear landscape effects on population differentiation and likely species histories were observable. Also, ecological gradients (especially of precipitation -related variables) could be shown to correlate with allelic patterns of certain genetic loci, especially for the generalist species, indicating potential divergent selection pressures among populations of *Aeonium* species on the island scale.

1.37 The effect of historical land connectivity on ant species composition in the Japanese Archipelago

Patricia Wepfer[1], Benoit Guénard[2], Evan P. Economo[1]
[1] Okinawa Institute of Science and Technology
[2] University of Hong Kong
Contact: patricia.wepfer@oist.jp

The occurrence of a species in an area is determined by multiple factors. Dispersal barriers in the form of water gaps often limit the spread of terrestrial species. However, sea level fluctuations in geologic times caused temporary land bridges, which may be reflected in the species distribution patterns observed today. We test the effect of land connections at the last glacial maximum (LGM) on species composition relative to the current land connectivity, environmental factors, and distance. We compiled occurrence records of 952 ant species in 160 insular and non-insular areas around the Japanese archipelago including neighbouring continental areas. Historic land connectivity was inferred by mapping sea depth exceeding -120 m using the NOAA ETOPO1 database. The explanatory distance matrices were regressed to ant species dissimilarity by the MRM function {ecodist} in R. The model could significantly explain 44% of the variation, partitioned among significant effects of temperature, elevation, geographic distance, and historical land connections. The insignificance of current land connections could indicate an ecologically minor effect of the time span since LGM on ant species distributions.

Keywords: ants, island biogeography, Japan, land bridges, Pleistocene, Japan

P2 Climate-change biogeography

2.1 Assessing the exposure of *Hemitriccus Mirandae* (AVES, Tyrannidae) to future climate change

Carlos Eduardo Arlé[1], Michelle Tavares Cardoso Andreu[1], Vanessa Schwan[1], Maria Lucia Lorini[1], Rafael Fortes[1]
[1] Laboratório de Ecologia Bêntica - Departamento de Ecologia e Recursos Marinhos - Centro de Ciências da Saúde - Instituto de Biociências - Universidade Federal do Estado do Rio de Janeiro – UNIRIO
Contact: kaduarle@gmail.com

Climate Change (CC) is one of the main threats to biodiversity conservation. CO_2 anthropic emissions will affect climate and will have far-reaching impacts on biodiversity. Thus, assessing species' climate change vulnerability has great importance to support decision in management and conservation actions. We applied Ecologic Niche Models (ENM) approach in order to estimate the exposure of the *Hemitriccus mirandae* to future CC and the implications for the species' conservation status (Vulnerable - IUCN). This bird is endemic to the northeastern portion of Atlantic Forest Hotspot. We performed the ENM associating occurrence records to six bioclimatic variables, selected by criteria of lower correlation and greater biological importance. We used six algorithms in an ensemble forecasting approach to model the current and future A2a scenario – 2050. We did the ensembles of forecasts including only models that showed good performance. The extent of the occurrence area will be severely affected, showing a significant loss of 97.8% and should be then categorised as Critically Endangered. This study suggests that CC can be a severe threat increasing the extinction risk to this species.

Keywords: Ecologic Niche Modelling, Ensemble Forecast, Climate Change, Hemitriccus mirandae

2.2 ⚡ Alpine treeline responses to experimental climate change: germination and seedling establishment

Maaike Bader[1], Gerhard Zotz[2], Hannah Loranger[2]
[1] Ecological Plant Geography, Faculty of Geography, University of Marburg, Germany
[2] Functional Ecology of Plants, Department of Biology and Environmental Sciences, University of Oldenburg, Germany
Contact: maaike.bader@geo.uni-marburg.de

Alpine treelines are likely to shift as a result of climate change. Warming would move thermal limits to tree growth upslope, but for treelines to track these new isotherms, trees need to be able to establish in the current alpine zone. Physiological requirements and microclimatic conditions can be very different for seedlings than for adult trees, which may cause distributional limits to mismatch tolerance levels of adults. We studied constraints on forest expansion into the alpine zone using germination and seedling-growth experiments with five European treeline tree species. Seeds were sown and seedlings were grown near treeline in the French Alps with warming, shading, vegetation and watering treatments. We found species-specific and weather-specific responses. For example, vegetation increased mortality in some species, but only in the wettest year. Responses were also process-specific, with partly opposing patterns for germination, mortality and growth. These interactions between macro- and microclimate, species properties and life stage may explain much of the great variation found in alpine treeline patterns and predict heterogeneous treeline responses to climatic changes.

Keywords: alpine treeline, climate change, ecophysiology, regeneration niche, seedling ecology

2.3 Climate adaptation is not enough: warming does not facilitate success of southern populations at northern latitudes in an Arctic tundra ecosystem

Anne Bjorkman[1], Greg Henry[2], Mark Vellend[3]
[1] German Centre for Integrative Biodiversity Research
[2] University of British Columbia
[3] Université de Sherbrooke
Contact: annebj@gmail.com

Rapidly rising temperatures are expected to cause poleward shifts in suitable climate space for many species. If local populations cannot respond to increased temperatures through phenotypic plasticity, they may become maladapted

to the warmer conditions in their current locations. Many researchers have hypothesized that northern populations might be "rescued" by gene flow from southern, warm-adapted populations, or will otherwise be replaced by the immigration of southern species tracking their optimal climate northward. However, these predictions rely on the assumption that warmer temperatures will allow southern immigrants to establish and prosper in an otherwise novel environment. Conversely, a lack of adaptation to environmental conditions other than climate – for example photoperiod, biotic interactions, or edaphic conditions – might limit the success of southern immigrants despite hospitable climatic conditions. Here we test the hypothesis that warmer temperatures at northern latitudes will confer a fitness advantage to southern immigrants relative to native populations.

Keywords: climate change, tundra, Arctic, range shifts, adaptation

2.4 ⚡ Dynamics of canopy dieback in the montane rainforest belt of a tropical volcanic island

Juergen Boehmer[1], Linda Mertelmeyer[2], James D. Jacobi[3]
[1] University of the South Pacific, School of Geography, Earth Science and Environment
[2] Technical University of Munich, Department of Ecology and Ecosystem Management
[3] U.S. Geological Survey, Pacific Island Ecosystems Research Center
Contact: boehmer_h@usp.ac.fj

A major forest decline on the island of Hawaii in the 1970s has provided a unique opportunity to analyse the landscape-level dynamics of the rainforest canopy. How did the distribution of dieback change between 1989 and 2012? Which abiotic factors correlate with dieback? Which areas are predisposed to new dieback? The study area on the island of Hawaii was remapped based on aerial photographs taken in 2009-2012. 1330 random points were established. Overstory species, understory species and current dieback status were sampled. 25 permanent plots monitored since 1976 were used for ground truthing. The abiotic factors annual rainfall, moisture availability index (MAI), elevation, slope gradient and substrate type were determined for each point. 80% of the former dieback plots were classified as healthy. The most significant changes in dieback status occurred along the former boundary between dieback and non dieback areas. The probability of dieback was found to correlate with elevation, moisture availability and substrate age. Dieback risk areas were found on elevational ranges from 347 to 1435 m where MAI ranges from 3148 to 4901 mm.

Keywords: forest decline, vegetation dynamics, Hawaii, Metrosideros polymorpha, resilience, cohort dynamics, long-term observation, natural disturbance, Pacific forests

2.5 Consequences of abrupt climate change on biodiversity

Filippo Botta[1], Anders Svensson[2], David Nogués-Bravo[3]
[1] University of Copenhagen
[2] Center for Ice and Climate, University of Copenhagen
[3] Center for Macroecology, Evolution and Climate, University of Copenhagen
Contact: botta@nbi.ku.dk

Understanding species response to past abrupt climate change is vital to anticipate future responses and extinction risk. Recent findings from Greenland ice cores and other paleoclimate records during the Late Pleistocene show frequent changes on less then decennial scale from cold stadial to warm interstadial periods associated with Greenland temperature changes of 10°C. Similar magnitudes of abrupt climate change are predicted for the next century and biodiversity assessments predict multiple extinctions. However, global extinctions in the Late Pleistocene are scarce except for megafauna species. This contradiction challenges the current biological theories on how species and populations react to climate change. In this study we will investigate how to combine paleoclimate data from the Greenland ice cores, climate model results, and macroecological models in an attempt to reconstruct biodiversity change over those climatic events, and evaluate the robustness of the large scale models when natural adaptations that track rapid environmental change are included.

Keywords: Abrupt climate change, biodiversity

2.6 ⚡ Modelling changing distribution ranges of *Betula utilis* in the Himalayan region under climate change conditions

Maria Brobrowski[1], U. Schickhoff
[1] CEN Center for Earth System Research and Sustainability, Institute of Geography, University of Hamburg
Contact: maria.bobrowski@uni-hamburg.de

Global warming causes shifts in species distributions and threatens biodiversity and ecosystem services, in particular in mountain regions such as the Himalaya, which shows above-average warming rates. However, species distribution modelling studies have hardly been conducted to date in this mountain system. This study aims at investigating how the distributionalrange ofa dominant treeline species (*Betula utilis*) will change under climate change conditions. In order to predict the future distribution range, an ensemble modelling approach was applied based on geo-coded information of current species occurrences linked to 19 bioclimatic variables and a digital elevation model (DEM). The potential habitat of *Betula utilis* is predicted to shift from lower to higher elevations and to expand into new habitats northward of the Himalayan range until 2070. Gaining a better understanding of potential range shifts of alpine treeline species under climate change scenarios is supported by such model results which also provide insights to decision makers with regard toclimate change mitigation and biodiversity conservation.

2.7 ⚡ Climate induced “dark needle conifers” mortality in Siberia

Viacheslav Kharuk[1]
[1] Forest Monitoring Lab, Sukachev Institute of Forest
Contact: kharuk@ksc.krasn.ru

The project “TREELINE” aims at investigating the sensitivity and response of the near-natural treeline ecotone of the Rolwaling valley, Central Himalayas, Nepal to climate warming. First results of the sub-project ‘vegetation ecology’ are presented, which aims at phytosociological mapping and analysing vegetation – environment relationships. Observations in the field showed that the two dominant tree species *Abies spectabilis* and *Betula utilis* need certain shelter elements for successful recruitment. Requirements for establishment have been analysed by correlating patterns of naturally established seedlings with microhabitat conditions. In the *Rhododendron campanulatum* krummholz-belt recruitment of *A. spectabilis* and *B. utilis* is inhibited. The potential allelopathic effect of *R. campanulatum* is therefore experimentally tested with bioassay species and with seeds of the native tree species. Above the treeline ecotone open top chambers have been installed and seedlings of *A. spectabilis* were replanted at the sites of experimental warming. A first monitoring in 2014 shows an increase in mortality of seedlings with increasing altitude level - regardless of temperature conditions.

Keywords: treeline, recruitment processes, climate warming, allelochemicals, Nepal, Himalaya

2.8 ⚡ Traits of European terrestrial gastropods indicate response to novel climates

César Capinha[1], Dennis Rödder[2], Henrique Pereira[1], Heike Kappes[3]
[1] Centre for Environmental Biology, University of Lisbon
[2] Zoologisches Forschungsmuseum Alexander Koenig, Museumsmeile Bonn
[3] Department of Ecology, Cologne Biocenter, University of Cologne
Contact: capinha@uevora.pt

Anticipating the propensity of species to persist outside the climatic conditions in which they are observed is important in assessing how they will respond to climate change. We use data from 27 European terrestrial gastropods (slugs and snails) that are established in new regions to investigate the degree of climate match between native and non-native ranges. We found that species with narrow native climatic niches, native ranges elongated in a north–south direction or native ranges with the southern limit at lower latitudes were more frequently found in novel climates. We also found that slugs were occupying a higher diversity of novel climates than snails. These results indicate that the accuracy of climate-matching is largely dictated by the levels of distributional equilibrium of species in their native ranges. In addition, analyses of the species’ ecological, biological and biogeographic attributes can provide important insight on how their ranges will respond to climate change.

Keywords: climate-matching, niche conservatism, species traits, terrestrial gastropods

2.9 ⚡ The relationship of climate and land cover with vegetation phenology: a scale-specific analysis using wavelets across central Europe

Gudrun Carl[1], Daniel Doktor[2], Oliver Schweiger[1], Ingolf Kühn[1]
[1] Community Ecology, Helmholtz Centre for Environmental Research - UFZ
[2] Computational Landscape Ecology, Helmholtz Centre for Environmental Research - UFZ
Contact: ingolf.kuehn@ufz.de

Assessing relationships between ecological and environmental variables as a function of spatial scale is a challenging problem. It was frequently stated that e.g., land-use is ecologically more important at smaller scales while climate is more important at larger scales. Nevertheless, a valid and reliable tool to examine and evaluate scale-dependencies is a serious problem. Here, we present a method for applying two-dimensional wavelet analysis to multiple linear regressions to evaluate the relative importance of several environmental variables across different spatial scales, with 1km^2 as smallest resolution. We tested whether climate or land cover is more important to explain variation in annual greening in Central Europa. Our results indicate that land-use is more important to explain the variation in greening than climate at smaller resolution while climate is more important at larger resolution with a shift at intermediate resolution.

Keywords: spatial scales, wavelet, multimodel inference, normalized difference vegetation index, remote sensing

2.10 State and expected changes of animal biodiversity in the northwestern Italian Alps

Cristiana Cerrato[1], Ramona Viterbi[2], Antonello Provenzale[1]
[1] Institute of Atmospheric Sciences and Climate, National Research Council
[2] Gran Paradiso National Park
Contact: cri.entessa@virgilio.it

In 2007, three alpine parks in N-W Italy started a field program to determine the factors influencing animal biodiversity. Twelve altitudinal transects (from montane to alpine belt) were defined, each composed of 4-7 sampling units, for a total of 69 monitored plots. In each station, five taxonomic groups (Rhopalocera, Staphylinidae, Carabidae, Araneae, Aves) were systematically sampled; topographic, environmental and microclimatic variables were recorded. The data analysis showed that species richness and community composition of invertebrates are determined mainly by altitude and microclimate, whereas birds are more sensitive to habitat structure. The use of presence-only distribution models then allowed to estimate the effects of a moderate temperature increase on the multi-taxa distributions. The results indicate small expected changes in the overall biodiversity patterns, but reveal different responses depending on habitat and degree of specialization. Changes in species richness are more pronounced in the alpine belt and for vulnerable species. Community composition significantly shifted, maintaining the separation between vegetation belts.

2.11 ⚡ The diversity and abundance of North American bird assemblages fail to track changing productivity

LuAnna L Dobson[1], Frank A La Sorte[2], Lisa L Manne[3], Bradford A Hawkins[1]
[1] Ecology and Evolutionary Biology, University of California, Irvine, California
[2] Cornell Laboratory of Ornithology, Cornell University, Ithaca, New York
[3] Ecology and Evolutionary Biology, College of Staten Island, Staten Island, New York
Contact: LDobson@uci.edu

Plant productivity and species richness of birds are associated across a range of spatial scales. Species-energy theory is generally assumed to explain these correlations. If true, bird richness should also track productivity temporally, and there should be spatial and temporal relationships between productivity and both bird abundance and richness. Using summer NDVI from 1982 – 2006 and the North American Breeding Bird Survey, we evaluated the response of avian richness and abundance to changes in plant production. We found positive spatial relationships between richness and NDVI all 25 years. Temporally, richness and NDVI were positively associated at 1,579 survey sites and negatively associated at 1,627 sites (mean $r^2 = 0.09$). Further, total abundance and NDVI were unrelated spatially (r^2s spanning <0.01 and 0.03) and weakly related temporally (mean $r^2 = 0.10$). We found no evidence that productivity drives bird richness temporally. Spatial relationships may be spurious, arising via covariance between plant productivity and vegetation structural complexity, consistent with the MacArthurs' classic hypothesis that the vertical profile of foliage drives bird species diversity.

Keywords: bird species richness; Breeding Bird Survey; climate; community richness; diversity gradients, more individuals hypothesis; NDVI; productivity hypothesis; species-energy theory; species richness

2.12 Estimating climate change impacts on forests: How does tree species distribution relate to tree growth and mortality?

Klara Dolos[1], Agnes Bauer[2], Steffen Albrecht[1]
[1] Institute for Geography and Geoecology, Karlsruhe Institute of Technology
[2] BayCEER, University of Bayreuth, Chair of Biogeography
Contact: dolos@kit.edu

Climate dependent models for species distribution (SDMs) are widely used to investigate species ecological niches. However, species distributions are caused by the joint effect of environment, competition and further biotic interactions on demographic processes. Therefore, demographic processes such as tree growth and mortality can be used to estimate site suitability similarly to SDMs. Furthermore, models for demographic processes increase the understanding of species distributions and their reaction to changing climatic conditions. In this study statistical models for *Picea abies*, *Fagus sylvatica*, *Abies alba* and *Pinus sylvestris* were calculated based on the German national forest inventories. Model predictions were jointly discussed regarding their indication of site suitability. Correlations among model predictions were assessed to identify processes driving species distribution. Species distribution models and demographic models did not provide the same answer regarding site suitability if interpreted improvidently. This is important to notice when they ought to be used to evaluate site suitability, particularly under climate change.

Keywords: forest, climate change, biogeographical modelling, statistics, tree growth, NFI

2.13 ⚡ Climate refugia and impacts of global climate change on threatened status of endemic plant species in southwestern South America

Milen Duarte[1], Pablo Guerrero[2], Ramiro Bustamante[1]
[1] University of Chile / IEB-Chile
[2] Departamento de Botánica, Facultad de ciencias naturales & oceanográficas, Universidad de Concepción
Contact: mylenduarte@gmail.com

The future climate regufia, are a crusial aspect for species conservation. We assessed the relationship between the climatic niche and the effect of global climate change on the future distribution of the species of two South America native genera: *Chaetanthera* and *Malesherbia*. The climatic niche was evaluated using principal component analysis, analyzing the niche breadth and niche conservatism. Using maximum entropy models, we generated current and future potential distribution of the species, assessing climate refugia between the two models.The results show that there is a positive relationship between niche breadth and refugias to climate change. The stable area will be greater for those species with higher niche breadth. Following the criteria established by the IUCN (UICN 2010), both genera could be threatened in their area of occupation. The genera *Malesherbia* could be affected by 53% of its species, and for *Chaetanthera* 39% of the species could be affected. This thesis confirmed that species with greater niche breadth have greater climate refugia. This idea is central to focus conservation, because the species with climatic ranges restricted are the central conservation target to climate change.

Keywords: Climate refugia, niche breadth, niche conservatism, threatened species

Continued next page

2.14 ⚡ Drought as well as nutrients and herbivores shape tree distribution in tropical forests: implications under global climate change

Bettina Engelbrecht[1], Julian Gaviria[1], Delicia Pino[1], Ben Turner[2], Rick Condit[2]
[1] Plant Ecology, BayCEER, University of Bayreuth, Germany
[2] Smithsonian Tropical Research Institute, Panama
Contact: bettina.engelbrecht@gmail.com

Understanding which factors shape species distributions, community composition and ecosystem function in tropical forests is one of the most pressing issues in global change vegetation modelling. The most pervasive patterns of tree distributions and diversity in tropical forests worldwide are correlations with rainfall and/or soil moisture. Evaluating the role of potential factors producing these patterns requires a mechanistic understanding of the underlying processes. Here we directly link extensive comparative experimental data sets on whole-plant responses to drought and fertilization, and on integrated plant defenses to quantitative assessments of species occurrence across a pronounced rainfall gradient at the isthmus of Panama. We show that species' differential drought sensitivity directly determine plant performance and distributions in tropical forests. Additionally, differential nutrient requirements and herbivore defenses indirectly shape the patterns. The results underline the importance of incorporating climate as well as nutrients and species interactions into models predicting species distribution, community composition and ecosystem function of tropical forests under global change scenarios.
Keywords: climate change, tropical forest, rainfall, precipitation, phosphorus, tree, distribution, diversity

2.15 ⚡ What can life-history traits tell us about species' ability to cope with climate change? A multi-taxon approach

Alba Estrada[1], Catarina Meireles[1], Ignacio Morales-Castilla[2], Peter Poschlod[3], David Vieites[4], Miguel B. Araújo[5], Paul Caplat[6], Regan Early[7]
[1] CIBIO/InBIO, University of Evora, Portugal
[2] Department of Biology, McGill University, Montreal, QC, Canada
[3] Universität Regensburg. Institut für Botanik. Regensburg, Germany
[4] Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain
[5] Imperial College London, Silwood Park Campus, Ascot, UK
[6] Centre for Environmental and Climate Research, Lund University, Sweden
[7] Centre for Ecology and Conservation, University of Exeter, UK
Contact: albaestradaa@gmail.com

Understanding the factors that govern species' geographic ranges is of utmost importance to predict potential range shifts triggered by climate change. Species' ranges are partially limited by their tolerances to extrinsic environmental conditions such as climate and habitat, and partially determined by species' capacity to disperse, establish new populations, and proliferate, which are in turn dependent on species' intrinsic life-history traits. Yet most forecasts of range shifts consider only climate and dispersal. In order to ask whether other factors should be considered, we investigate how range filling and range size of European plants, birds and mammals is determined by these factors. We found that traits related to ecological generalization, such as habitat breadth, were important for all groups of species. Dispersal and seed-banks that permit survival during unsuitable environmental conditions were highly important for plants, whereas fecundity-related traits were important for animal groups. We suggest that considering these traits would improve assessments of extinction vulnerability under climate change.
Keywords: birds, Europe, mammals, plants, range filling

2.16 Plant endemism patterns across China are shaped by glacial-interglacial climate change

Gang Feng[1], Lingfeng Mao[2], Brody Sandel[1], Nathan G. Swenson[2], Jens-Christian Svenning[1]
[1] Aarhus University
[2] Michigan State University
Contact: gang.feng@biology.au.dk

China is a major diversity hotspot for temperate and subtropical plants and harbours numerous endemic species. Previous studies have shown that small-ranged (endemic) species on a global scale are concentrated where

Quaternary climate oscillations have been small. China has overall been relatively mildly affected by these oscillations, so it is unclear if they nevertheless shape endemism patterns within this biodiversity hotspot. Using distribution maps for China's nearly 8,000 endemic seed plant species, we find that endemics are particularly concentrated in parts of southern China. We find consistent support for a positive relation between Quaternary temperature stability and endemic species richness, supplementing effects of topography and current climate. Importantly, endemics are concentrated in long-term stable areas irrespective of growth form or whether they are paleo- or neoendemics. These findings indicate that Quaternary climate changes have overridden any growth-form-dependent differences in climate sensitivity and acted via effects on both extinction and diversification.

2.17 Using models and connectivity analysis to predict current and future patterns of invasion in a transfrontier context – a case study of *Acacia dealbata* invasion in the Galicia-North of Portugal Euro-region

Rui F. Fernandes[1], João P. Honrado[2,3], Antoine Guisan[1], Alice Roxo[2], João Martins[2], Joana R. Vicente[2,3]
[1] Department of Ecology and Evolution, and Faculty of Geoscience and the Environment, University of Lausanne, Switzerland
[2] Faculdade de Ciências da Universidade do Porto (Departamento de Biologia),Portugal
[3] InBIO - Rede de Investigação em Biodiversidade e Biologia Evolutiva, Laboratório Associado; CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Portugal
Contact: ruifilipe.freitasfernandes@unil.ch

To protect native biodiversity, ecosystems and productive landscapes from the effects of biological invasions, comprehensive studies and measures to anticipate impacts on species and habitats with highest conservation value are required. Species distribution models (SDMs) can be used to predict the distribution of invasive species, both for current conditions and future scenarios of environmental changes. We applied a combined predictive modelling framework, coupled with connectivity analysis, to determine whether predicting invasions and conflicts in a transfrontier context would provide additional insights on the patterns and drivers of invasion, when compared to models obtained from predictions for individual regions. The framework is illustrated for the alien woody invader *Acacia dealbata* in Galicia-North of Portugal region. The results show that SDMs obtained in a transfrontier context provided additional information, with higher predictive performance, than models for individual regions. Transfrontier context predictions are more informative to anticipate impacts of invasions, providing additional support to international cooperation when tackling issues of global change.

Keywords: Invasions, Transfrontier context, Portugal, Galicia, Distribution

2.18 ⚡ Elevation gradients in islands: Variation in bryophyte community structure at different spatial scales

Rosalina Gabriel[1], Jacques Bardat[2], Olivier Flores[3], Juana Gonzalez-Mancebo[4], Terry Hedderson[5], Dominique Strasberg[6], Silvia Calvo Aranda[7], Márcia C. M. Coelho[1], Débora S. G. Henriques[1], Raquel Hernandez-Hernandez[4], Lovanomanjanahary Marline[5], Nicholas Wilding[5], Claudine Ah-Peng[6]
[1] University of the Azores, DCA, Azorean Biodiversity Group (CE3C), Angra do Heroismo, Portugal
[2] Muséum National d'Histoire Naturelle, Dep. Systematique e Evolution, Paris, France
[3] CIRAD, UMR PVBMT, Pôle de Protection des Plantes, Saint-Pierre, La Réunion, France
[4] Universidad de La Laguna, Dep. Botany, La Laguna, Tenerife, Canary Islands, Spain
[5] University of Cape Town, Biological Sciences Department, Rondebosch, South Africa
[6] Université de La Réunion, UMR PVBMT, Saint-Dennis, La Réunion, France
[7] Museo Nacional de Ciencias Naturales, Madrid, Spain
Contact: rgabriel@uac.pt

Biodiversity patterns and responses to climate change may be studied using elevational gradients, since they simulate a vast array of climatic conditions. Bryophytes are of paramount importance in ecosystem functioning and respond quickly to environmental change which renders them ideal candidates for spatial ecological studies. The MOVECLIM Project is the first comparative study between oceanic (La Palma, La Réunion, Pico, Terceira) and continental islands (Madagascar) and aims to investigate spatial changes in diversity across elevational gradients. A homogeneous hierarchical sampling strategy was used for each transect, setting up two permanent plots ($100\ m^2$) and climatic sensors (if possible) at 200 m elevation intervals. Results show that the diversity patterns tend to be

congruent among the islands. Species show hump-shaped patterns with altitude, which explains the largest fraction of Beta-Diversity; no general trends appear to exist for Rapoport's rule; tropical systems exhibit a higher proportion of short ranged species across the altitudinal gradient, conforming with Janzen's Hypothesis. The Mid-Domain Effect, could not explain three of the five species richness patterns.

Keywords: Bryophytes, climate change, elevational gradients, ecology, spatial scale

2.19 Lean pattern in an altitude range shift of a tree species (*Abies pinsapo* Boiss.)

Antonio González-Hernández[1], Julio Peñas[1], Diego Nieto-Lugilde[2], Francisca Alba-Sánchez[3]
[1] Dpt. Botany, University of Granada
[2] Appalachian Lab. University of Maryland Center for Environmental Science
[3] Dpt. Botany, University of Granada
Contact: aglezhdez@gmail.com

Differences between rates of extinction and colonization at the rear and front edges explain different geographical patterns of range shift. We explored the range shift along the altitudinal gradient of a threatened tree species, its pattern and the consequences for the species conservation. Assuming the species is established under climatic conditions that fits its reproductive niche, the range of different age classes varies if climatic change exists. We collected the occurrences of different age classes and modeled with MaxEnt the suitability of three sets of occurrences (mature, sapling, and the whole set of species occurrences) with three climate predictors. We compared areas where suitability of each set is the highest to determine persistence (mature), optimum (whole) and migration (sapling) areas. Results show that persistence areas are larger than optimum and migration occupying most of the mountain bases. Optimum areas form a higher altitudinal belt, leaving just the mountain submits as potential migration areas. This pattern is not alarming in short term, but could derive into a crash pattern in an upper-limited range in long term. Acknowledgement: P11-RNM-7033

2.20 ⚡ Elevational shifts in plant communities is more pronounced at high elevations

John-Arvid Grytnes[1], Vivian A. Felde[1], Hanne Henriksen[2], Jutta Kapfer[3], Kari Klanderud[2], Mikael Ohlson[2], Fride H. Schei[3], Richard Telford[1], Risto Virtanen[4]
[1] University of Bergen
[2] Norwegian University of Life Sciences
[3] Norwegian Forest and Landscape Institute
[4] University of Oulu
Contact: grytnes@bio.uib.no

There has been observed a general tendency for species and communities to move upwards in elevation during the last decades. However, considerable variations exist between regions in how large proportion is moving upwards and the magnitude of upward movements. We resampled data on species composition along seven elevational gradients in in Fennoscandia. A relationship between species composition of the original data set and elevation was established and a transfer function was used to predict the elevation based on the species composition of the new data set. If the predicted value was below the observed value it indicates that the species composition corresponded to a "warmer" vegetation type at higher elevation, and that the communities had shifted upwards. For five of the seven regions we found a statistically significant upward movement of species assemblages along the whole gradient, and for five of the regions the difference changed with elevation so that upward movement was most pronounced at higher elevations. Our results indicate that lowland communities lag behind climate warming compared to communities at higher elevations.

2.21 ⚡ Bioclimatic transition zones as bridges for migration of tree species under global change.

Laura Hernández[1], Isabel Cañellas[1], Fernando Montes[1], Helios Sainz-Ollero[2], Rut Sánchez de Dios[3]
[1] Silviculture and Forest Management Department, INIA-CIFOR
[2] Unidad de Botánica, Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid
[3] Departamento de Biología Vegetal I, Facultad de Biología, Universidad Complutense de Madrid
Contact: hernandez.laura@inia.es

Bioclimatic transition zones are sensitive areas for global change monitoring. Based on the comparison of sequential forest inventories in Northern Spain, this work assess the range shifts of a transitional, a sclerophyllous, a mountain conifer and a temperate deciduous species along the Temperate-Mediterranean bioclimatic transitional gradient as response of global change. We found a shift of the sclerophyllous species towards transitional territories along with an associated retreat of the temperate, mountain conifer and transitional taxa supporting the previous hypothesis of a "mediterraneization" of this zone. Simultaneously, the transitional and temperate species have shifted their altitudinal ranges towards higher elevations while for the sclerophyllous and the mountain conifer species a downslope range shift is detected. The effect of recent climate warming and land use changes driving range shifts is species-dependent. The results highlight the need of considering the overall range of the species along geographical gradients to ascertain species range shifts and the importance of accounting for biogeographical and anthropogenic factors to interpret them.

Keywords: shifts, global change, Submediterranean bioclimatic transition zone, Quercus subpyrenaica, Quercus ilex subesp. ballota, Pinus sylvestris, Fagus sylvatica

2.22 ⚡ The global variation of thermal tolerances: what can the integration of physiology and biogeography tell us about species' vulnerability to climate change?

Christian Hof[1], Imran Khaliq[1], Roland Prinzinger[2], Katrin Böhning-Gaese[3], Markus Pfenninger[3]
[1] Biodiversity & Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung, Frankfurt, Germany
[2] Metabolic Physiology, Institute for Ecology, Evolution and Diversity, Department of Biological Sciences, Goethe University Frankfurt, Germany
[3] Biodiversity & Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung; Institute for Ecology, Evolution and Diversity, Department of Biological Sciences, Goethe University, Frankfurt, Germany
Contact: christian.hof@senckenberg.de

The relationships among species' thermal capacities and the geographical variation of ambient climatic conditions are crucial to understand how species may respond to climate change. We assembled data on thermal tolerances from physiological experiments for about 400 species of birds and mammals and analyzed them, along with data on ambient climate and species' geographical distributions. We found incongruent macro-physiological patterns for birds and mammals: birds, e.g., showed a strong link between climatic variability and thermal tolerances, whereas there was no such relationship in mammals. The differences between the two taxa imply different potential responses to current and future climate change for mammals and birds. Overall, we show that vulnerability to climate change increases from polar to tropical regions. However, we also show that many species may be able to tolerate projected temperature increases across significant proportions of their ranges. Our findings underline the need for cross-disciplinary research among physiologists, ecologists, and biogeographers, to improve future scenarios for biodiversity in a changing world.

Keywords: macroecology, macrophysiology, climate change, birds, mammals, thermal tolerance

Continued next page

2.23 Elevational distributions of tropical epiphyte species indicate potential risk due to climate change

Emily Hollenbeck[1], Dov Sax[1]
[1] Ecology and Evolutionary Biology, Brown University
Contact: Emily_Hollenbeck@brown.edu

Elevational range shifts may help tropical montane species mitigate risk from climate change, but only if they can track an appropriate precipitation regime as well as temperature. Currently, scarce data on species distributions in the tropics makes risk analysis difficult. We surveyed the presence and abundance of 49 epiphytic species in two genera, *Peperomia* (Piperaceae) and *Elaphoglossum* (Pteridophyta) across several transects near Monteverde, Costa Rica. On the seasonally dry Pacific slope, diversity of species increased with elevation, peaking in cloud forest habitat. In contrast, on the wet Atlantic slope, diversity increased slightly with decreasing elevation. 13% of these species are restricted to cloud forest habitats, which are projected to be lost from the mountain range with only moderate climate change, and 23% of species are in danger of local mountaintop extinction due to projected temperature increases alone. If these patterns are representative of other tropical taxa, distributions and elevational gradients, then they suggest that a great number of species in these systems will be at risk of extinction with changes in climate that occur during this century.

Keywords: elevational gradients, tropical montane forests, climate change, epiphytes

2.24 Characteristics of beech forests communities at their warm dry distribution limit

Daniel Hornstein[1], Ewald Jörg
[1] HSWT
Contact: daniel.hornstein@hswt.de

This research it is focused on forests with beech as dominant tree species at its warm and dry range limit (margin, distribution edge). We searched and detected *Fagus sylvatica* close to its warm and dry range limit based on a climatic niche model and regional expert knowledge. We sampled nine old growth beech forest plots in Bulgaria, Romania, Slovenia and Italy, that had neither been planted nor managed for a long time. Marginality of plots has been ranked according to the results of an ensemble of three different species distribution models. They show different distances (based on probabilities of occurrence) to the niche margin. Plots were characterised by vegetation relevées, stand parameters, dendroecological measurements, leaf traits and soil descriptions. Ellenberg indicator values for moisture and temperature are correlated with climatic marginality. Plant species composition is rather similar to the one found in the centre of the distribution range, however, there are differences in vegetation structure. Topographically induced microclimate conditions are apparently modulating the macroclimatic drivers at the xeric edge of beech and therefore favor its persistance.

Keywords: margin, Fagus sylvatica, climate, growth-trend, xeric edge, indicator values

2.25 Plant water-use strategies in serious soil erosion area: surviving the experimental drought

Zheng Huaizhou[1], Zhu Jinmao[2], Zhong Xiaohui[2], Zheng Liwei[2], Duan Lili[2], Zhang Yunfei[2]
[1] Institute of Geography, Fujian Normal University
[2] College of Life Science, Fujian Normal University
Contact: zhz@fjnu.edu.cn

Forest ecosystems are sensitive to climate changes, especially to the drought. In serious soil erosion area of south China, the soil is so poor and drying. The main native tree specie is only *Pinus massoniana,* other trees are hard to live there without artificial measures. We studied on typical *P. massoniana* forestry by using artificial isolation rainfall, with the aim of better understanding the mechanisms of tree adaptation to drought. After one year of completely isolated rain experimental, trees are still alive. Although the observed decrease in soil water potential, trees maintained lower leaf water potential than it, so trees still remain transpiration, even in the winter. The leaves accumulate more carbohydrates to keep them low water potential, so that trees are still some potential gradient and

poor soil. We find most of the transpired water was being taken from groundwater sources and fog water. This study shows that changes in groundwater levels in serious soil erosion area should be monitored, because of its direct relation to the impact on plant survival.

Keywords: Drought;Water-use strategies;serious soil erosion area

2.26 Terrestrial primary production scaling is unimodal and hierarchical

Dave Jenkins[1]
[1] Dept. of Biology, University of Central Florida
Contact: David.Jenkins@ucf.edu

In theoretically ideal systems, terrestrial net primary production (NPP) should scale with plant biomass (B) as a power law with $b \sim$ ¾, where log(NPP) = a + b(logB). However, two factors may change that linear shape; competition by larger plants and hierarchical levels of complexity beyond organisms (i.e., populations, communities, ecosystems, biomes). If so, terrestrial log(NPP) should scale with log(B) as a unimodal (quadratic) function and a negative effect of hierarchical levels. Here I show strong support for that hypothesis within and among hierarchical levels, based on 711 compiled above-ground NPP and B values. Asymmetric competition by large plants may be the main regulator of terrestrial NPP relative to a theoretical ideal. Moreover, terrestrial systems converge to a nonlinear log(NPP) scaling trajectory that indicates regime shift in response to rapid changes in biomass, with a tipping point ~ 10^3 g dry mass m^{-2}. The general scaling relationship may describe past terrestrial NPP scaling after woody flowering plants radiated out of the tropics > 30 MYA, as well as future changes due to growing human appropriation of plant biomass and climate change.

Keywords: macroecology metabolic theory allometric scaling asymmetric competition ecological hierarchy nonlinear tipping point

2.27 Thresholds of European grassland resilience in the face of climatic extremes - The SIGNAL Experiment

Anke Jentsch[1], SIGNAL Consortium
[1] Disturbance Ecology, BayCEER, Universtity of Bayreuth
Contact: anke.jentsch@uni-bayreuth.de

Grasslands are spatially and economically highly important for European agriculture and biodiversity. However, they might be threatened by climate extremes and invasive species. Within the SIGNAL experiment, we adress stability and resilience of grassland towards extreme drought and invasive pressure across a pan-European precipitation gradient with standardized field experiments at 10 sites between Belgium and Israel. We found a surprisingly high stability towards both extreme drought and invasive species within mesic grassland, as biomass production was not reduced by a severe drought event, and as invaders were not able to spread and showed high mortality. However, we also found that drier (more southern and more continental) sites along the gradient suffered more from drought, showing losses in biomass production directly after drought, which did not persist until the end of the growing season. Our multisite-experiment highlights a surprising degree of stability against extreme drought and invasive species in mesic grasslands.

Keywords: Coordinated Experiment, Climatic Extremes, Invasion,

2.28 Endotherms in a warming world: limits to metabolic heat generation and phylogenetic constraints

Imran Khaliq[1], Susanne A. Fritz[1], Katrin Böhning-Gaese[1], Markus Pfenninger[1], Christian Hof[1]
[1] Biodiversity and Climate Research Centre (BiK-F) and Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, 60325 Frankfurt, Germany
Contact: imran.khaliq@senckenberg.de

In an age of global warming, we need to understand how energetic and evolutionary constraints influence species' vulnerability to climate change. The amount of heat dissipation has been proposed as a factor that influence endotherms overall energetics. To understand influence of heat dissipation and evolutionary constraint on thermal

traits, we collated a large global data set of endotherms' body masses, BMR, upper and lower critical temperatures, and data of species' phylogenies. We found that in endotherms, upper and lower critical temperatures show a strong negative association with BMR that indicated that under predicted future rising temperatures, to meet the energetics requirements, endothemrs need to alter their heat dissipation capacities. We also found that tropical endotherms showed strong phylogenetic signals in all thermal traits, while these were much weaker in temperate species. Our results highlight the vulnerability of tropical endotherms to climate change due to energetic and evolutionary constraints. We suggest that the potential effects of heat dissipation should be included in projections of species' future distributions in order to increase their predictive power

Keywords: Endotherms, energetics, global warming, phylogenetic constraints,

2.29 ⚡ Spatial patterns of floristic richness and threatened plant species of Caatinga biome (Brazil) under climate change conditions

Robert Koch[1], Markus Günther[1], Birgit Kleinschmit[1]
[1] Technical University of Berlin
Contact: robert.koch@tu-berlin.de

Climate change and human activities cause impacts to ecosystems resulting in environmental problems such as loss of biodiversity. Our scientific focus is on impacts of climate change on spatial patterns of floristic richness in the Caatinga. The study area is located in the northeast of Brazil and has a size of ca. 850.000 km^2. The biome is classified as a seasonally dry tropical forest, which was already affected by severe drought periods in the last decades.

As the Caatinga is poorly researched, we are dealing with imperfect data conditions. Therefore, we decided to use a maximum entropy approach (MaxEnt) for modeling current and future simulations runs of plant species distributions to detect spatial patterns of the Caatinga flora and identify areas of threatened plant species at a very high spatial resolution of 1x1 km per cell. Climate change scenarios from the 4th IPCC report were integrated into the model to assess the consequence of environmental changes on species distributions and on endangered species. We used a quantitative GIS-based approach to create floristic richness maps to gain suitable information for detecting priority areas and to support conservation planning.

Keywords: biodiversity, species distribution modeling, dry tropical forest, climate change, threatened species

2.30 Increasing precipitation buffers plant species against climate warming

Martin Kopecký[1], František Máliš[2], Petr Petřík[1], Jozef Vladovič[3]
[1] Institute of Botany, Czech Academy of Sciences
[2] Technical University in Zvolen, Slovakia
[3] National Forest Centre, Slovakia
Contact: ma.kopecky@gmail.com

Upward shifts of plant species are expected in response to climate warming. However, evidence for large-scale distributional shifts is based on snapshot studies with contradictory results. We therefore analyzed plant distributional shifts in 1435 forest plots resurveyed after three decades.

Despite considerable warming, species did not shift upslope, likely because increasing precipitation compensated higher evaporative demand. Regionally increasing precipitation thus buffered plant species from global warming through maintaining constant water availability.

This suggests variable reshuffling of plant assemblages according the spatially heterogeneous changes in water availability, resulting in novel ecosystems and spatial mismatch between dependent species. Knowledge of water availability is therefore crucial for understanding of climate change effects on world biota.

Keywords: climate change, distributional range shifts, elevation shifts, global warming, vegetation resurvey, semi-permanent plots,temperate forests, water deficit

2.31 ⚡ The implications of mid-latitude climate extremes for migratory birds

Frank La Sorte[1], Daniel Sheldon[2]
[1] Cornell Lab of Ornithology
[2] University of Massachusetts, Amherst
Contact: fal42@cornell.edu

The frequency of climate extremes has increased under global climate change with the greatest concentration occurring at mid-latitudes in the Northern Hemisphere. Migratory birds may be under greater risk of population loss due to their complex life-history phenologies and high mid-latitude concentrations during the breeding season. The mid-latitudes in North America experienced an extreme warming event during March, 2012 that resulted in lower ecological productivity during subsequent months. Due to geographic proximity and more flexible migratory behavior, we expect populations of short-distance migrants to be the most affected. To test this, we used weekly occurrence data for 268 migratory species from the eBird database. As expected, short-distance migrants whose winter and breeding ranges intersected mid-latitudes presented the strongest phenological response. Contrary to expectations, population declines were most evident for long-distance migrants. Thus, populations of long-distance migratory birds must contend both with phenological mismatches under global warming and disruptions in seasonal patterns of ecological productivity due to mid-latitude climate extremes.
Keywords: eBird, ecological productivity, global climate change, migration phenology, seasonal bird migration, temperature, vegetation greenness

2.32 ⚡ How will climate change alter vegetation geography in the temperate steppe of China?

Hongyan Liu[1], Fengjun Zhao[1], Xu Liu[1], Shuang Qiu[1]
[1] College of Urban and Environmental Sciences, Peking University
Contact: lhy@urban.pku.edu.cn

A large area of the temperate steppe zone in northern China is threatened by climatic drying, which raises the following question: Will steppe or even desert expand and replace forest? To answer this question, we systematically recorded species composition of 532 plots and measured plant functional traits of dominant species along environmental gradients, mainly precipitation gradient. Based on a space-for-time-substitution approach, we intend to project how climatic drying will alter vegetation geography in the temperate steppe of China. Particularly, we test whether there is a compensation effect between plants on the level of plant functional groups, species, or plant functional traits, and whether the compensation effect will stabilize the steppe vegetation under changing climate.

We project that compensation effect between plant functional groups should benefit a stabilized steppe distribution under changing climate. Persistent warming and drought, however, might reduce wood and perennial rhizomatous grass. Soil coarsening may also lead to increase in dominance of annual and biennial plants and C4 plants.
Keywords: Temperate steppe; Plant functional groups; Plant functional traits; Compensation effect; Climatic drying

2.33 ⚡ Continental-scale phylogenetic assemblage patterns in angiosperm and gymnosperm trees across North America

Ziyu Ma[1], Brody Sandel[1], Jens-Christian Svenning[1]
[1] Department of Bioscience, Aarhus University
Contact: ziyu.ma@biology.au.dk

The response of forests to past climate change may help us predict their dynamics in a warming world. We used distribution ranges and phylogenies to map phylogenetic diversity (PD), phylogenetic endemism (PE) and net relatedness index (NRI) of North American tree assemblages at a 50km resolution and analysed their relations to current climate, climate stability since the Last Glacial Maximum (LGM), as well as postglacial accessibility. We tested the following two predictions: 1. PD and PE should be higher under warmer, wetter and less seasonal current climate conditions, while NRI should be lower, i.e., representing co-occurrence of more distantly related species. 2. PD and PE should be higher at lower climate-change velocity and higher accessibility, while NRI could be either higher or lower. Simultaneous autoregressive modelling of these potential relations for the whole continent as well as its major forest regions generally confirmed these predictions, with exceptions that can be related to angiosperm-gymnosperm competition, historical evolutionary and biogeographic differences between gymnosperms and angiosperms, and regional differences in current and glacial environments.

Keywords: phylogenetic diversity, phylogenetic endemism, net relatedness index, climate-change velocity, tropical conservatism hypothesis, tree migration, water-energy relations

2.34 ⚡ Plant responses to climatic extremes: within-species variation equals among-species variation

Andrey Malyshev[1], Carl Beierkuhnlein[1], Hugh A. L. Henry[2], Mohammed A. S. Arfin Khan[1], Anke Jentsch[1], Manuel Steinbauer[1], Juergen Dengler[1], Evelin Willner[3], Juergen Kreyling[1]
[1] BayCEER, University of Bayreuth
[2] University of Western Ontario
[3] Leibniz Institute of Plant Genetics and Crop Plant Research
Contact: amalyshe@alumni.uwo.ca

High ecotypic variation complicates comparisons of variation among species although the two forms of variation have not been compared explicitly. We compared intra and inter-species variation in response to two of the main stresses anticipated with climate change: drought and frost. We simulated summer warming and drought and spring frost for 4 common European grass species and their ecotypes collected from 4-6 European countries. We also conducted a subsequent mid-winter thaw/frost experiment which included 4 grasses, 2 non-leguminous and 2 leguminous forbs, in addition to 11 European ecotypes of a representative grass species. Biomass, C:N ratio, chlorophyll content, plant greenness and root ^{15}N uptake were measured. Out of the total 81 within-vs among species comparisons with respect to coefficients of variation (CV) (for each species vs country comparison in every experiment and for every parameter), within-species CV exceeded among-species CV for 6 out of the 12 significantly different CV. This result has important implications for niche conservatism and the insurance hypothesis as well as species distribution models, which stand to benefit from the inclusion of within-species components.

Keywords: intra-specific variation, inter-specific variation, extreme climatic events, insurance hypothesis, genetic diversity, niche models.

2.35 ⚡ Temperature-size rule in insects: evidence from natural populations

Aigi Margus[1]
[1] Department of biological and environmental science, University of Jyväskylä
Contact: aigi.margus@jyu.fi

Body size has typically been shown to decrease with increasing temperature (= temperature-size rule) in laboratory conditions. This has led to a prediction that the body sizes in many organisms will decrease due to the climate warming. Furthermore, these experimental responses have been documented in rather simple environments, using unnaturally large gradients of temperature (typically 10-15°C) and constant within-treatment temperatures. By contrast, the response of species' body sizes to temperature variations in complex natural environments is poorly known. To fill this gap, we measured yearly variation in body size (forewing length in nine common moth species sampled from natural populations in Estonia (N=1899), and correlated these data with interannual variation in temperatures. Correlations between body size and temperature substantially varied across the set of species examined. However, those showing clear associations were mostly negative confirming the temperature-size rule. Our results suggest that the responses of different species to climate warming are likely to range from no change to a considerable decrease in body size.

2.36 Broad-extent vs small extent distribution models: an alternative by updating broad-extent models with small-extent data

A.L. Márquez[1], R. Real[1]
[1] Biología Animal, Universidad de Málaga
Contact: almarquez@uma.es

We modelled the ecogeographical favourability for 20 threatened non-volant vertebrate species in Andalusia (Spain), under different climate change scenarios (GGCM2-A2/B2-ECHAM4-A2/B2). We considered three approaches: a) Using national models trained in mainland Spain and projected on Andalusia (NAT model), b) Performing a new model for Andalusia only (REG-model), c) Using the national models recalibrating them with the presence/absence data for Andalusia (UPD-model). For all the models we assessed their calibration power, by calculating the Root Mean Square Error (RMSE) of their predicted and observed presences in probability intervals, and their parsimony, discrimination and classification power and the probability function domain. For each species we selected for projection to the future the model approach with the best assessment scores. Approaches b) and c) were usually the best. We propose to take advantage of national species distribution models, but proceeding to update them to the regional target area before projecting them to the future.

Keywords: Andalusia, emission scenarios, favourability function, threatened species, species distribution model

2.37 How does contemporary climate vs. climate change velocity affect endemic plant species richness in China?

Chunjing Qiu[1], Zehao Shen[1]
[1] Peking University
Contact: qiuchunjing2011@163.com

Climate change is considered a top threat to biodiversity, but the relative roles of contemporary climate versus the rate of climate change in determining spatial patterns of biodiversity are far from clear. We explores the geographic patterns of a representative sample of 555 endemic seed plant species in China. Ordinary least squares and spatial autoregressive models were compared to assess the relationship between richness of endemics and the rate of climate change in the past century, as well as several contemporary climate variables. In China, a high level of endemism was associated with high elevation and low rate of climate change. However, contemporary climate had a stronger impact than climate change velocity in the past century on endemic species richness patterns.Specifically, mean annual precipitation and annual range of temperature were important contemporary climatic factors.The rate of change of annual mean temperature also significantly contributed to the spatial pattern of endemic species richness.We found no significant relationship between topographic variation and endemic species richness, while temperature variability was strongly correlated with the species richness pattern.

Keywords: Species richness, Endemic plant, Climate change, Geographical pattern, Topography, Contemporary climate, China

2.38 Abrupt versus gradual environmental change: Effects on species adaptation

Viktoriia Radchuk[1], Jörns Fickel[1], Andreas Wilting[1], Norbert Marwan[1], Jürgen Kurths[1], Christian Voigt[1], Alex Greenwood[1], Juliane Maaß[1], Renata Martins[1], Riddhi Patel[1], Stephanie Kramer-Schadt[1]
[1] Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research (IZW), Germany
Contact: radchuk@izw-berlin.de

The effects of sudden versus gradual environmental change on the adaptation of the species are hotly debated. The consequences of such changes are most often explored with theoretical models, however their predictions are rarely underpinned with empirical data. In this project we aim to understand how much the speciation of primates, carnivorous and hoofed mammals in South East Asia was affected by an abrupt environmental event, the super-eruption of the Toba volcano ~70,000 years ago. To this end we will employ process-based evolutionary modelling, in which species traits (e.g. ecological niche, dispersal ability) will be allowed to evolve. The models will be run under alternative environmental change scenarios to produce plausible phylogenetic trees. These trees will then be contrasted with the ones inferred

from the genetic data to allow an insight into the mechanisms behind the observed results of the evolution. Understanding the main cause of mammalian evolution in Sunda Shelf region will help to suggest more effective conservation guidelines for the endangered species in the current rapidly changing environment.

2.39 Berkeley Ecoinformatics Engine: Rescuing and integrating biological and environmental data in the face of global change

Giovanni Rapacciuolo[1], Rosemary Gillespie[1], Sarah Hinman[1], Maggi Kelly[1], Michelle Koo[1], Kevin Koy[1], George Roderick[1], Charles Marshall[1]
[1] Global Change Biology, University of California, Berkeley, USA
Contact: roderick@berkeley.edu

Predicting biotic responses to global environmental changes necessitates a holistic understanding of the complex interactions and feedbacks among organisms, climate, and their physical and biotic environments across space and time. The newly launched Berkeley Ecoinformatics Engine (ecoengine.berkeley.edu) addresses this challenge by creating web-based building blocks that access and integrate data from established biological and environmental data repositories as well as newly digitized historical datasets rescued from orphaned or remote labs. These datasets include specimens from natural history collections, field surveys and observations, photographs, environmental sensor networks, GIS baselayers of paleo, present, and future climate scenarios and more. This unique combination of features and data makes the Ecoengine an invaluable tool for biodiversity and global change research. Users can access Ecoengine through their pathway of choice from directly tapping the Application Programming Interface (API), to R (via rOpenSci's Ecoengine package), to using Holos (holos.berkeley.edu) our newly launched exploratory mapping interface. Case studies are illustrated including animal and plant responses to changes in land use and climate.

Keywords: Global change, ecoinformatics, data science, climate change, species distributions, R, rOpenSci, Ecoengine

2.40 ⚡ SDM ensembles cannot overcome bias: caveats for inferring range dynamics

Francisco Rodriguez-Sanchez[1], Jordano Pedro[1]
[1] Integrative Ecology Group, Estacion Biologica de Donana - CSIC
Contact: frodriguez.work@gmail.com

Species Distribution Models (SDM) are widely used to infer climate change impacts on species ranges. But the species distribution data used to calibrate these models are only uncertain –and often biased– indicators of species' climatic requirements (e.g. due to sampling bias or disequilibrium of species distributions with climate). SDM ensembles, which aggregate outputs from different models to produce consensus predictions, are now a common strategy to accommodate uncertainty and deal with the typically large variability between model projections. Here we show, using simulated data, that SDM ensembles are unable to overcome biases in the distribution data, affecting their ability to project range dynamics under climate change. Since all models of the ensemble are calibrated on the same dataset, all are affected by the bias in the distribution data, which impairs the quality of the final ensemble. In fact, some models perform consistently better than the ensemble. We thus advocate for applying bias correction techniques on the distribution data and aiming for single good, sensible models rather than averaging over many different models of more dubious quality.

Keywords: species distribution modelling; climate change; range dynamics; uncertainty;

2.41 ⚡ *Fagus sylvatica* leading edge in North-Western Iberia: Holocene migration inertia, forest recovery and recent climate change

Rut Sánchez de Dios[1], Laura Hernández[2], Fernando Montes[2], Helios Sainz-Ollero[3]
[1] Biología Vegetal I, University Complutense of Madrid
[2] INIA-CIFOR, Madrid, Spain
[3] Autonoma University of Madrid (UAM), Spain
Contact: rut.sanchez@bio.ucm.es

Fagus sylvatica presents its south-western distribution edge in Spain. Here its abundance decreases from E to W being absent in the most western part. This area appears climatically suitable when modelling the species distribution. Recent palaeopalynologic and genetic data have demonstrated the existence of glacial refugia in NW

Iberia. They also establish the beginning of *F. sylvatica* forests expansion at the Mid Holocene associated with anthropic activities. By comparing data from different cycles of National Forest Inventories (1990-2010) we find that that the expansion of *F. sylvatica* may be still in progress. However, future species distribution models show a significant surface reduction. Our results also point out the expansion of *Fagus* forests instead of *Q. petraea*. Both species present thus different types of distribution margins: a trailing edge and a leading edge respectively. Finally we analyse *F. sylvatica* and *Q. petraea* dynamics during the last decades in NW Iberia and explore the role of forest management and biotic interactions in the recent and future species trends using GLM and SEM models and demographic and recruitment variables as response variables

Keywords: Fagus sylvatica, Quercus petraea, forest migration, forest management, global change

2.42 ⚡ The fate of deep subterranean biodiversity under climate change

David Sánchez-Fernández[1], Valeria Rizzo[1], Alexandra Cieslak[1], Arnaud Faille[2], Javier Fresneda[2], Ignacio Ribera[1]
[1] Institute of Evolutionary Biology (CSIC-UPF)
[2] Zoologische Staatsammlung, Muenchhausenstrasse, Munich, Germany
Contact: davidsan@um.es

Most assessments of species extinction risk under climate change have been based on niche modelling of their current distribution, overlooking small scale heterogeneity (with the potential of behavioral adjustments), phenotypic plasticity or adaptive evolution to face new environmental conditions. Here we study a model system in which most of these uncertainties do not apply: the deep subterranean environment, characterized by homogeneous and constant conditions with simple biological communities. We focus on a clade of highly modified troglobitic beetles (tribe Leptodirini) living in the NE Iberian Peninsula, for which we have comprehensive phylogenies, detailed distributions, and experimental thermal tolerances of some species. Our aims are to estimate i) the range of conditions to which these species are currently exposed and those which they may have experienced in the recent past (LGM); ii) the minimum range of temperatures they should have experienced through their evolutionary history, and the minimum rates of thermal niche evolution to sustain these changes, and finally; iii) their fate under future scenarios of global change.

Keywords: thermal niche evolution, cave beetles, thermal tolerance, risk of extinction

2.43 ⚡ Do Himalayan treelines respond to recent climate change? An evaluation of sensitivity indicators

Udo Schickhoff[1], Maria Bobrowski, Juergen Boehner, Birgit Buerzle, Ram Chaudhary, Lars Gerlitz, Helge Heyken, Jelena Lange, Michael Mueller, Thomas Scholten, Niels Schwab, Ronja Wedegaertner
[1] Geography, University of Hamburg
Contact: schickhoff@geowiss.uni-hamburg.de

Climate warming is expected to induce treelines to advance to higher elevations. Empirical studies in diverse mountain ranges, however, give evidence of both advancing alpine treelines as well as rather insignificant responses. This paper reviews the current state of knowledge regarding sensitivity and response of Himalayan treelines to climate warming. Since most Himalayan treelines are anthropogenically depressed, observed advances are largely the result of land use change. Near-natural treelines are usually krummholz treelines which are relatively unresponsive. Nevertheless, intense recruitment of treeline trees suggests a great potential for future treeline advance. Competitive abilities of seedlings within krummholz thickets and dwarf scrub heaths will be a major source of variation in treeline dynamics. Tree growth-climate relationships show mature treeline trees to be responsive to temperature change, in particular in winter and pre-monsoon seasons. High pre-monsoon temperature trends will most likely drive tree growth performance in W and central Himalaya. Ecological niche modelling suggests that bioclimatic conditions for a range expansion of treeline trees will be created during coming decades.

Keywords: Recruitment, Treeline form, Treeline shift, Treeline type, Tree Growth-Climate Relationship

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2.44 ⚡ How gradual warming, extreme weather and landscape interactively affect ecosystem processes

Corinna Schillinger[1], Andreas Schweiger[1], Carl Beierkuhnlein[1]
[1] Biogeography, BayCEER, University of Bayreuth
Contact: schillingerco@aol.com

Gradual climatic shifts and abrupt extreme weather events are expected to have major ecological implications on various scales. However, most future projections about climate change impacts are rather coarse and are not able to model ecological effects on the relevant (regional-) scale. Plant communities of springs response very sensible to water chemistry, which in turn integrates biogeochemical catchment processes that are sensible to climate and land use changes. By studying plant communities and hydrochemistry of springs in Central Europe, we are able to investigate the interactive effect of climatic extreme events, gradual climatic shifts and landscape characteristics on a regional scale. Based on 25 years of investigation we can show visible effects of gradual warming on landscape scale. However, the impact of climatic extreme events which strongly interacts with additional stressors linked to land use practice significantly modifies this long-term response. By combining these findings with our already existing knowledge about the ecological response characteristics of these systems we can provide a sound tool to assess regional effects of future climate change.

Keywords: biomonitoring, global change, community indication, crenal communities, forest catchments

2.45 ⚡ Near natural treeline ecotone, species patterns and species transitions influenced by soil factors in Rolwaling Himal, Nepal

Niels Schwab[1], Birgit Bürzle[1], Michael Müller[2], Udo Schickhoff[1], Thomas Scholten[2], Ram P. Chaudhary[3]
[1] Physical Geography, Center for Earth System Research and Sustainability (CEN), University of Hamburg, Germany
[2] Chair of Physical Geography and Soil Science, University of Tübingen, Germany
[3] Research Centre for Applied Science and Technology (RECAST), Tribhuvan University, Kirtipur, Nepal
Contact: niels.schwab@uni-hamburg.de

Main objective of the project "Sensitivity and Response of the Treeline Ecotone in Rolwaling Himal, Nepal, to Climate Warming" (TREELINE) is to detect hitherto poorly understood driving forces for spatially differentiated treeline dynamics under climate warming at small scales. We implement an integrated landscape approach focusing on topography, climate, soils and vegetation. Vegetation and dendrochronological analyses include the sampling of randomly selected forest stands along elevational transects (3700-4200 m) across the ecotone with regard to growth rates, age structures, tree physiognomy, stand densities and tree recruitment. Moreover we analyse site conditions and mechanisms (geomorphic controls, soil temperature, physical and chemical conditions, plant interactions).

We present details on the treeline ecotone stand structure including dendroecological data and results of treeline response pattern analyses. We identified several transitions of all occurring ecotone tree species regarding various tree growth parameters. Analyses of these transitions result in different transition intensities ranging from smooth to abrupt, enabling further analyses to explain growth patterns.

Keywords: treeline, species transitions, growth patterns, dendroecology, soil factors

2.46 ⚡ Advantages on the dark side of insect colouration

Andreas Schweiger[1], Manuel Steinbauer[1], Carl Beierkuhnlein[1]
[1] Biogeography, University of Bayreuth
Contact: andreas.schweiger@uni-bayreuth.de

Body colouration has direct implications for the evolutionary success of animals. For ectotherms, which rely on external heat sources, thermoregulation through colouration seems to be crucial to sustain energy balance and overcome the rising energy demand linked to increasing body size and decreasing ambient (habitat) temperatures. Although theoretical background exists about the compensatory importance of colouration, evidence is still lacking especially on large spatial and taxonomic scales. Here we show that colour traits of two divers groups of insects, namely ground beetles and bumble bees in Central Europe strongly depends on endo- and exogenic thermal constraints. For ground beetles we found a strong positive correlation between mean body size and colour darkness.

For bumble bees, we could show a strong positive correlation between body darkness and the upper elevational range limit for working females but not for drones (males). Both findings elucidate, that body colouration plays a crucial role for thermo-regulation in completely differing groups of insects, which emphasize the trans-taxonomic, evolutionary relevance of this still neglected trait.

Keywords: adaptive colouration, Coleoptera, Hymenoptera, insects, melanism, pigmentation, thermoregulation

2.47 ⚡ Resilience of freshwater wetland habitats for migrating shorebirds under climate change

Valerie Steen[1], Susan Skagen[2], Barry Noon[1], Gordon Reese[2]
[1] Colorado State University
[2] U.S. Geological Survey
Contact: valerie.steen@gmail.com

In the U.S., millions of migrating shorebirds use freshwater wetlands throughout interior grassland ecosystems. Two component ecoregions, the Playa Lakes and the Rainwater Basin, contain primarily ephemeral wetlands whose variable existence depend on seasonal precipitation and temperature-driven evaporation. Here, future climate projections indicate more frequent dry conditions, and thus, reduced availability of ephemeral wetland habitats. The third component ecoregion, the Prairie Pothole Region (PPR), contains seasonal and semipermanent wetlands. These larger and deeper wetlands can retain water through dry periods. We examined the importance of the PPR to migrating shorebirds by comparing shorebird abundance and distribution at the flyway scale under historical droughts and wet periods using systematic surveys and citizen science-based Ebird datasets. We found important differences in shorebird numbers and distribution at the flyway scale and indication of the importance of the more permanent wetland habitats in the PPR during droughts. While patterns differed by species, overall our results indicated the importance of the PPR to flyway scale shorebird habitat resilience.

Keywords: Shorebirds, migration, climate change, freshwater wetland habitats

2.48 Targeted conservation planning accounting for the effects of climate and land-cover change on Borneo's terrestrial mammals

Matthew J. Streubing[1], Andreas Wilting[2], David Gaveau[3], Eric Meijaard[3], Robert J. Smith[1], The Borneo Mammal Distribution Consortium[4], Manuela Fischer[2], Kristian Metcalfe[1], Stephanie Kramer-Schadt[2]
[1] Durrell Institute of Conservation and Ecology, School of Anthropology and Conservation, University of Kent, UK
[2] Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany
[3] Center for International Forestry Research (CIFOR), Bogor, Indonesia
Contact: kramer@izw-berlin.de

Habitat loss and climate change pose a double jeopardy to many species. To identify the best area to effectively conserve Borneo's mammals this century we modelled suitable habitat under multiple climate and land-cover change scenarios prior to spatial prioritisation. We first refined Maxent to predict present-day habitat suitability and project to the 2020s, 2050s and 2080s. Future climates were derived from four IPCC model and emission scenario combinations, and future land-cover estimated by a predictive deforestation model. Despite variation in model projections, Marxan-derived spatial plans for distributional changes during the projection time-frame required more land outside conservation reserves than prioritisation just for present-day. Conserving a consensus area identified by the majority of models would meet ~85% of present-day species targets in 31000-58000km2, the majority in forest reserves and logging concessions. The remaining land is allocated for timber production (64%) or conversion (36%), warranting further conservation partnerships with logging and oil palm companies in these areas.

Keywords: mammal diversity, climate change, land-cover change, species distribution modelling, spatial prioritisation, conservation planning

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2.49 ⚡ Have British birds extended northward?

Shirin Taheri[1], Babak Naimi[1], Miguel Araújo[1]
[1] Department of Life Science, Imperial College London
Contact: taheri.shi@gmail.com

No doubt exists that climate limits the distributions of species. However, detecting these changes and attributing casual effects requires simultaneous examination of changes across northern, eastern, southern, and western quadrants. Here we provided the first evidence of non-directional shifts in species distributional range using 154 breeding bird species in the UK. Then considered two comparison scenarios given the three time periods, firstly 1968 -72 vs. 1988-91 and secondly 1988-91 vs. 2008-11. To measure distributional shift, local extinction and expansion were counted (into neighbor cells) for every species and quadrants. No clear directional shift were detected. The proportion of contracting or expanding marginal cells was not significantly different among quadrants for both group of species. Range expansions and contractions are non-directional, suggesting that climate change has not caused any shift in margins of the birds in past 40 years. Distributional dynamics of species are affected by a cocktail of factors, including aspects of their life histories or habitat changes. Attributing cause and effect requires more sophisticated methods than typically used in studies.

Keywords: Species range shift, climate change, extinction risk, expansion

2.50 Defining risk zones for Chikungunya Fever in Europe: A biogeographical approach

Nils Tjaden[1], Stephanie Thomas[1], Anja Jaeschke[2], Dominik Fischer[3], Carl Beierkuhnlein[1]
[1] Department of Biogeography, BayCEER, University of Bayreuth
[2] Department of Biogeographical Modelling, BayCEER, University of Bayreuth
[3] TU München
Contact: nils.tjaden@uni-bayreuth.de

Until recently epidemic outbreaks of Chikungunya, a viral disease transmitted by mosquitoes, were geographically restricted to Southeast Asia, India and Africa. This changed in December 2013, when the first case of autochthonous (local) transmission on the Caribbean Island of St. Martin was reported. In the following months, a rapid spread across the Caribbean was observed, accompanied by cases on the Central- and South American Mainland. From continental Europe, sporadic cases of autochthonous transmission have been reported since 2007. Given the pervasive presence of the Asian Tiger Mosquito *Aedes albopictus* (a competent vector for Chikungunya) in southern Europe, increased influx of potentially infected travelers as observed by the European Centre for Disease Prevention and Control (ECDC) poses a serious threat to public health. In close collaboration with the ECDC, we aim to identify European risk zones for Chikungunya, utilizing the current and potential future climatic suitability for the vector, flight patterns of travelers from affected regions, and other environmental parameters that affect potential disease spread. Here we present our approach as well as first results.

Keywords: Chikungunya Aedes albopictus Climate Change vector-borne diseases species distribution modelling

2.51 Potential climate-driven impacts on the distribution of generalist treefrogs in South America

Tiago Vasconcelos[1], Bruno Nascimento[1]
[1] Sao Paulo State University
Contact: zoologia@ig.com.br

Climate change has been considered a serious threat to biodiversity. If populations have no longer physiological, morphological, or behavioral adaptations to novel climatic conditions, or are unable to change the timing of crucial life cycle events to avoid those months with unfavorable climate, the only alternative may be tracking appropriate conditions in space and follow them. In this study, we evaluate the spatial potential effects that climate change can exert on four generalists wide-ranged South American anurans. Using six ecological niche modelling methods and different climate change scenarios for 2050, we found that all treefrogs are predicted to contract their geographical ranges by 2050 at a magnitude varying from 13.90% (*Dendropsophus nanus*) to 57.66% (*D. minutus*) loss of climatically suitable areas. These areas are mainly located in the northern geographical rim of the species distribution. Conversely, only minor gains in climatically suitable areas are expected for the species (except for *D. minutus*). Finally, all species are expected to be mainly associated to the Brazilian Atlantic Forest and absent from the lowlands of the Pantanal floodplain by 2050.

Keywords: Anura, Ecological niche modelling, Ensemble forecast, Hylidae.

2.52 Range collapse in the Diana fritillary, *Speyeria diana (Nymphalidae)*

Carrie Wells[1], David Tonkyn[2]
[1] Biological Sciences, University of North Carolina at Charlotte
[2] Biological Sciences, Clemson Uniersity
Contact: cwells19@uncc.edu

Global warming can affect the distributions, phenology and, ultimately, conservation status of species, but most published studies on its biological effects have focused on higher latitude species. We examined the Diana fritillary, a butterfly which once ranged throughout the Southeastern USA but now is severely restricted in range. We searched for all records of this species, from publications, specimens in public and private collections in the USA and Europe, online databases, contemporary field surveys by scientists and amateurs, and our own field surveys. We analysed records for shifts in latitude, longitude, elevation and phenology. The Diana fritillary has disappeared entirely from the Atlantic coastal plain, and from interior lowland sites. It now persists in two disjunct parts of its former range, and is shifting to higher elevations at about 18 m/decade. Females are being collected 4.3 days earlier per decade. These shifts in distribution and phenology are consistent with predicted effects of global warming, but we review other changes to the region which also might contribute to these patterns. We also comment on implications for the conservation of this species.

Keywords: Butterfly; climate change; distribution; elevation; habitat loss; phenology; range collapse

2.53 Drivers of body size evolution in pikas *(Ochotona)* vary between taxonomic levels

Marie Westover[1]
[1] Biology, University of New Mexico
Contact: mariewestover@gmail.com

Body size is a universal character among organisms that strongly influences life history, behavior and physiology, including climatic tolerance. The pattern that species within a genus generally have larger body sizes at higher latitudes is known as Bergmann's rule. The underlying mechanism for Bergmann's rule, and how well it holds between biological levels is not well understood. Here, I test the extent to which pikas *(Ochotona)* conform to Bergmann's rule for: a) species within the genus, and b) subspecies and populations within a widely distributed species, *O. princeps*. I hypothesize that pikas will follow Bergmann's rule, with larger individuals or species found in cooler climates. I compared the body mass of georeferenced *O. princeps* specimens and the centroids of *Ochotona* species with bioclimatic variables from worldclim.org in ArcMap. Preliminary analyses suggest that body size variation at both species and subspecies level is not strongly correlated with latitude or temperature. Pika body size at the subspecies and species level is most strongly correlated with precipitation, suggesting that availability or quality of food may be an important influence on pika body size.

Keywords: Bergmann's rule, body size evolution, abiotic drivers, climate

2.54 The effects of dispersal ability and climate velocity on the extent of species range shifts

J. Eric Williams[1], Jessica L. Blois[1]
[1] University of California, Merced
Contact: jwilliams45@ucmerced.edu

Understanding how species will respond to future climate change is at the forefront of conservation biology. Species distribution models (SDMs) have been widely used to determine how species ranges change over time in relation to

climate change. However, these models rarely incorporate dispersal mechanisms or varying rates of climate change through time and across space. These factors are likely important in determining the ability of a species to respond to changing climates. In this study we assess how climate velocity and the dispersal ability of a species affect the extent to which a species can shift its range in response to climate change. We build SDMs for 29 small mammals in western North America and hindcast them to various times over the past 21,000 years. Preliminary results indicate that mammals showed a variety of responses, including stable, expanding, and contracting ranges. We then determine the extent to which individual life history traits and local climate velocities influence the amount of range shift observed in individual species. These results will help generalize the types of responses that can be expected for species and regions in the future.

2.55 The exposure, sensitivity and vulnerability of natural vegetation in China to thermal climate variability (1901-2013): An multiple indicators-based approach

Yue Xu[1], Zehao Shen[1]
[1] Peking University
Contact: xuyue10@pku.edu.cn

The anthropogenic climate changes since 20th century have intensified risks to degradation of ecosystem structure and functions. Vulnerability assessment for natural ecosystems to the climate change is expected to support adaption and/or mitigation strategies, but a contented indicator system for this purpose is still in need. Focusing on the primary stress of climate thermal variability (of January minimum temperature and July maximum temperature), the buffering capacity of habitat, and vegetation resistance, this study proposed three indicators to implement an vulnerability assessment for 46 natural terrestrial vegetation types in China to the climate change in the past century (1901-2013). The result suggested contrasting patterns of vulnerability to the threat of low and high thermal limits in the past century. Several regions showed concentrated high vulnerability value in the north of China, including Northeast China plains, Central Junggar Basin, and northern part of Qinghai-Tibet Plateau, while the Northeast China mountains, Qinling-Daba Mountains, Hengduan Mountains and East China hills exhibited low vulnerability value, although there are also some areas of middle-high values scattered in the subtropic region.

Keywords: Climate change, thermal variability, vegetation, spatial fragmentation, lifespan, vulnerability, China

2.56 Seasonal relationships of avian diversity with climate in Australia

Juliane Zenner[1], Thomas Müller[2], Katrin Böhning-Gaese[2], Susanne A. Fritz[3]
[1] Biodiversity and Climate Research Centre (BiK-F) & Goethe University Frankfurt
[2] Biodiversity and Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung & Goethe Universität Frankfurt
[3] Biodiversity and Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung
Contact: JulianeZenner@web.de

Most previous studies of large-scale spatial patterns in avian diversity have concentrated on breeding ranges only, but how does seasonal change within a year affect these? The aim of this study was to detect how species richness and phylogenetic diversity of birds in Australia are related to climate across seasons. We expected no seasonal change in spatial diversity patterns for resident birds, so the relationships between diversity and climate variables may change between seasons. In contrast, migratory and nomadic species may track their climatic niches through the seasons. We used presence-absence data from 'The New Atlas of Australian Birds' for 658 species recorded over 4 years, and extracted seasonal climate data for the same timeframe. Species richness and phylogenetic diversity were higher in tropical and temperate than in arid areas. Differences in spatial diversity patterns and relationships with climate between the species groups were larger than differences within a group between different seasons. Our study implies that to understand the environmental drivers of avian diversity, it is essential to tease apart seasonal climatic effects for different migration types.

Keywords: birds - diversity - macroecology - Australia - seasonal migration - species richness - phylogenetic diversity -

2.57 ⚡ Global warming favours light-coloured insects in Europe

Dirk Zeuss[1], Roland Brandl[1], Martin Brändle[1], Carsten Rahbek[2], Stefan Brunzel[1]
[1] Department of Ecology, University of Marburg
[2] Center for Macroecology, Climate and Evolution, the Natural History Museum of Denmark
Contact: dirk.zeuss@biologie.uni-marburg.de

Associations between biological traits of animals and climate are well documented by physiological and local-scale studies. However, whether an ecophysiological phenomenon can affect large-scale biogeographical patterns of insects is largely unknown. Insects absorb energy from the sun to become mobile, and their colouration varies depending on the prevailing climate where they live. Here we show, using data of 473 European butterfly and dragonfly species, that dark-coloured insect species are favoured in cooler climates and light-coloured species in warmer climates. By comparing distribution maps of dragonflies from 1988 and 2006, we provide support for a mechanistic link between climate, functional traits and species that affects geographical distributions even at continental scales. Our results constitute a foundation for better forecasting the effect of climate change on many insect groups.

2.58 Does biogeographic origin influence leaf-out phenology?

Constantin Zohner[1], Susanne Renner[1]
[1] Systematic Botany and Mycology, University of Munich (LMU)
Contact: constantin.zohner@t-online.de

Gaining phenological knowledge about plants is necessary for predicting impacts of climate change on ecosystem processes, but locally adapted phenological strategies are still poorly documented and understood. Here, we demonstrate how phenological data (experimental and *in situ* from a common garden) can be used to study leaf-out in woody species from different native climates and thus to forecast how climate-induced shifts in the floristic composition might affect community phenology. Twig-cutting experiments for 100 species were conducted to examine the relative importance of leaf-out triggering factors such as photoperiod, chilling, and forcing temperatures. We are presenting two new approaches to link our phenological research with species' climatic provenance, one relying on the Köppen system, the other on Worldclim data. In combination, these approaches reveal climate-related phenological patterns and species-specific sensitivity to external signals. Thus, southern-climate-adapted species flush later than Munich natives, and photoperiod- and chilling- sensitive species all flush late; other unexpected differences between southern- and northern-climate adapted species will be documented with new data on our poster.

Keywords: Phenology, Biogeography, Leaf-out

P3 Gradients, range limits, and beta diversity

3.1 ⚡ Boundaries of Saharo-Arabian and Sudanian regions in Saudi Arabia

Abdulatif Alnafie[1]
[1] College of Social Sciences, Geography, Dep., Al-Imam Muhammad Ibn Saud Islamic University
Contact: aalnafie@gmail.com

The Arabian Peninsula comprises parts of two phytogeographical regions that cover some parts of the Middle East and North Africa: (1) The Saharo-Arabian (or Sindian) region; and (2) The Sudanian (Sudano-Zambezian) region. Unfortunately, the boundaries of these two regions in Saudi Arabia are still debatable, ill-defined and very difficult to delimit. The delimitation of the frontier between the two regions in the Arabian Peninsula in its southern part has always created some difficulties for a few biogeographers as well as phytogeographers who have studied the region. This paper will present the phytogeography of Saudi Arabia and examines its phytogeographic location within the complex plant geographical regions of the Middle East.

Keywords: Saudi Arabia, Saharo-Arabian, Sudanian regions

3.2 A fuzzy implementation of binary similarity indices for assessing biogeographic associations, biotic regions, and beta diversity

A. Márcia Barbosa[1]
[1] CIBIO/InBIO, University of Evora
Contact: barbosa@uevora.pt

Binary similarity indices are widely used for detecting associations between species occurrence patterns, performing biotic regionalization, and assessing beta diversity, including spatial and temporal species loss and turnover. Such indices are commonly calculated upon binary presence/absence (or sometimes modelled suitable/unsuitable) data, which are both incomplete and more categorical than their underlying natural patterns. Spatial proximity is disregarded, such that occurrences at adjacent, even interspersed, but not strictly coincident localities are considered as dissimilar as occurrences at opposite ends of the study region. This amplifies the effects of data deficiencies and the scale-dependence of the results. I propose fuzzy-logic versions of these binary similarity indices, which can be applied to continuous (modelled or interpolated) rather than binary occurrence values. The procedure is robust to data source disparities, gaps or other errors in occurrence data, even for restricted species for which slight inaccuracies can affect substantial parts of their range. It is implemented in a free and open-source R package and in a graphical user interface extension for QGIS.

Keywords: chorotypes, biotic regionalization, specific composition, beta diversity, fuzzy logic, species distributions

3.3 ⚡ The debate on beta diversity partitioning: linking measures to concepts

Andrés Baselga[1], Fabien Leprieur[2]
[1] University of Santiago de Compostela
[2] Université Montpellier 2, France
Contact: andres.baselga@usc.es

Quantifying the differences among biological communities is a major step for understanding how and why biodiversity is distributed in the way it is. Biological communities can differ because they are composed of different species or because they have a different number of species. These two facets of biotic dissimilarity can be separated using two alternative methods. Both approaches separate a “species replacement” component, but there is a debate on whether the other component should account for dissimilarity associated to species richness difference or nestedness. This is not trivial because total dissimilarity is additively partitioned. Therefore, subtracting from total dissimilarity the dissimilarity associated to nestedness or to richness difference yields a different measure of species replacement. We thus have two alternative measures for a same ecological concept, “species replacement”. Are they really interchangeable or, instead, are they linked to different ecological processes? Here I perform a systematic comparison of measures of species replacement, richness difference and nestedness-resultant dissimilarity, aiming to link measures to clear ecological concepts.

Keywords: beta diversity, dissimilarity, methods, nestedness, species richness

3.4 ⚡ Individualistic Gleasonian patterns in beta diversity prevail along elevational gradients

Jan Beck[1], Christy McCain[2]
[1] Environmental Science (Biogeography), University of Basel
[2] University of Colorado
Contact: jan.beck@unibas.ch

Species turnover is thought to influence the pattern of species richness on elevational gradients, but it has yet to be examined systematically (1) for ecological structuring that go beyond null expectations, (2) for general, repeated patterns along elevational gradients, or (3) for coincident trends with species richness. We used 62 elevational gradients for different vertebrate groups. We measured beta diversity as total beta of the gradient, and as turnover and nestedness patterns along neighbouring elevation bands. We derived expectations for randomized ranges with the mid-domain model and two other null models. Total beta increased with latitude and was higher among ectotherms than endotherms. Gradients of turnover were highly idiosyncratic, multi-peaked and without consistent elevational trends. There was little concordance between turnover and species richness. No clearly repeated and predictable patterns existed for turnover and nestedness, although both were more structured than predicted by null models. These results support Gleason's (1926) view on range limits, where each species' range is determined individualistically and not as part of a larger community's limits.

Keywords: beta, diversity, ecotones, elevation, nestedness, range limits, turnover, vertebrates

3.5 Synthetizing Worldwide Ecology, Evolution and Physiology (sWEEP): Unifying marine and terrestrial biodiversity at the interplay of macroecology, macroevolution and macrophysiology

Joanne. M Bennett[1], Adam. C Algar[2], Miguel .B Araújo[3], Piero Calosi[4], Susana Clusella-Trullas[5], Jose Alexandre Felizola Diniz-Filho[6], Bradford A. Hawkins[7], Sally A. Keith[8], Ingolf Kühn[9], Brezo Martínez[10], Carsten Rahbek[8], Laura Rodríguez[10], Jennifer Sunday[11], Fabricio Villalobos[12], Ignacio Morales-Castilla[13], Miguel Ángel Olalla-Tárraga[10]
[1] German Centre for Innovative Biodiversity Research (iDiv) Halle-Jena-Leipzig
[2] School of Geography, University of Nottingham
[3] Department of Life Sciences Faculty of Natural Sciences, Imperial College London
[4] School of Marine Science and Engineering, University of Plymouth
[5] Centre for Invasion Biology, Department of Botany and Zoology, Stellenbosch University
[6] Departamento de Ecologia, Instituto de Ciências Biológicas, Universidade Federal de Goiás
[7] Department of Ecology and Evolutionary Biology, University of California
[8] Center for Macroecology and Climate, University of Copenhagen
[9] Department Community Ecology, Helmholtz Centre for Environmental Research
[10] Biodiversity and Conservation Unit, Rey Juan Carlos University
[11] Department of Biological Sciences, Simon Fraser University
[12] Departamento de Ecologia, Universidade Federal de Goias
[13] Department of Biology, McGill University
Contact: joanne.bennett@idiv.de

Macroecology, macroevolution and macrophysiology have an overlapping goal to explain the patterns and process that drive global biodiversity distributions. Despite this, these fields are traditionally studied in isolation. Similarly, large scale studies generally focus on terrestrial, coastal and marine realms separately, leading to a lack of unified theories, methodologies or a mechanistic explanation of biodiversity gradients. sWEEP aims to bring together these realms and scientific fields using Climatic Niche Conservatism as a unifying theoretical framework. By collating a large dataset on the geographic distributions, associated physiological and phylogenetic relatedness of both terrestrial and marine taxa we aim to assess (1) how much macrophysiology and macroevolution contribute to generating diversity gradients, (2) how climatic niches are conserved *through evolution* and (3) how close species' realized niches are to their potential niches. Our results will allow us to make predictions of species' relative vulnerabilities to global change and assess whether predictions are similar across realms, bringing us closer to mechanistic explanations for biodiversity gradients.

3.6 ⚡ Biodiversity across varying environments: accumulation, loss, or stasis?

Jessica Blois[1], Stephen T. Jackson[2]
[1] Life and Environmental Sciences, School of Natural Sciences
[2] Southwest Climate Science Center, US Geological Survey; Department of Geosciences and School of Natural Resources and Environment, University of Arizona
Contact: jblois@ucmerced.edu

Understanding mechanisms of biodiversity change is important given the many factors that may influence future biodiversity. To provide a long term context for recent biodiversity changes, I investigate links between local biodiversity and environmental change over the past 21,000 years. I assembled records of fossil pollen genera from lake sediment cores in eastern North America and determined richness change at each site through time. The majority of sites showed no substantial directional changes and the mean richness across all sites did not significantly change through time. However, some individual sites had either significant increases or decreases in richness through time. I then examined the taxa underlying those changes to determine 1) if more compositional change occurred during times of rapid climate change and 2) the spatiotemporal patterns underlying taxonomic changes (i.e., average direction and distance of colonization or extirpation); I compared these changes to similar metrics of climate change. These results will illuminate whether environmental change maintains diversity in fluctuating environments by influencing colonization and extirpation of different species.
Keywords: biodiversity, richness, colonization, extirpation, late Pleistocene, pollen

3.7 ⚡ Bergmann's rule applies but Rensch's rule does not: two species rich moth taxa along a Neotropical elevational gradient

Gunnar Brehm[1]
[1] Phyletisches Museum, University of Jena
Contact: gunnar.brehm@uni-jena.de

Body size patterns (Bergmann's rule), sex ratios, sexual size dimorphism (SSD) and Rensch's rule were investigated using a large and unique dataset of two species rich groups of moths (Lepidoptera: Geometridae and Arctiinae) from a complete elevation gradient in Costa Rica.

Fore wing lengths (WLs) were measured, using (1) mean WLs of each species at each site, and (2) mean WLs of complete local assemblages. In total, 15,047 specimens (794 species) of Geometridae and 4,167 specimens (308 species) of Arctiinae were analysed. WLs increase significantly with elevation in both sexes and both taxa either linearly or asymptotically. Unexpectedly, wing loading increases with elevation. Females were far less frequently sampled than males, but their proportion is significantly lower in larger than in smaller geometrid species.

Bergmann's rule of increasing body sizes in cooler climates is clearly supported. Several mechanisms can be rejected: WL and body size are not or negatively correlated with ambient temperature, estimated net primary productivity and rainfall. Rensch's rule is not supported, which predicts smaller SSD with increasing size when females are the larger sex.
Keywords: elevation gradient, Rensch's rule, Bergmanns's rule

3.8 Species interactions across varying phylogenetic depths

Chelsea Chisholm[1], Jonathan Davies[2]
[1] Center for Macroecology, Evolution and Climate, University of Copenhagen
[2] McGill University
Contact: chelsea.chisholm@gmail.com

Phylogenetic patterns can provide a powerful approach for exploring the structure of ecological communities. Using measures that capture the phylogenetic distance and spacing of community members, researchers have tended to focus at the tips of the phylogeny in order to infer process from pattern. In this study we use a node-based phylogenetic metric in order to assess co-occurrence at each level of the phylogenetic tree., where we assess the co-occurrences of both external nodes (species) and internal nodes on the evolutionary tree linking co-occurring species. Through the use of simulations, we explore assembly rules in which species interactions can be either

negative (i.e. competitive) or positive (i.e. facilitative). We show that both significantly segregated and aggregated nodes can be detected using phylogeny. We employ our method on the Barro Colorado Island Forest Dynamics Plot, and reveal that although many of the interactions found were not different from that expected from the null distributions, we were able to detect significant interactions among particular nodes within the phylogeny, and illustrate their phylogenetic placement.

Keywords: phylogeny, node-based measures, community ecology, species interactions

3.9 ⚡ Temperature versus resource constraints: which factors determine bee diversity on Mount Kilimanjaro (Tanzania)?

Alice Claßen[1], Marcell Peters[1], William Kindeketa[1], Tim Appelhans[2], Connal Eardley[3], Mary Gikungu[4], Andreas Hemp[5], Thomas Nauss[2], Ingolf Steffan-Dewenter[1]
[1] Department of Animal Ecology and Tropical Biology, University of Würzburg
[2] Environmental Computer Sciences, University of Marburg
[3] School of Biological and Conservation Sciences, University of KwaZulu-Natal
[4] Zoology Department, National Museum of Kenya
[5] Department of Plant Physiology, BayCEER, University of Bayreuth
Contact: alice.classen@uni-wuerzburg.de

Temperature and resources are assumed to be the major predictors of latitudinal and elevational diversity gradients. While recent studies found high support for diversity limitations by resources, the mechanisms behind are still a matter of debate and have largely been analysed for vertebrate taxa. However, in ectothermic organisms temperature-limitations may be of considerably higher importance than resource-limitations, as temperature modulates the access of animals to resources. Along a 3.6 km elevational gradient on Mount Kilimanjaro, we disentangled the effects of temperature and floral resources on bee diversity. Floral resources had a weak but significant effect on bee richness, via bee abundances. We found that temperature outweighed the impact of floral resources on bee richness, as it controlled (a) the access of bees to floral resources (indirect effect) and (b) ecological and evolutionary processes that drive the maintenance and origination of diversity (direct effect). We conclude that temperature-mediated resource use processes improve our understanding of how ectothermic animals respond to environmental changes on macroecological scales.

Keywords: elevational gradient, productivity-hypothesis, physiological-tolerance hypothesis, energy-richness hypothesis, temperature-speciation hypothesis, pollination, land use change, macroecology, Apoidea

3.10 Spatial distribution and diversity of parasites: macroscale estimations based on host-parasite inferences

Jean-Francois Cornu[1]
[1] CNRS
Contact: Jean-Francois.Cornu@univ-montp2.fr

The spatial distribution and the estimation of diversity of life is of paramount importance for understanding biogeographical patterns and ecological processes. A significant number of global or near-global scale studies have been realised on “macroscopic” organisms but only few attempts have been done to assess spatially the richness and diversity of parasites at a similar scale. Despite their importance for the understanding of evolutionary processes, the functioning of ecosystems and their key role in infectious diseases, the low symbolic and appealing value for conservation of parasites associated with the low number of taxonomists specialised for these organisms have impede the realisation of large scale, spatialized study of parasite richness and diversity. However, the use of large database about host-parasite relationship associated with “macroscopic” geographical range can be an elegant solution to throw foundations to fill this gap. In this communication, we will present an easy approach based upon host-parasite relationships inferences to map the parasite richness and throw the foundation of large scale study on the biogeography of parasites.

Keywords: parasites, richness, host-parasite relationships

Continued next page

3.11 ⚡ A spatial analysis framework for population genetics in river networks

David Cowley[1], Erin Peterson[2], Sabela Lois[3], Daniel Isaak[4]
[1] Fish, Wildlife & Conservation Ecology, New Mexico State University
[2] CSIRO, Brisbane, Australia
[3] Zoology, University of Santiago de Compostela
[4] U.S. Forest Service, Idaho
Contact: dcowley@nmsu.edu

Biogeography of genes is embraced in landscape genetics, which links causal factors to the spatial genetic composition of populations, and species. Wright first described how isolation by distance could lead to increased genetic difference as distance increases. Sokal *et al.* showed that correlogram shape for Moran's *I*, a measure of kinship between individuals, could provide inference about causes of evolution. Most landscape-genetic papers since then have used Moran's *I* and/or Mantel correlograms for inference. Although landscape genetic models continue to be refined, there has been little work to develop spatial population genetics in rivers, where the topology of the network and water flow direction defines ecosystem processes. We will summarize historical developments in evolutionary theory in the framework of spatial statistics, and present new ideas for landscape genetics in the context of the spatial stream-network (SSN) model developed by Ver Hoef *et al*. Our objective is to extend that spatial-statistical mixed-model framework to provide a method of inference in biogeography based on accurate mapping of genetic attributes and pattern attribution to environmental covariates.

Keywords: spatial stream network freshwater biogeography landscape genetics gene-environment gene flow conservation genetics

3.12 ⚡ Is environmental heterogeneity a driver of species richness at local and regional scales? A comparison of lichen families across North American forests

Jessica Coyle[1], Allen Hurlbert[1]
[1] Dept. of Biology, University of North Carolina
Contact: jrcoyle@live.unc.edu

Environmental heterogeneity has been proposed as a primary driver of contemporary biodiversity patterns across a wide range of spatial scales. Species' persistence also depends on whether environmental conditions meet fundamental niche requirements, and spatial patterns of diversity may reflect the 'optimality' of certain environments for species pools under evolutionary constraints. By integrating environmental data with a U.S. forest inventory, herbarium records, and a global trait database, we have shown that for macrolichens, local richness is substantially influenced by diversity of the regional species pool, but that environmental heterogeneity explains little variation in species richness at both local and regional scales relative to variables characterizing environmental optimality. This is surprising given that the two largest families in the data set exhibit species richness patterns that track apparently different environmental niche requirements. We explore the implications of these niche and trait differences for evaluating heterogeneity versus optimality hypotheses across local and regional scales in the two lichen families.

Keywords: lichen, species richness, heterogeneity, environment, North America, SEM, spatial scale

3.13 ⚡ Robust techniques for regionalization reveal historical and ecological fingerprints on species assemblages

Leonardo Dapporto[1], Gianni Ciolli[2], Roger Dennis[1], Vlad Dinca[3], Simone Fattorini[4], Richard Fox[5], Matteo Ramazzotti[6], Tim Shreeve[1], Gerard Talavera[7], Roger Vila[7], Raluca Voda[7]
[1] Oxford Brookes University
[2] 2nd Quadrant
[3] Guelph University
[4] Azorean University
[5] Butterly Conservation
[6] Florence University
[7] Institut de Biologia Evolutiva (CSIC-UPF)
Contact: leondap@gmail.com

Elucidation of beta-diversty indices has led to renewed interest in regionalization methods and applications. The use of Sørensen or Jaccard indices paired with hierarchical clustering has become the preferred method. These indices

can be partitioned into turnover (species replacements between areas) and nestedness (the ordered increase of richness among areas) components. Turnover is largely influenced by historical factors (vicariance and endemism), thus being a favoured choice for identifying regionalization. Nevertheless, turnover indices produce a large number of low (zero) dissimilarity values that generate multiple equivalent solutions in most clustering algorithms and can produce highly biased results. We developed consensus techniques to solve this issue that are available in the R package recluster. Using butterflies as a model system we have shown how these novel techniques can unravel complex biogeographic fingerprints for historical and ecological determinants over the Mediterranean and expose how the different components of beta-diversity over the UK have changed in time, probably in response to natural and anthropogenically induced environmental changes.

Keywords: regionalization, beta-diversity, turnover, nestedness, recluster R package, bias, consensus, Mediterranean, British islands, butterflies

3.14 ⚡ Neutral species distributions yield non-random food webs

Christoph Digel[1], David Ott[1], Björn C. Rall[1], Brose Ulrich[1]
[1] Systemic Conservation Biology, University of Göttingen
Contact: cdigel@gwdg.de

We analyzed 48 forest soil communities and 40 lake communities. We analyzed the effects of spatial distance and environmental dissimilarity on the species dissimilarity (beta diversity) and the dissimilarity in food web structure. We show that the mechanisms proposed by neutral theory can predict the beta diversity of multitrophic species communities quite well as effects of spatial distance on beta diversity are much stronger than effect of environmental dissimilarity. Furthermore, we show that food-web structure is robust and affected neither by spatial distance (random dispersal) nor by environmental filtering. We additionally analyzed model food webs (random and niche topology) and compared their dissimilarities to our dataset of food webs. Highest dissimilarity between model food webs was reached in random food webs, niche model food webs were in between and lowest distances were expressed by empirical food webs. Food-web structure appears to be energetically optimized with local species adapted to energetic niches. This suggests that different species could be adapted to the same energetic niches, and therefore following random drift, still yield similar food web structures.

Keywords: neutral theory, food webs, food-web structure, niche theory

3.15 Towards spatial coherence of biogeographical regions

Jan Divíšek[1]
[1] Department of Geography, Masaryk University
Contact: divisekjan@mail.muni.cz

Classification of world's biota into biogeographical regions is one of the main aims in the field of biogeography, however, issues concerning spatial properties of biogeographical regionalisations have been somewhat neglected to date. Here, I address following questions: Are mammalian and avian regions statistically delineated on the basis of assemblage distinctiveness spatially coherent across two spatial scales, i.e. in the perspective of western-central Europe (with grid resolution 50 × 50 km) and in national perspective of the Czech Republic (with grid resolution 11.1 × 12 km)? Which factors shape spatial pattern of biogeographical regions at these different scales? At broader scale of western-central Europe, both mammalian and avian regions were highly spatially coherent, whereas, at finer spatial scale of the Czech Republic, regions disintegrated into spatially discontinuous patches. Analysis of these spatial patterns revealed that, at broader scale, membership of grid cells in particular cluster may be explained by their geographical distance, whereas, at finer spatial scale, spatial pattern of delineated regions may be ascribed rather to environmental similarity.

Keywords: Biogeographical regions, spatial scale, spatial coherence, distance decay of similarity, Central Europe

3.16 ⚡ Phenotypic plasticity of Central European herbs is negatively related to niche breadth and commonness

Petr Dostal[1], Daniel Prati[1], Markus Fischer[1]
[1] Institute of Plant Sciences, University of Bern
Contact: dostal@ibot.cas.cz

The hypothesis on the relationship between niche breadth and range size posits that species which can use wider arrays of resources or tolerate larger ranges of environmental conditions should be more widespread. In plants, a larger niche breadth may result from high phenotypic plasticity, i.e. changes of traits in response to environmental conditions, and therefore more plastic species are assumed to be more common. We estimated the magnitude of phenotypic plasticity in five functional traits in response to three experimental treatments across 105 European grassland species and calculated trait plasticity for each species. We then related plasticity with niche breadth and commonness for all species. Unexpectedly, we found that more plastic species have narrower niches along light and moisture gradients. More plastic species were also found to be less common, i.e. both to be less abundant locally and to have smaller range sizes. Our results indicate that phenotypic plasticity is related to the sensitivity of species towards environmental change rather than contributing to increased ecological tolerance and species commonness.

Keywords: environmental heterogeneity, plasticity, rare species, SLA, temperate grasslands

3.17 ⚡ Effects of climate and land use on alpha and beta diversity of birds at Mt. Kilimanjaro

Stefan Ferger[1], Matthias Schleuning[1], Katrin Böhning-Gaese[2]
[1] Biodiversity and Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung
[2] Biodiversity and Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung; Department of Biological Sciences, Johann Wolfgang Goethe-University
Contact: stefan.ferger@yahoo.de

Tropical mountains offer unique opportunities to study the simultaneous effects of climate and land use on biodiversity. We assessed bird communities in 13 habitat types with different land-use intensities along a 3700-m elevational gradient at Mt. Kilimanjaro, Tanzania. We recorded abiotic (e.g. temperature, precipitation) and biotic variables (e.g. vertical vegetation heterogeneity, invertebrate prey biomass, fruit abundance) and used structural equation modeling to study their direct and indirect effects on bird species richness. Climate affected bird species richness mainly indirectly through vertical vegetation heterogeneity and food availability. We further investigated the impacts of climate and land use on avian beta diversity and its richness difference and replacement components. Temperature explained most variation in richness differences, whereas land use explained most variation in replacement, indicating that different processes drive beta diversity along the temperature and land-use gradients. Temperature and land use exhibited a synergistic interaction on beta diversity, suggesting that their joint effects on beta diversity will exacerbate in the future.

3.18 Flying plants and crustaceans: waterfowl as vectors of passively dispersing organisms in endorheic lakes

Jose Antonio Gil-Delgado[1], Andreu Castillo-Escriva[2], Luis Valls[2], Xavier Armengol[1], Antonio Camacho[1], Rafael U. Gosálvez[3], Daniel Guijarro[4], Germán López-Iborra[5], Adrian Ponz[6], Carlos Rochera[2], Angel Velasco[7], Francesc Mesquita -Joanes[2]
[1] ICBIBE, University of Valencia
[2] Microbiology and ecology
[3] Department of Geography, University of Castilla La Mancha.
[4] CBIBE, University of Valencia
[5] Department og Ecology, University of Alicante
[6] University of Zaragoza
[7] Department of Environment Science, University of Castilla La Mancha
Contact: gild@uv.es

One of the aims of the multidisciplinary Ecolake project is to evaluate the proposed hypetheses of the main structure processes in biological communities, and for this purpose role of waterfowl as dispersal vectors of plants and invertebrates in the Mancha Húmeda Biosphere Reserve (Central Spain). For this purpose, we collected faeces of two duck species, the mallard and the shellduck, in Manjavacas lake, and both presented propagules of several plants (*Ruppia* sp., *Juncus* sp, Cyperaceae), and macroalgae (Characeae) as well as of invertebrate taxa (insects and crustaceans). In addition to the search for propagules in duck faeces we performed a viability experiment with the *Ruppia* seeds found in these excrements. Out of 164 seeds planted under controlled laboratory conditions 117 (71.3%) germinated. The germination time had a range of 3-18 days. Manjavacas Lake does not harbour *Ruppia* meadows at present, nor the other species found in the samples so they were likely transported from other lakes, stressing the important role of waterfowl for the dispersal of aquatic organisms in wetland systems metacommunities.

Keywords: Ducks, faeces, dispersion, germination, propagules, seeds.

3.19 Species diversity, habitat and food specialisation in Australian birds

Lenka Harmáčková[1], Vladimír Remeš[1]
[1] Department of Zoology, Palacky University
Contact: harmlen@seznam.cz

Environmental conditions affect species diversity and ecological traits of organisms in communities. We studied effects of environmental conditions including temperature, precipitation, and productivity on species richness and ecological specialisation of Australian birds. We calculated specialisation in habitat use, type of food, and selection of feeding site using Levins' index, which put every species on the specialist-generalist continuum. As a background for the spatial analyses we used a geographical grid (1^o resolution) overlapping Australia and Tasmania. We analysed average values of traits in each geographical cell with two methods: 1) classical ordinary least squares (OLS) and 2) generalized least squares (GLS), which take spatial autocorrelation into account. We found the highest species diversity and a high concentration of small families (families with low number of species) along the eastern coast, while large families were more evenly distributed. Species richness increased with the productivity of environment and with increasing precipitations. Birds in cells with high species richness were habitat and feeding specialists, but generalists in terms of food consumed.
Keywords: species diversity, specialisation, habitat, Australia, songbirds

3.20 ⚡ Competition may shape species ranges at global scales and forces regional extinction

Janin Hochheimer[1], Matthias Hoffmann[1]
[1] department of geobotany and botanical garden, Martin-Luther-University Halle-Wittenberg
Contact: janin_hochheimer@posteo.de

It has been widely shown that plant species distributions may be easily modeled with climatic factors. However, climatic modeling not always works for species with strikingly disjunctive distributions. Unavailable climatic and abiotic parameters for modeling appear not a likely explanation and reasons need to be sought at the biotic level. We use two *Artemisia* (Asteraceae) species, which are almost extinct in Europe but possess large Central Asian distribution ranges to infer reasons for large disjunctions that cannot be explained by climate. Both species are salt tolerant throughout their ranges and the availability of saline soils may not be a cause for the disjunctions. Competition between glycophytes and the halophytic *Artemisia* species may also not explain the distribution pattern. A detailed analysis of distribution patterns of halophytic species of Western Eurasia revealed that competition with congeners having similar life and growth patterns is most likely the cause for the enigmatic disjunctions. This can be supported by either completely excluding or equiform ranges. We can show that competition can seriously shape current species distributions at the global scale.
Keywords: global-scale competition, global range analysis, extinction

3.21 ⚡ Variation in fine-scale functional and phylogenetic diversity of assemblages: scale, detection, and multi-species models

Marta Jarzyna[1], Walter Jetz[1]
[1] Ecology and Evolutionary Biology, Yale University
Contact: marta.jarzyna@yale.edu

Estimates of functional and phylogenetic diversity can provide insights into the mechanisms controlling the dynamics of biological communities. While coarse-grain patterns of biodiversity are relatively well described, the fine-scale variation in functional and phylogenetic assemblage structure remains relatively poorly explored. Our goal was to investigate spatial variation in fine-grain estimates of functional and phylogenetic diversity of birds across large spatial extents, while accounting for imperfect detection of species comprising communities. We used hierarchical multi-species occupancy models (MSOMs) to estimate true probabilities of species occurrence, which were then incorporated into the estimates of community functional and phylogenetic diversities (CFD and CPD, respectively). To evaluate CFD, we quantified the multivariate trait dissimilarity between all species in a community. To assess CPD, we quantified mean phylogenetic distance between all species in a community. Accounting for imperfect detection improved the estimates of true community composition, thus allowing deeper insights into functional and phylogenetic assemblage structure across fine spatial grains.
Keywords: functional diversity hierarchical modeling imperfect detection occupancy modeling phylogenetic diversity

3.22 ⚡ Evolution of elevational diversity patterns

Michael Kessler[1], Dirk N. Karger[2]
[1] University of Zurich
[2] University of Turku
Contact: michael.kessler@systbot.uzh.ch

Geographic patterns of diversity, such as latitudinal and elevational gradients, continue to baffle biogeographers. Among the numerous explanations, the hypothesis of evolutionary niche conservatism proposes that adaptation to new environments requires time. Under this scenario, the older a taxonomic group is, the higher its chance to occupy and diversify in a wide range of habitats. We tested this by comparing elevational richness patterns of >40 taxonomic groups, ranging from bacteria to specific plant and animal families. We quantified the distinctness of the diversity pattern as the steepness of the decline of richness from the elevational of maximum richness towards higher elevations. We found a significant decrease in the steepness with increasing age of the taxonomic group, so that older groups have less pronounced diversity patterns. This result was even clearer when the estimated number of generations since the origin of the taxon was considered. This supports the notion that geographic patterns of species richness are at least partly determined by the time lag between the origin of a taxon and it's evolutionary ability to occupy and diversify in a wide range of habitats.

3.23 Mass elevation effect, continentality and isolation – drivers of global treeline elevation?

David Kienle[1], Severin D.H. Irl[1], Carl Beierkuhnlen[1]
[1] Biogeography, BayCEER, University of Bayreuth
Contact: david.kienle@web.de

Treelines are one of the few fundamental borders in ecology, separating forests from treeless alpine systems. Already a century ago the concept of mass elevation effect (MEE; i.e. area of mountain chains) and continentality (i.e. distance from the ocean) were proposed to have positive effects on treeline elevation but have never been quantified. This study aims at globally quantifying the influence of MEE, continentality and isolation (i.e. the nearest distance to a mountain region with similar elevation) on the treeline elevation, by using the currently largest dataset of global treeline elevations (n = 672). We applied an innovative sampling method (GoogleEarth), enabling a global coverage of treeline elevations (74°N to 66°S). The global treeline pattern showed a distinct double hump, which may result from a tropical depression or from the lack of high mountains in the equatorial tropics. The MEE and continentaliy positively affected treeline elevation, probably because an increased solar radiation leads to better growing conditions at high elevations. However, evolutionary process might lead to fewer high elevation-adapted tree species with increasing isolation.

Keywords: Alpine treeline; mass elevation effect; global pattern; GoogleEarth

3.24 ⚡ Does the number of species or individuals change along temperature and moisture gradients?

Ching-Feng Li[1], David Zelený[1], Tze-Ying Chen[2], Chang-Fu Hsieh[3]
[1] Department of Botany and Zoology, Masaryk University
[2] Department of Nature Resources, National Ilan University
[3] Institute of Ecology and Evolutionary Biology, National Taiwan University
Contact: chingfeng.li@gmail.com

Pattern of alpha-diversity, the number of species (NSP), along temperature and moisture gradients and the possible explanations are interesting issues in biogeography. However, NSP is highly correlated with the number of individuals (NID). This relationship is explained by the neutral theory: in a given species pool, while all the species have the same ecological equilibrium, NSP is the result of NID. This would change the focus of asked question: from 'why are there more species co-existing together?' into 'why are there more individuals growing together?' National Vegetation Database of Taiwan contains 3564 plots which cover the long gradients of temperature and moisture. Sampling size of each plot is 20 by 20 square meters. All the individuals of woody species with Diameter at Breast Height more than 1 cm in the plot are recorded. In this study, we try to answer the following questions by using this database: (1) What is the pattern of NSP on both gradients? (2) Does NSP do relate to NID? (3) What is the pattern of NID on both gradients? After partitioning the relationship between NID and NSP, is there any remained pattern of NSP on both gradients?

Keywords: neutral theory, Taiwan, variance partitioning, woody species

3.25 Spatial effects on niche evolution in *Mimulus*: climate to microhabitat

Qin Li[1], Amy L. Angert[2]
[1] Department of Botany, Biodiversity Research Centre, University of British Columbia
[2] Department of Botany & Zoology, Biodiversity Research Centre, University of British Columbia
Contact: qin.li@biodiversity.ubc.ca

Niche conservatism is invoked to explain many patterns, from historical biogeography to species responses to climate change. However, the evidence for niche conservatism versus niche evolution is mixed. Spatial scale and species interaction could be essential modifying factors in the relative importance of niche conservatism. In this study we focus on the monkeyflower genus *Mimulus*, and aim to examine niche conservatism at two spatial scales (climate and microhabitat) and the impact of range overlap (as a proxy for competition). Climatic niche was estimated based on locality data and corresponding climate data. Microhabitat attributes were collected in the field and published floral sources. Phylogenetic niche conservatism was not found for climatic niche. Conversely, microhabitat water affinity showed a clustered pattern of two major clades with wet and dry preference respectively. Climatic niche similarity increased as range overlap increased, while there was more divergence in microhabitat in sympatry compared to allopatry. These results suggest that niche conservatism is only apparent in some niche dimensions and that niche divergence is influenced by patterns of range overlap.

Keywords: niche conservatism, niche evolution, geographic range overlap, climatic niche, microhabitat preference, *Mimulus*

3.26 ⚡ Biotic interactions in river networks: An example with the freshwater pearl mussel and its host fish

Sabela Lois[1], David E. Cowley[2]
[1] Zoology, University of Santiago de Compostela
[2] New Mexico State University, USA
Contact: sabela.lois@gmail.com

Consideration of many factors and their spatial and temporal interactions are necessary to understand species distribution and abundance. Biotic interactions can influence species distribution and abundance through predation, competition, parasitism or mutualism. Interspecific interactions may also affect species' responses to abiotic factors across space and time that may influence abundance patterns of two or more species. Riverine aquatic systems are especially interesting because they are dendritic networks with a directional flow that lie in drainage basin retaining spatial and temporal information about the surrounding terrestrial landscape. They are anisotropic ecosystems with multiple sources of spatial autocorrelation. We present analyses of abundance 20 river networks by using a freshwater mussel species and its host fish. Geostatistical mixed models for stream networks are applied to analyse abundance patterns. This study shows the importance of including biotic interactions when modelling and the need to account for the spatial characteristics of river ecosystems when modelling biodiversity patterns on river networks.

Keywords: Dispersal, freshwater ecosystems, geostatistical mixed model, macroecology, multivariate analysis, parasite–host, river networks, spatial autocorrelation.

3.27 Geomorphological, climatic and spatial drivers of amphibian beta diversity in Atlantic Forest lowlands of southeastern Brazil

Amom Luiz[1], Thiago Pires[1], Ricardo Sawaya[2]
[1] State University of Campinas (UNICAMP)
[2] Federal University of São Paulo (UNIFESP)
Contact: sawayarj@gmail.com

Amphibian assemblages are affected by contemporary climate but historical processes remain poorly understood. We assess and disentangle geomorphological, climatic and spatial drivers of amphibian beta diversity in coastal Atlantic Forest of southeastern Brazil. We mapped 15,259 geographic distribution records. Sampling area was divided in four spatially explicit geomorphological units. Climatic descriptors were represented by PCA axes and spatial predictors were described by Moran Eigenvector Maps. Redundancy Analysis was implemented to partition the explained variation of species composition by all predictors. We also tested neutral theory predictions by spatial autocorrelation analyses. Shared fraction of climatic and geomorphological variables was an important predictor

(16%), as well as broad scale spatial predictors (11%). Neutral theory predictions were confirmed. Geomorphological units were the most important predictor (36%), and must have played a crucial role in structuring amphibian beta diversity. We highlight the importance of combining spatially explicit historical and contemporary predictors for understanding and disentangling major drivers of beta diversity patterns.

Keywords: Atlantic Forest, Beta diversity, Biogeography, Climate, Community ecology, Geomorphology, Historical factors, Lowlands, Spatial variables, Variation partitioning

3.28 ⚡ The unification of unified biodiversity theories fails at predicting spatial patterns in a tropical forest

Felix May[1], Andreas Huth[1], Sebastian Lehmann[1], Thorsten Wiegand[1]
[1] Department of Ecological Modelling, Helmholtz Centre for Environmental Research - UFZ
Contact: felix.may@ufz.de

Several unified theories of biodiversity and biogeography combine ideas of area, species richness and abundances to predict biodiversity patterns as the species–area curve (SAC) and the species abundance distribution. It was recently argued that all existing “unified theories” can be unified by three simple assertions: (1) species abundances follow a hollow curve distribution (2) species show intraspecific aggregation (3) species are randomly placed with respect to other species. We test the predictive power of these assertions using a spatial simulation model in combination with forest census data from Barro Colorado Island, Panama. We parameterize the model using the three “unifying” assertions and predicted additional biodiversity patterns, e.g. the SAC and the distance decay of similarity. The model correctly predicted the SAC, which was not used in model calibration, but failed to predict the distance decay. The three “unifying” assertions are not sufficient to completely characterize the spatial biodiversity patterns in a tropical forest. Improved predictions will likely require further information on species-specific dispersal and species habitat requirements.

Keywords: species-area curve, distance decay, species aggregation, neutral theory, modelling

3.29 ⚡ Large-scale distribution patterns of arbuscular mycorrhizal and non-mycorrhizal plant species

Andreas Menzel[1], Stefan Hempel[2,3], Ameur M Manceur[4], Lars Götzenberger[5], Mari Moora[6], Matthias C Rillig[2,3], Martin Zobel[6], Ingolf Kühn[1,7,8]
[1] Helmholtz Centre for Environmental Research - UFZ, Department of Community Ecology, Halle (Saale), Germany
[2] Freie Universität Berlin, Institut für Biologie, Dahlem Center for Plant Sciences, Berlin, Germany
[3] Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB), Berlin, Germany
[4] Helmholtz Centre for Environmental Research – UFZ, Department of Computational Landscape Ecology and Community Ecology, Leipzig, Germany
[5] Institute of Botany, Czech Academy of Sciences, Czech Republic
[6] Institute of Ecology and Earth Sciences, University of Tartu, Estonia
[7] German Centre for Integrative Biodiversity Research (iDiv), Leipzig, Germany
[8] Martin-Luther-University Halle Wittenberg, Institute of Biology/Geobotany and Botanical Garden, Halle, Germany
Contact: andreas.menzel@ufz.de

About 75% of all vascular plant species form associations with arbuscular mycorrhizal fungi (AMF). Three arbuscular mycorrhizal states of plant species can be defined: (1) obligatory mycorrhizal species that are always colonized by AMF, (2) facultative mycorrhizal species that are colonized under some conditions but not under others, and (3) non-mycorrhizal species that are never found to be colonized by AMF. We analysed the spatial distribution of these different states across the German country scale (grid cells of c. 130 km²). Using a vector generalised additive model, the distributions can be explained as a function of eight environmental predictors (D^2=0.58). Proportion of obligatory arbuscular mycorrhizal plant species increased with temperature range, mean annual temperature, urban area and lime as geological parent material, and decreased with increasing area of mixed and coniferous forest. The most important predictor was annual temperature range. Our results refine previous knowledge of the symbiosis' biogeography and its related plant traits. Therefore, we encourage integrating mycorrhizal status as a functional trait in future analyses of plant species distributions.

Keywords: arbuscular mycorrhiza, Central Europe, distribution model, functional plant trait, macroecology, MycoFlor, mycorrhizal status, vector generalised additive model

3.30 ⚡ Inferring species associations from occurrence data – a cautionary tale

Naia Morueta-Holme[1], Benjamin Blonder[2], Brian J. McGill[3], Brian J. Enquist[2], Jens-Christian Svenning[4], The BIEN Working Group
[1] Integrative Biology, University of California - Berkeley, USA
[2] Ecology and Evolutionary Biology, University of Arizona, USA
[3] Sustainability Solutions Initiative / School of Biology and Ecology, University of Maine, USA
[4] Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Denmark
Contact: morueta-holme@berkeley.edu

Understanding how species communities assemble across spatial scales is a major unresolved question. Stacking species distribution models to predict local communities is not meaningful if species are associated due to e.g. biotic interactions or local environmental filtering. The explosion in data availability has led to renewed efforts to use species occurrence data to infer associations, disentangle drivers, and improve community assembly predictions. Ecological networks may be a powerful tool to achieve these goals. We developed a framework that combines network approaches with a large tree occurrence dataset for North America and tested it on local communities. We found positive and negative associations in the network, but slight changes in methods (regional null model definition, abundance vs. presence/absence data, association metric, etc.) always yielded different associations, and none could be explained by the drivers tested. Our results provide a warning against underestimating the temporal and spatial complexity of species associations and putting too much faith on occurrence data and network approaches to infer mechanisms. So far, their promise remains unfulfilled.

Keywords: species associations, network, community assembly, co-occurrence data, North American trees

3.31 Plant-soil feedback as potential factor driving distribution of dominant species in the landscape

Zuzana Münzbergová[1], Lucie Hemrová[2], Jana Knappová[3]
[1] Institute of Botany
[2] Academy of Sciences of the Czech Republic & Department of Botany,
[3] Faculty of Science, Charles University, Prague
Contact: zuzmun@natur.cuni.cz

We studied determinants of distribution of four dominants in grasslands. We used reciprocal transplant experiment to study performance of the dominants at their own localities and at localities dominated by other dominants. We also collected data on habitat conditions at the localities and performed a garden experiment to study the importance of plant-soil feedback. No major environmental differences between localities with different dominants were found. The results of transplant experiment show that the local dominants perform worse at their own localities than at localities with the other dominants. In agreement with this, the garden experiment indicated that plants perform worse when grown in their own soil indicating negative feedback effect. All this suggest that the local dominants are not the best competitors at their own sites. Rather, their distribution might be given by stochastic processes during colonization. Afterwards, the dominants maintain their dominant position thanks to their extensive clonal growth, but are not able to successfully reproduce generatively at their localities. In the long run, it can thus be expected that the dominant identity might change.

Keywords: species distribution, dominant, dry grasslands

3.32 ⚡ Finescale latitudinal and altitudinal patterns of selected Andean plant genera at the continental scale

Jens Mutke[1], Maximilian Weigend[1]
[1] Nees Institute for Biodiversity of Plants, Rheinische Friedrich-Wilhelms-Universität Bonn
Contact: mutke@uni-bonn.de

The tropical Andes are a hotspot of biodiversity, but detailed altitudinal and latitudinal distribution patterns of species are poorly understood. We compare the distribution and diversity patterns of the Andean plant genera Nasa

(Loasaceae), Ribes (Grossulariaceae), and Urtica (Urticaceae) on the basis of georeferenced specimen data. In the tropical Andes, these often grow together, especially in (naturally or anthropogenically) disturbed or secondary vegetation at middle to upper elevations. The Amotape-Huancabamba Zone between 3-8°S shows a clear diversity peak of overall species richness as well as for narrowly endemic species. Latitudinal ranges are generally larger towards the margins of overall range of the group. Species number of our taxa peak at elevations of 2,500 - 3,500m in the tropical Andes. Altitudinal diversity patterns correspond well with the altitudinal distribution of slope inclination. We hypothesize that the frequency of landslides at steeper slopes translates into temporal habitat heterogeneity. The frequency of landslides may be causally connected to diversification especially for the numerous early colonizing taxa, such as Urtica and annual species of Nasa.

3.33 ⚡ Large extent and small grain monitoring data provide new insights into scale-dependent plant diversity patterns in southern Africa

Jens Oldeland[1], Ute Schmiedel[1], Norbert Jürgens[1], Alexander Gröngröft[2], Jürgen Dengler[1]
[1] Biodiversity, Ecology and Evolution of Plants, University of Hamburg
[2] Institute of Soil Science, University of Hamburg
Contact: jens.oldeland@uni-hamburg.de

We studied patterns of plant diversity at three spatial scales (100 m², 1000 m², and 1 km²) from northern Namibia to the Cape of Good Hope in South Africa, covering six biomes and a steep rainfall gradient. For the analyses, we used the data sampled on the 37 standardised Biodiversity Observatories arranged along the BIOTA Southern Africa transects. We analysed alpha diversity, i.e. species richness, as well as *z*-values as measures of beta-diversity. We related the biodiversity parameters with multiple regressions to potential drivers such as land use, climate, soil parameters and environmental heterogeneity. Highest α-diversity of the Fynbos biome was equalled by the Succulent Karoo at the 1-km² scale, whereas beta-diversity was highest in the Succulent Karoo and in the Namib Desert. Consistent across all spatial scales, mean annual precipitation and percentage winter rainfall were the strongest predictors of alpha-diversity. However, other parameters differed between scales. Environmental heterogeneity and land-use intensity played an important role not only at the 1-km² scale but also at smaller scales.

Keywords: scale dependence; species richness; species-area relationship; vegetation plot; winter rainfall

3.34 Unifying elemental stoichiometry and metabolic theory in predicting species abundances

David Ott[1], Christoph Digel[1], Björn C. Rall[2], Mark Maraun[1], Stefan Scheu[1], Ulrich Brose[1]
[1] Department of Biology, University of Goettingen
[2] Departments of Aquatic and Terrestrial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands
Contact: dott@gwdg.de

While metabolic theory predicts variance in population density within communities depending on population average body masses, the ecological stoichiometry concept relates density variation across communities to varying resource stoichiometry. Using a data set including biomass densities of 4959 populations of soil invertebrates across 48 forest sites we combined these two frameworks. We analyzed how the scaling of biomass densities with population-averaged body masses systematically interacts with stoichiometric variables. Simplified analyses employing either only body masses or only resource stoichiometry are highly context sensitive and yield variable and often misleading results. Our findings provide strong evidence that analyses of ecological state variables should integrate allometric and stoichiometric variables to explain deviations from predicted allometric scaling and avoid erroneous conclusions. In consequence, our study provides an important step towards unifying two prominent ecological theories, metabolic theory and ecological stoichiometry.

Keywords: Allometric scaling, body mass, leaf litter, population density, soil communities

3.35 ⚡ Patterns and predictors of biodiversity at Mt. Kilimanjaro across taxa

Marcell Peters[1], Andreas Hemp[2], Tim Appelhans[3], Christina Behler[4], Alice Classen[5], Andreas Ensslin[6], Stefan Ferger[7], Maria Helbig-Bonitz[4], Claudia Hemp[5], William Kindeketa[8], Ephraim Mwangomo[9], Christine Ngereza[10], Juliane Röder[3], Gemma Rutten[6], David Schellenberger Costa[11], Giulia Zancolli[5], Connal Eardley[12], Ralph Peters[13], Mark-Oliver Rödel[14], Axel Ssymank[15], Victor Kakengi[16], Jie Zhang[5], Katrin Böhning-Gaese[7], Roland Brandl[3], Elisabeth Kalko[4], Michael Kleyer[11], Thomas Nauss[3], Marco Tschapka[4], Markus Fischer[6], Ingolf Steffan-Dewenter[5]
[1] Department of Animal Ecology and Tropical Biology, University of Würzburg
[2] University of Bayreuth
[3] University of Marburg
[4] University of Ulm
[5] University of Würzburg
[6] University of Bern
[7] Biodiversity and Climate Research Centre (BIK-F)
[8] Tanzania Commission for Science and Technology
[9] Mount Kilimanjaro National Park
[10] National Museum of Tanzania
[11] University of Oldenburg
[12] University of KwaZulu-Natal
[13] Zoological Research Museum A. Koenig
[14] Museum für Naturkunde Berlin
[15] Falkenweg 6, Wachtberg
[16] Tanzania Wildlife Research Institute
Contact: marcell.peters@uni-wuerzburg.de

Since nearly two centuries naturalists try to explain the remarkably heterogeneous distribution of biodiversity on earth. Temperature and primary productivity have been suggested as major structuring forces but available results for different taxa provide conflicting support, motivating an intense scientific discussion in the past decade. We compiled the hitherto largest data set on trends in the elevational distribution of biodiversity encompassing data on eight vascular plant and thirteen major animal groups collected on 30 study sites along a 3.6 km elevational gradient at Mt. Kilimanjaro, Tanzania. Here we present patterns of elevational species richness across plant and animal taxa and infer the support for the major drivers of biodiversity.

Keywords: elevational species richness, elevational gradients, species energy theory, macroecology, temperature theory, tropical mountains, metabolic theory of ecology

3.36 ⚡ Large-scale patterns of variation in species richness in the Páramo region and its environmental determinants

Gwendolyn Peyre[1], J.Sebastián Tello[2], Xavier Font[3], Henrik Balslev[1]
[1] Ecoinformatics and Biodiversity, Department of Bioscience, Aarhus University, Denmark
[2] Center for Conservation and Sustainable Development, Missouri Botanical Garden, St. Louis, Missouri , USA
[3] Department of Plant Biology, Faculty of Biology, University of Barcelona, Barcelona, Spain
Contact: g.peyre@ub.edu

Understanding the spatial distribution of richness, whether it is for a particular taxonomic group or a biogeographic region, has important implications for biodiversity theory and conservation. Although the influence of environment on richness patterns has been studied in various areas, lack of appropriate data often prevents broad scale analyses of diversity. The páramo region in the northern Andes is a hotspot for diversity and evolution, with more than 3400 vascular plants species and very high endemism. Our goals are (1) to describe the large-scale patterns in the distribution of species richness throughout the entire Páramo and (2) to understand the unique and combined effects of energy, heterogeneity and seasonality on shaping this pattern. Using the VegPáramo biological database (www.vegparamo.com; ~2100 vegetation plots), we calculated the relative species richness in raster cells using rarefaction. We observe a decrease in species richness on a south-north gradient from Peru and Ecuador to Colombia followed by a slight increase towards Venezuela. Strong differences between eastern and western slopes were noted. We detected redundancy between the three environmental predictors of richness (energy, heterogeneity, seasonality). Our results represent the best attempt to date to describe and understand the spatial patterns in biodiversity across the entire Páramo extent.

Keywords: species richness, large-scale pattern, vegetation, vascular plants, Andes

3.37 ⚡ The “centre-periphery hypothesis”: a biogeographical paradigm revisited

Samuel Pironon[1], Amy Angert[2], Daniel Doak[3], William Morris[4], Guillaume Papuga[5], John Thompson[5], Jesus Villellas[6], Maria Begoña Garcia[1]
[1] Instituto Pirenaico de Ecologia (IPE-CSIC)
[2] University of British Columbia
[3] University of Colorado
[4] Duke University
[5] Centre d'Ecologie Fonctionnelle et Evolutive (CEFE-CNRS)
[6] University of Uppsala
Contact: samuel.pironon@free.fr

Current global change is leading numerous taxa, communities and ecosystems to shift their geographic range. The response of species to changing environments is likely to be determined largely by population responses at range margins. A major paradigm in the field of biogeography, the “center-periphery hypothesis”, predicts that marginal populations are genetically less diverse, exhibit lower vital rates and abundances, because they tend to occur in less favorable habitats. These populations are then predicted to be more prone to extinction. By reviewing most of the studies that empirically tested this hypothesis since its formulation, we give an overview of all the different approaches used, and examine the extent of its validity. Moreover, by using extensive data (demographic rates, genetic diversity) on one short-lived (*Plantago coronopus*) and two long-lived (*Silene acaulis*, *Polygonum viviparum*) plants across their continental ranges, and recent advances in species distribution modeling, we propose a new approach testing whether measures of environmental or historical centrality/marginality describe better the distribution of species performance than geography.

3.38 ⚡ Response shapes of dominant and subdominant plant species in Amazonian rain forests

Kalle Ruokolainen[1], Hanna Tuomisto[1], Gabriela Zuquim[1], Gabriel Moulatlet[1], Glenda Cárdenas[1]
[1] Dept. of Biology, University of Turku
Contact: kalle.ruokolainen@utu.fi

A recent study by ter Steege and collaborators showed that the most abundant Amazonian tree species have wider environmental niches than the rarer ones but no other biological differences were observed. We ask if dominant and subdominant species among two understorey plant groups in Amazonia (ferns and Melastomataceae) differ in terms of species response shape along the gradient of the summed concentration of soil cations (Ca, K, Mg and Na). The analysis is based on about 300 species inventory transects with analyses of soil chemistry in Amazonian lowland *terra firme* rain forests of Brazil, Colombia, Ecuador and Peru. We first investigate with one mathematical model family (Huisman-Olff-Fresco models) if species response type vary as a function of total abundance in the data set. The types are described as 1) no response, 2) monotonic, 3) plateau, and 4) unimodal symmetric or 5) unimodal skewed response. Thereafter we take apart species with either one of the two types of unimodal species responses and investigate with another model (beta functions) if the flatness of the response depends on total abundance. The results of these analyses will be discussed.

Keywords: Amazonia, Melastomataceae, pteridophytes, soil

3.39 ⚡ Comparison of altitudinal patterns of plant diversity between East Himalaya and Taiwan Island: determinents and linkage

Zehao Shen[1], Ye Liu[1], Rong Li[2], Hang Sun[2]
[1] Department of Ecology, Peking University
[2] Kunming Institute of Botany, the Chinese Academy of Sciences
Contact: shzh@pku.edu.cn

Altitudinal patterns and the determinants of species diversity is a central issue in biogeography, and the theory of island biogeography has been applied as a explanative framework, with little attention paid for the difference between mountain and island. We compared the altitudinal patterns of vascular plant diversity between Mt.

Gaoligong and Taiwan Island, two comparable terrains hosting over 4,000 species. The similarity of the two floras reaches the maximum at 1400-1500 m a.s.l. The altitudinal patterns of species richness, endemism, and taxon-subtaxon ratio are distinct, with hump-shaped patterns more common in Gaoligong and more monotonous gradients in Taiwan. The maximum floristic differentiation ratio in Gaoligong is twice as much as in Taiwan. The average angiosperm family age in Taiwan is older than in Gaoligong. Area and spatiotemporal variation of precipitation dominate the species richness pattern in Gaoligong, while the pattern in Taiwan is primarily related with energy availability. The comparisons reflect distinct environmental and geographical contexts of flora development, and imply a more active speciation process in Gaoligong, especially at the high elevation.

Keywords: Mt. Gaoligong, Taiwan Island, altitudinal pattern, plant diversity, environmental explanation, isolation, area

3.40 ⚡ Partitioning beta diversity into turnover and nestedness components in assemblages of breeding birds and lizards on inundated land-bridge islands

Xingfeng Si[1], Andrés Baselga[2], Ping Ding[1]
[1] College of Life Sciences, Zhejiang University
[2] Departamento de Zoología, Facultad de Biología, Universidad de Santiago de Compostela
Contact: xingfengsi@gmail.com

Partitioning beta diversity provides better understandings on the variation of species composition in fragmented habitats that has particular relevance for potential applications in conservation planning. Here, we decomposed beta diversity of breeding bird and lizard communities into spatial turnover and nestedness-resultant components to assess their relative contributions and respective relationships to differences in island attributes on islands in an inundated lake in China. Our results showed spatial turnover contributed more to beta diversity than nestedness. The degree of isolation had no significant effect on total beta diversity or their components, neither for birds nor for lizards. In both groups, the nestedness component increased with larger differences in island area and habitat richness, respectively, while turnover component decreased with them. The major difference among birds and lizards was a higher relevance of nestedness dissimilarity in lizards, suggesting that they are more prone to local extinctions derived from habitat fragmentation. Based on these findings, we suggest all islands have potential conservation values for breeding bird and lizard communities.

Keywords: Additive partitioning, conservation, land bridge, nestedness, spatial turnover, Thousand Island Lake.

3.41 ⚡ Which spatial patterns do the indices actually measure, and which indices measure the same thing? – Systemizing measures that compare species compositions in areas and linking them to spatial phenomena

Arnošt L. Šizling[1], Eva Šizlingova[1], Kathleen M.C. Tjørve[2], Even Tjørve[2]
[1] Charles University, Prague
[2] Lillehammer University College
Contact: even.tjorve@hil.no

Studying large-scale biodiversity trends and effects of human influence require effective and sound indicators. Indices that compare the composition of species in two or more areas or compare spatial ranges of two or more species constitute important tools in conservation biogeography and ecology. They measure and uncover patterns of β-diversity, species spatial turnover, species nestedness, co-occurrence, and species-richness gradients. However, a plethora of indices has bewildered us, leaving few answers to what indices to choose or what they actually measure. Moreover, many indices have been re-invented times over, each time disguised with a different formula. Recent attempts to prune the thicket have not resolved the confusion. We synthesize the ideas behind the indices and introduce a procedure to attribute each index to an idea, thereby unveiling which indices measure the same spatial phenomena. First, we describe and delimit five phenomena by their constraints. Secondly, we fit data to 36 indices assessing their scaling properties and then derive analytically the relationships between index pairs that scale uniquely. Thirdly, we systemize them into four consistent families.

Keywords: conservation biogeography, macroecology, β-diversity, between-assembly indices, similarity indices

3.42 ⚡ Invariances and non-invariances in biogeography and macroecology: Looking for fundamental scales

Arnošt, L. Šizling[1], William E. Kunin[2], Even Tjørve[3], David Storch[1]
[1] Charles University in Prague, Czech Republic
[2] The University of Leeds, UK
[3] Lillehammer University College, Norway
Contact: sizling@cts.cuni.cz

In recent decades macroecologists have been searching for general patterns in ecology. However, most of the patterns were shown to be scale, location or taxon dependent. To give some examples, (i) frequency distribution of species abundances in a site (SAD) depends on SADs in its sub-sites, and (ii) increase of species richness with sampled area (SAR) is slower for taxa with smaller individuals. In some cases, the patterns for different parameters such as the area or taxon in question can be mathematically converted to each other. For instance, the SAD of a site can be computed from the SADs for sub-sites, and SAR for two taxa can be mathematically composed from the SARs of its sub-taxa. Such mathematically constrained relationships between patterns at different scales or for different taxa raise two questions: What is the fundamental scale and taxonomical level at which the processes beyond the patterns act? and What are the scales and taxonomical levels for which the ecological patterns are derived?
We suggest that the next decade should be devoted to searching for fundamental levels in ecology and demonstrate a method to test their existence.

Keywords: generality, general laws, taxon invariance, area invariance, scale invariance

3.43 Testing diversity hypotheses: A global analysis of ant diversity across elevations

Tim Szewczyk[1], Christy McCain[1]
[1] Ecology and Evolutionary Biology, University of Colorado at Boulder
Contact: tim.szewczyk@gmail.com

Many hypotheses have been proposed to explain patterns of diversity. Investigating the predictions on a global scale may yield a more complete understanding of these processes. Mountain ranges are ideal systems for testing these hypotheses and allow the separation of predictions. I used published data on ant elevational diversity to test multiple predictions of four hypotheses: area, the mid-domain effect (MDE), temperature, and precipitation with temperature. Robust datasets, representing 6 biogeographical provinces, humid and arid mountains, and temperate and tropic gradients, showed four main patterns. Most studies showed a hump-shaped pattern with highest diversity at mid-elevations, though low plateaus with a mid-elevation peak, low plateaus with a monotonic decrease, and monotonic decreases were also seen. Area predicted most diversity patterns well with 80% of transects with a significant relationship according to $S=cA^z$. Though mid-peaks were common, the MDE was not supported. Temperature was largely inconsistent as well. The datasets showed fair support for precipitation and temperature. Thus, ant diversity on mountains is most likely driven by a combination of factors.

Keywords: Elevational climate model, elevational gradient, environmental gradient, Formicidae, insect, mid-domain effect, mountains, species-area relationship, species richness, temperature

3.44 ⚡ Exploring the drivers of mammalian diversity patterns in the Himalayas

Krishnapriya Tamma[1], Uma Ramakrishnan[1]
[1] National Centre for Biological Sciences, TIFR
Contact: priya.tamma@gmail.com

The Himalayas, an east-west spanning mountain range, are located at the transition of the Palaearctic and the Oriental biogeographic regions and are part of two biodiversity hotspots. Diversity patterns and the underlying processes remain poorly understood here. We investigate the patterns and processes driving mammal diversity in the Himalayas using macroecological and phylogenetic methods, in the context of the surrounding biogeographic realms. Our macroecological analyses reveal differing drivers of species richness in the eastern and in the western ends of the Himalayas. Further, we demonstrate nested patterns of community assembly along an east-west axis in the Himalayas. To explore the processes driving the diversity patterns, we conducted field sampling for 3 genera of rodents, in 7 sites across the Himalayas. Phylogenetic trees reconstructed for the three genera reveal - 1. Endemic cryptic diversity in the Himalayas, 2. In situ speciation and colonization from surrounding biogeographic realms drive the evolution of Himalayas diversity. Our results emphasize on a complex biogeographic history of the Himalayas, one that is largely dominated by east-west diversity patterns.

Keywords: Himalayas, rodents, phylogenetics, nestedness

3.45 Environmental determinants of migration distances of large mammalian herbivores

Claire Teitelbaum[1], William Fagan[2], Gunnar Dressler[2], Thomas Mueller[1]
[1] Biodiversity and Climate Research Centre; University of Maryland, College Park
[2] University of Maryland, College Park
Contact: claire.teitelbaum@gmail.com

Maximum migration distances of animal species have previously been linked to body size, where biomechanical and energetic constraints explain longer migration distances in larger species. Here, we focused on land migrations of large mammalian herbivores and examined how the environment affects variability in migration distance among populations. We examined 95 migrations ranging from 10 to 1638 km of populations of large herbivores with a mean body mass from 19 to 3900 kg. We found no effect of body size on migration distance. Instead, environmental covariates that reflect food resources had a negative relationship with migration distance. This result holds even when only maximum migration distances per species are used, which reflects the robustness of the relationship. Our results demonstrate that the environment, rather than body size, shapes migrations of large mammalian herbivores and that animals living in environments with scarcer resources need to travel farther to fulfill their resource needs.

Keywords: migration distance, NDVI, foraging resources, scaling relationships, land migrations, mammalian herbivores, ungulates

3.46 ⚡ Impact of herbaceous vegetation on post-disturbance forest dynamics – effects across an elevation gradient

Timothy Thrippleton[1], Harald Bugmann[1], Rebecca Snell[1]
[1] Forest Ecology, ETH Zurich
Contact: timothy.thrippleton@usys.ethz.ch

Herbaceous understorey vegetation (i.e. grass, ferns, forbs and herbs) is an important, however often overlooked, component of forest ecosystems. The herbaceous layer competes with tree species in their early life stages and can change forest dynamics and species composition. The impact can be especially strong following a disturbance event, as a dense understory layer may delay or alter successional pathways. However, knowledge about these impacts is scarce, particularly at larger spatio-temporal scales. Here we used the forest model LandClim to study vegetation dynamics on a landscape scale. Forest gap models typically neglect the herbaceous layer. The present study thus provides a first approach to include this component and investigates the impact on post-disturbance forest dynamics. Simulation results showed that the presence of herbaceous vegetation delayed forest succession and shifted forest composition by favouring shade-tolerant tree species. Furthermore, the approach highlighted the importance of considering a landscape scale, since patterns varied across an elevation gradient, with the highest changes occurring in mixed-deciduous forests at low and mid-elevations.

Keywords: herbaceous vegetation, forest modelling, landscape ecology, long-term dynamics, elevation gradient

Continued next page

3.47 ⚡ Regions, Range and Redundancy – Correlating chorology and taxonomy in marine gastropods

Benedikt Wiggering[1], Matthias Glaubrecht[2]
[1] Humboldt Universität zu Berlin
[2] Centrum für Naturkunde der Universität Hamburg
Contact: B.Wiggering@gmx.net

Ever since Wallace, biogeographers aim at a regionalisation of the world's biota. While those of marine systems are still under debate, recent studies mainly based on fish distribution suggest broader regions with established provinces unaltered. Due to the frequent lack of systematic revisions, invertebrates are regularly left out of these models. We here present the application of a marine regionalisation on the littoral gastropoda family Planaxidae.

Our current revision of the planaxids validates 7 genera with, at least, 11 species distributed throughout the warm regions. We discuss how the reconstructed species distributions fit into the known regionalisation, finding strong support for one developed based on vertebrate chorology. Additionally, the planaxids allow insights into the dependence of the degree of taxonomic redundancy and species range. We use three range categories to describe in how many provinces a given species occurs. Based on the systematic revision of the family our results corroborate the conjecture that species with wider distribution tend to be described more often than species with narrow or even restricted range.

4.1 Rarity, niche differentiation and species formation in Hawaiian Philodromid spiders

Ellie Armstrong[1], Andrew Rominger[2], Rosemary Gillespie[2]
[1] University of Hawaii
[2] University of California, Berkeley
Contact: ellieearmstrong@gmail.com

We test the role of rarity and evolution of ecotypes in two Hawaiian endemic sister genera of Philodromid spiders. We use molecular markers to reconstruct the phylogeny of Pagiopalus and Pedinopistha using Philodromid outgroups from around the globe. Both genera appear to have originated from a single colonization event. Pedinopistha is found in low abundance while different species of Pagiopalus maintain a variety of abundances. Species of Pedinopistha also conform to similar ecomorphologies. Conversely, Pagiopalus species have evolved three ecomorphologies, one generalist with a brown-green color and two substrate specialists, one short-legged red ecomorph suited for crypsis in mosses and a longer-legged green ecomorph suited for crypsis in live vegetation. The rare Pedinopistha species have diversified in allopatry with functionally similar, yet genetically distinct species on different islands. The most generalist and abundant Pagiopalus species show little population structure across islands, while less abundant specialists show clear population breaks across the islands. Our results show that rarity appears to be important for diversification.

4.2 Dated phylogeny and biogeography of the genus *Selaginella*

Dennise Stefan Bauer[1], Kristina Vanessa Klaus[1], Christian Schulz[1], Thomas Stützel[1]
[1] Institute of Evolution and Biodiversity of Plants, Ruhr-Universität Bochum
Contact: dennise.bauer@rub.de

Selaginella P. Beauv. is the only extant genus within the family Selaginellaceae and the order Selaginellales. The genus comprises approximately 700 species which can be divided into different subgenera (e.g., Jermy 1986). The genus has a cosmopolitan distribution with main distribution areas in the tropics and subtropics of Asia and South America (e.g., Setyawan 2011). Here, we present a global time tree for the genus *Selaginella* based on a concatenated sequence dataset. Calibration was performed using fossil data. The taxon sampling comprises species from all major distribution areas. The biogeographic reconstruction suggests that *Selaginella* originated in today's Asia around 300 MA in the Carboniferous. Furthermore, the ancestral areas and ages of the different subgenera and extant species were reconstructed. Ancestral areas as well as historical long distance-dispersal versus vicariance events were discussed under the aspect of plate tectonic and historical climate conditions.
Keywords: Selaginella, Phylogeny, Molecular Clock, Biogeography, Ancestor Area Reconstruction, Long-Distance Dispersal, Vicariance

4.3 ⚡ The lycophyte genus *Isoetes* from South America: Evidence to Understanding its Evolution

Jovani B. de Souza Pereira[1], Christian Schulz[1], Paulo H. Labiak[2], Thomas Stützel[1]
[1] Department of Evolution and Biodiversity of Plants, Ruhr-Universität Bochum, Germany
[2] Department of Botany, Universidade Federal do Paraná, Brazil
Contact: jovanibio@gmail.com

Isoetes is a cosmopolitan group of predominately aquatic plants. The quite ancient divergence between *Isoetes* its sister group relationship, *Selaginella*, has resulted in considerable genetic and morphological differences between them. Nevertheless, *Selaginella* can be used as an outgroup of *Isoetes*. Studying the phylogeny and the biogeography of *Isoetes* is important because it may help us to clarify the long evolutionary history of a lineage of plant that first emerged in the Paleozoic. Recent molecular studies have improved our knowledge about *Isoetes* by establishing well-supported clades. However, the lack of important taxa from South America has limited our knowledge about the biogeographic events that have led to its current diversity. In our study, we used plastid and nuclear markers of some Brazilian species. The aim of our analysis is to understand the phylogenetic relationships of these species within the established clades, as well as to understand the biogeographical history of the genus in South America. Here we present some preliminary results of our phylogenetic analyses, as well as the various biogeographical scenarios so far.
Keywords: BEAST, Biogeography, Paleozoic, Phylogeny, South American Phytogeographical Domains.

4.4 ⚡ Node-based analysis of species distributions

Michael Borregaard[1], Carsten Rahbek[1], Jon Fjeldså[1], Juan Parra[2], Robert Whittaker[3], Catherine Graham[4]
[1] Center for Macroecology, Evolution and Climate, University of Copenhagen
[2] University of Antioquia
[3] University of Oxford
[4] Stony Brook University
Contact: mkborregaard@snm.ku.dk

The integration of species distributions and evolutionary relationships is one of the most rapidly moving research fields today, and has led to considerable advances in our understanding of the processes underlying biogeographical patterns. Here, we develop a set of metrics, the specific overrepresentation score and the geographic node divergence score, which avoids many of the problems that characterise community phylogenetic methods in current use. This approach compares the distributions of all sister clades in the phylogeny to a null model. The method is independent of phylogeny size and allows an intuitive visualisation of the results. We demonstrate the metrics with two case studies: a local-scale dataset of hummingbirds in the Andes, and a large-scale dataset of New World flycatchers. The analysis generates a set of intuitively interpretable patterns that are consistent with current biogeographical knowledge. Importantly, the results are statistically tractable, opening many possibilities for their use in analyses of evolutionary, historical and spatial patterns of species diversity. The method is implemented as the R package *nodiv*, which makes it accessible and easy to use.
Keywords: allopatry, bird biogeography, distribution, evolution, macroecology, macroevolution, null model, phylogeny, R, range.

4.5 ⚡ Miocene divergent species lineages contributed to high levels of species diversity in the Atlantic Forest and Cerrado biomes of South America

Plauto Carvalho[1]
[1] Botânica, Universidade Estadual de Goiás
Contact: plauto.decarvalho@gmail.com

Myrtaceae phylogeny from Neotropics did not show conflict with modern concepts of genera, with the exception of *Blepharocalyx*. The position of *B. salicifolius*, hasn't conclusive and considered enigmatic by many taxonomists. Divergence times were estimated using the Bayesian inference including haplotypes from 136 samples of *B. salicifolius* and a Myrtaceae matrix. Molecular dating suggests that divergence of *B. salicifolius* lineage from its closest relative (*Pimenta*) occurred during the Miocene (c. 19 Ma) followed by geographical structuring with one clade subsequently diverging in the Southern Atlantic rainforest and the other in transitional ecosystems in the Northern Atlantic Forest and Cerrado Savannas of Central Brazil. Shortly before, other important species-rich genus (*Eugenia*, 20Ma; *Myrcia* group 22.2Ma) diversified. The diversification of *B. salicifolius* coincides broadly with estimates of divergence of the major suprageneric groups during the Miocene. Most suprageneric diversification also took place during the Miocene, from 27-18 Ma corroborating the importance of the Miocene climate dynamics to the diversification of important rich-species families in South America.
Keywords: Blepharocalyx salicifolius, Myrtaceae, plant, diversification.

4.6 ⚡ Impact of the Mio-Pliocene Messinian salinity crisis on large mammals

Julien Clavel[1]
[1] IBENS, Ecole Normale Supérieure/LGTPE, Université Lyon 1
Contact: julien.clavel@hotmail.fr

Deep time macroevolutionary analyses can provide a perspective on how global climatic and environmental changes in the past have affected species assemblages. Major environmental changes occurred in the late Miocene, when the repeated isolation of the Atlantic Ocean led to the drying of the Mediterranean Sea during the so called Messinian Salinity Crisis. Here I investigate the effect of such a large scale event on ecosystems from the peri-mediterranean area through an analysis of the large mammal's fossil record. First, I developed and applied new phylogenetic comparative methods to identify species phenotypic adaptive response to climate changes. Next, I evaluated the relative importance of various drivers of geographical diversity structure (environmental sorting, physiogeography, and historical factors) through a phylogenetic diversity analysis of different terrestrial basins surrounding the Mediterranean Sea. Overall, these analyses show that large mammal's diversity patterns have tracked climatically driven changes of the environment. I will discuss the implication of these results in the context of current climatic changes for threatened ungulates species.

Keywords: Macroevolution, Macroecology, fossil, ungulate, bovid, cervid, comparative methods, climate, phenotypic diversity, phylogenetic diversity

4.7 *Saxifraga* L. on a cold tin roof: Diversification and biogeography on the Qinghai-Tibetan Plateau and beyond

J. Ebersbach[1], A. Favre[1], N. Tkach[2], M. H. Hoffmann[2], A. N. Muellner-Riehl[3]
[1] Department of Molecular Evolution and Plant Systematics, Leipzig University
[2] Institute of Biology, Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle (Saale)
[3] Department of Molecular Evolution and Plant Systematics, Leipzig University and German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Contact: jana.ebersbach@uni-leipzig.de

Highly biodiverse regions of the world are often associated with mountain systems. With its surrounding areas, the Qinghai-Tibetan Plateau (QTP), the largest and highest plateau of the world, constitutes one of the few recognized biodiversity hotspots in the northern hemisphere. However, the environmental factors that contributed to the diversification of organisms in this region remain poorly understood. Using the highly diverse plant genus *Saxifraga* L. (Saxifragaceae) as a study system, we integrate genus-wide multi-gene phylogenies, molecular clock dating, biogeographic and niche analyses and investigate the effect of the QTP uplift on evolution and diversification of *Saxifraga* and the formation of this hotspot in general.

4.8 ⚡ Colonization and radiation of the hyperdiverse ant genus *Pheidole* in Madagascar

Georg Fischer[1], Lacey Knowles[2], Jen-Pan Huang[2], Evan Economo[1]
[1] Economo Unit, OIST
[2] University of Michigan
Contact: georgf81@gmail.com

Madagascar's ant fauna is highly diverse and exhibits an enormous degree of endemism. Although a number of studies have improved our understanding of biogeographic relationships between Madagascar and other parts of the World, relatively little knowledge exists about the colonization and radiation dynamics of lineages in the region. Here, we expand and analyze a large scale phylogeny of the hyperdiverse ant genus *Pheidole*, dominant in abundance and ecological roles across the world's tropics and subtropics, to reconstruct biogeographic relationships between the faunas of Madagascar, Africa, and other parts of the Old World. Our analysis supports previously defined species group hypotheses as monophyletic lineages, and reveals complex relationships between Madagascar, Africa and other Old World regions. We find the Malagasy *Pheidole* fauna has roots in both Afrotropical and in Autralasian clades, and discuss distributional patterns and the potential biodiversity dynamics generating those patterns.

Keywords: Ants, Madagascar, phylogeny, biodiversity, biogeographic relationships, Old World, Pheidole

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4.9 ⚡ Fossil mammalian diversity has tracked primary productivity over 20 million years

Susanne Fritz[1,2], Jussi Eronen[1,2,3], Jan Schnitzler[1,2,4], Christian Hof[1,2], Christine Janis[5], Andreas Mulch[1,2,4], Katrin Böhning-Gaese[1,2,4], Catherine Graham[6]
[1] Biodiversity & Climate Research Centre (BiK-F)
[2] Senckenberg Gesellschaft für Naturforschung
[3] University of Helsinki
[4] Goethe University Frankfurt
[5] Brown University Rhode Island
[6] Stony Brook University New York
Contact: sfritz@senckenberg.de

Spatial patterns of present-day global mammalian species richness are often strongly correlated to primary productivity, but it is debated whether this relationship holds across time. Here, we compile the largest dataset of terrestrial fossil mammals through the Neogene to date, spanning over 14,000 genus-level occurrences in North America and Europe through the Miocene and Pliocene. We find that mammalian diversity has been significantly correlated through space and time with productivity as estimated from a database of fossil plant sites. Comparison with present-day data shows that the diversity-productivity relationship seems to hold across the last 20 million years, although it may be threatened by future anthropogenic climate and land-use change.

Keywords: diversity mammals productivity fossils Neogene North America Europe

4.10 Niche divergence drives diversification in vertebrate clades

Carola Gómez-Rodriguez[1], Adrián Castro-Insua[2], Andrés Baselga[2], John J. Wiens[3]
[1] Natural History Museum, London
[2] University of Santiago de Compostela
[3] University of Arizona
Contact: andres.baselga@usc.es

Diversification rate is critically important to understanding patterns of species richness, among both clades and regions. Climatic niche width is a potentially important correlate of variation in diversification rate among clades, and patterns of variation in niche width may help reveal the causes of diversification (i.e. niche divergence or niche conservatism). Here, we test several hypotheses relating diversification rate and niche width across all amphibian and mammal clades. We found significant positive relationships between diversification rate and family niche width, but weak relationships between diversification rate and the mean niche width of all species in the family (despite both niche width variables being correlated). In fact, deviations from the relationship between family-level and species-level niche widths (i.e. residuals of family niche width vs. mean species niche width within the family) was the best predictor of diversification rate. This latter result suggests that climatic niche divergence among species within clades can be important in explaining large-scale diversity patterns.

4.11 ⚡ Cretaceous–Tertiary diversification among select Scolopendrid centipedes of South India

Jahnavi Joshi[1], Praveen Karanth[2]
[1] Centre for Ecological Sciences, Indian Institute of Science and Current Affiliation is Ecology and Evolution Group, National Centre for Biological Sciences
[2] Centre for Ecological Sciences, Indian Institute of Science
Contact: jj.jahnavi@gmail.com

Given that peninsular India was part of the Gondwanan super continent, part of its current biota might have Gondwanan origin. To determine the Gondwanan component of the peninsular Indian biota, a large number of species spanning diverse taxonomic groups need to be sampled from multiple, if not all, of the former Gondwanan fragments. Such a large scale phylogenetic approach will be time consuming and resource intensive. Here, we explore the utility of a limited sampling approach, wherein sampling is confined to peninsular India (PI), in identifying putative Gondwanan elements. To this end, samples of Scolopendrid centipedes from peninsular India were

subjected to molecular phylogenetic and dating analyses. Bayesian divergence date estimates suggested that the earliest diversifications within various genera were between 86 and 73 mya, indicating that these genera might have Gondwanan origin. In particular, at least four genera of Scolopendrid centipedes, *Scolopendra*, *Cormocephalus*, *Rhysida* and *Digitipes*, might have undergone diversification on the drifting peninsular India during the Late Cretaceous.

Keywords: historical and gondwanan biogeography, western ghats, molecular phylogeny

4.12 ⚡ Including fossils in phylogenetic climate reconstructions: A deep time perspective on the climatic niche evolution and diversification of Spiny Lizards (*Sceloporus*)

Michelle Lawing[1], David Polly[2], Diana Hews[3], Emília Martins[4]
[1] Ecosystem Science and Management, Texas A&M University
[2] Department of Geological Sciences, Indiana University
[3] Department of Biology, Indiana State University
[4] Department of Biology, Indiana University
Contact: alawing@tamu.edu

Fossils can improve phylogenetic comparative method estimates of phenotypic evolution. Here, we use fossil information to calibrate ancestral reconstructions of suitable climate for *Sceloporus* lizards in North America. Integrating data from the fossil record, general circulation models of paleoclimate during the Miocene, climate envelope modeling, and phylogenetic comparative methods provides a geographically and temporally explicit species distribution model of *Sceloporus* suitable habitat. We provide evidence to support the historic biogeographic hypothesis of *Sceloporus* diversification in warm North American deserts and suggest a relatively recent *Sceloporus* invasion into Mexico around six mya. We use a physiological model to map average daily hours of restriction, a variable that highly explains extinction risk. We suggest that hours of restriction limited *Sceloporus* from inhabiting Mexico until the climate cooled enough to provide suitable habitat approximately six mya. If the future climate returns to the hotter climates of the past, Mexico, the place of modern highest *Sceloporus* richness, will no longer provide suitable habitats for *Sceloporus* to survive and reproduce.

Keywords: fossils, phylogenetic comparative methods, climate niche evolution, paleoclimate, physiological model

4.13 Challenging disjunctions across the globe: the biogeographic history of Nartheciaceae

Ingo Michalak[1], Robert Kellner[1], Adrien Favre[1], Alexandra N. Muellner-Riehl[2]
[1] Department of Molecular Evolution and Plant Systematics, Leipzig University
[2] Department of Molecular Evolution and Plant Systematics, Leipzig University; German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Contact: ingo.michalak@uni-leipzig.de

The 35 species of Nartheciaceae (Dioscoreales) have an extremely disjunct distribution. Three of the five genera are endemic to Japan (*Metanarthecium*, 1 sp.), northern South America (*Nietneria*, 2 spp.) and eastern North-America (*Lophiola*, 1 sp.). *Narthecium* (7 spp.) is distributed in North America, Europe and Japan, while *Aletris* (24 spp.) occurs in eastern North America, China, Japan and western Malesia. To our knowledge, no attempt has yet been made to explain the biogeographic history of the family, as its genera were long associated with different families.

Ultrametric trees generally form the base for biogeographic analyses. Recently, this dogma was challenged, as different branch length estimations were found to lead to conflicting but *a priori* equally valid estimations. We estimate the biogeographic history of Nartheciaceae based on a cladogramm, a phylogramm and different dating schemes to assess a) if there are conflicting histories estimated from trees with different branch lengths and b) their respective plausibility based on the number of estimated events.

Keywords: ancestral area reconstruction, branch lengths, disjunct distributions, Nartheciaceae

Continued next page

4.14 ⚡ Improved phylogeny integrated estimates of abundance and their potential uses in macroecology

Rasmus Østergaard Pedersen[1], Søren Faurby[1], Jens-Christian Svenning[1]
[1] Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University
Contact: rasmus.pedersen@bios.au.dk

Upon entering the Anthropocene, natural animal ranges and densities are declining rapidly. Projects are trying to maintain populations at current densities, improve numbers, or restore populations to natural densities. Unfortunately, we rarely know what the natural densities are, because most populations have declined since the arrival of man. Knowing current and historical population densities is necessary to understand the differences between ecosystem function of the past and the present. Which ecological processes have ceased or declined on a macroecological scale during the last 130 000 years? Crude estimates of population densities are found from allometric models on body mass. Our allometric model of mammalian population densities (n=467) in relation to species body mass was built while incorporating the potential for different phylogenetic groups to have different responses to body mass. Recent range-maps of extant and extinct species distributions worldwide provides us with the opportunity to estimate mammal loss in terms of both numbers and biomass, and to investigate the implications of global change in ecosystem function.

Keywords: allometry, population densities, natural densities, predicting

4.15 ⚡ The elusive case for neotropical refugia

Danny Rojas[1], Omar Warsi[2], Liliana Davalos[2]
[1] Department of Biology, University of Aveiro
[2] Ecology and Evolution, SUNY Stony Brook
Contact: lmdavalos@gmail.com

The mechanisms underlying the high extant biodiversity in the Neotropics have been controversial since the 19th century. Using the ecologically diverse radiation of New World mammals (Chiroptera: Noctilionoidea) and multiple fossil calibrations to infer time-calibrated phylogenies, we tested the role of Pleistocene refugia in speciation by estimating ancestral areas and generating simulations. The distribution of the ancestor of the species-rich and ecologically diverse Phyllostomidae comprised multiple separate landmasses, and phyllostomids reached South America early in their evolutionary history. The divergence times between sister species in the phylogeny were compared to simulated birth-death trees to test Quaternary climate change as a mechanism of speciation. Simulations systematically show more speciation events in the Quaternary when modeling constant speciation and extinction rates for the entire phylogeny. Hence, the age of extant sister species cannot test the effect of Pleistocene glaciations on speciation. Instead, testing the Pleistocene refugia hypothesis, or any other proposed temporal driver of speciation, requires modeling diversification rates through time.

Keywords: Refugia, bats, neotropics, diversification

4.16 ⚡ Colonization and diversification patterns of passerine birds at the margins and in the centre of the Qinghai-Tibetan Plateau

Patrick Strutzenberger[1], Sun Yue-Hua[2], Martens Jochen[3], Tietze Dieter-Thomas[4], Päckert Martin[1]
[1] Museum of Zoology, Senckenberg Natural History Collections Dresden, Dresden, Germany
[2] Key Laboratory of Animal Ecology and Conservation, Institute of Zoology, Chinese Academy of Science, Beijing, China
[3] Institut für Zoologie, Johannes Gutenberg-Universität, Mainz, Germany
[4] Insitut für Pharmazie und Molekular Biotechnologie, Universität Heidelberg, Heidelberg, Germany
Contact: patrick.strutzenberger@senckenberg.de

Mountain forests along the southern and eastern margins of the Qinghai-Tibetan Plateau (QTP) represent a prominent biodiversity hotspot of the Northern Hemisphere. Earliest passerine radiations occurred in the mid to late Miocene when subtropical SE Asian faunal elements colonized the foothills of the Himalayas. This was followed by Pliocene faunal interchange between Sino-Himalayan subalpine forests and the Eastern Palearctic. The central plateau region itself is characterized by rather low species richness but nevertheless a good number of endemics. Some represent rather ancient phylogenetic lineages that date back to even pre-Pliocene colonization events. During long-term separation some alpine endemics underwent strong adaptations of body size and life history traits to (semi-) open alpine habitats. Using molecular dating and ancestral range analysis (with taxon-complete genus trees) we provide a spatial and temporal framework of passerine evolution in the QTP region. Recent diversification patterns at the interspecific level are analyzed by DNA-barcoding and backed by morphological and bioacoustics data for selected taxa.

Keywords: passeriformes

4.17 ⚡ Islands as refugia? - Are Macaronesian laurel forests 'Tertiary' relicts?

Mike Thiv[1], Paulina Kondraskov[1], Christina Schüßler[1], Nicole Schütz[1]
[1] Botany, Staatliches Museum für Naturkunde Stuttgart
Contact: mike.thiv@smns-bw.de

The Macaronesian laurel forests (MLF) of the Canary Islands, Madeira and Azores are composed of trees with a laurophyll habit comparable to evergreen humid forests which were scattered across Europe and the Mediterranean in the Neogene and Paleogene. Therefore, MLF are traditionally regarded as a ‘Tertiary’ relict vegetation type. We tested this hypothesis using molecular dating, ancestral trait and area reconstructions of 18 representative species. Our molecular dating showed that the origins of 14 species date back to the Plio-Pleistocene. This coincides with the decline of fossil laurophyllous elements in Europe since the Middle Miocene. Ancestral trait, habitat and area reconstructions further indicate that MLF evolved from pre-adapted taxa outside laurel forests from the Mediterranean, Macaronesia and the tropics. The establishment of the MLF happened in a narrow time window, possibly triggered by the intensification of the trade winds at the end of the Pliocene. Instead of surviving as relicts of a once more widespread vegetation, MLF are examples of plant communities which likely assembled newly through global recruitment possibly in response to climate change.

Keywords: Macaronesia, islands, laurel forests, refugia, Neogene

4.18 ⚡ Does evolution of habitat niche in tits (Aves: Paridae) follow distributional range shifts?

Dieter Thomas Tietze[1], Ulf S. Johansson[2]
[1] Institute of Pharmacy and Molecular Biotechnology, Heidelberg University
[2] Department of Zoology, Swedish Museum of Natural History, Stockholm
Contact: mail@dieterthomastietze.de

In the recent past, methods to reconstruct ancestral distribution and other trait states were significantly improved by probabilistic and Bayesian approaches, but historical biogeography and trait evolution have rarely been related to each other. The avian family Paridae (tits and chickadees) comprises some 63 species and is distributed in the Palearctic, Afrotropic, Indomalayan and Nearctic zoogeographic regions. Within these regions the tits are found in a wide range of habitats: from subtropical rainforest to boreal taiga and from dry tropical shrublands to high alpine tundra. In this study we analyze the temporal and spatial context in which these birds have adapted to these various habitats with specific focus on shifts along the temperature and precipitation gradients, respectively. We use a dated molecular phylogeny for all parid species to reconstruct ancestral areas. Preferences for certain temperature and precipitation ranges and forest types were inferred under a Multi-State Speciation and Extinction model. For all internal nodes of the phylogeny we ask if these preferences fit the historical distribution, i.e., how realistic the reconstructions are.

Keywords: historical biogeography, trait evolution, birds

5.1 Karasu dune vegetation (N Turkey), important and conservation problems

Seda Akkurt[1], Meral Avcı[2], Hatice Yılmaz[3]
[1] Department of Geography, Bilecik Seyh Edebali University, Faculty of Arts and Sciences
[2] Department of Geography, Istanbul University Faculty of Letters
[3] Department of Forestry, Istanbul University Faculty of Forestry
Contact: seda.akkurt@bilecik.edu.tr

The study area is Karasu dunes located on the coast of the Black Sea in the North of Turkey. Karasu dunes area is one of the rare dune beaches in the western section of the Black Sea. The dunes extend around 45 km. It takes attraction with its vegetation cover. During 4 excursions on the research area, various species of plants were collected and 75 types of different plants were determined. Two of them are *Centaura kilaea* and *Verbascum degenii* which are endemic plants bearing the danger to become extinct. According to the categories of IUCN (the International Union for Conservation of Nature) the status of *Centaura kilaea* is V, that is Vulnerable and *Verbascum degenii* is E, that is Endangered. *Verbascum degenii* is a species included in the Bern Aggrement Appendix I. On the other hand, *Peucedanum obtusifolium* is accepted to be under threat in the European scale and encountered in rare frequency in Karasu dunes. From 1800s to date, Turkish nomads destroyed the vegetation cover with the activities of agriculture and animal husbandry in the dunes. Currently, the devastation has started with private facilities and beach activities made for the purpose of recreation.

Keywords: Northern Turkey, biodiversity, sand dune vegetation, conservation biogeography

5.2 Determinants of aquatic macrophyte floras across North America

Janne Alahuhta[1], Jan Hjort[1], Jani Heino[2]
[1] University of Oulu, Department of Geography
[2] Finnish Environment Institute, Natural Environment Centre, Biodiversity
Contact: janne.alahuhta@oulu.fi

Modelling of biogeographical patterns has previously focussed on a few well-known taxonomic groups. One of the most understudied taxonomic groups at broad scales is aquatic plants, which are important contributors to multiple ecosystems services and ecosystem functions in freshwaters. We studied the geographical structure of 145 aquatic plant species covering the entire North America (25° to 70°N, 50° to 165°W) at 100 x 100 km resolution. We found that geographical location strongly distinguished aquatic plant floras at the continental scale. The primary determinants of aquatic plant floras were longitude and latitude, followed by annual maximum and minimum temperatures. Thus, there seems to be clear geographical barriers restricting dispersal of aquatic plants across the continent. Those barriers have wider importance in biogeographical regionalisation in the context of environmental assessment and biodiversity studies.

Keywords: Aquatic macrophytes, Broad scale, Freshwaters, North America

5.3 Vulnerability of marine mammals to projected climate change: potential consequences for the phylogenetic and functional components of biodiversity

Camille Albouy[1], Valentine Delattre[2], Séverine Boyer[3], Fabien Leprieur[2]
[1] Université du Québec à Rimouski
[2] Laboratoire Ecologie des Systèmes Marins Côtiers UMR 5119, CNRS, IRD, IFREMER, UM2, UM1, cc 093, Place E. Bataillon, FR-34095 Montpellier Cedex 5, France.
[3] 3 Institut Maurice-Lamontagne, Pêches et Océans Canada, 850 Route de la Mer, CP 1000, Mont-Joli, QC, Canada, G5H 3Z4
Contact: albouycamille@gmail.com

Growing evidence suggests that climate change is currently threatening marine biota. However, a global assessment of marine mammal vulnerability to climate change is currently lacking while 37 % of marine mammal species are already included in the IUCN Red List. In this study, we built a vulnerability index that combine the intrinsic sensitivity

of each species to climate change and their degree of exposure according to different scenarios of climate change. We then explored the potential impact of climate change-driven extinctions on the functional and phylogenetic components of marine mammal biodiversity. Our results show that (i) the Arctic region hosts the most vulnerable species; (ii) climate change may induce greater losses of both functional and phylogenetic diversity than expected by random extinctions. These results emphasize that projected climate change would not randomly erode both the functional and phylogenetic trees of life of marine mammals. Future conservation strategies should therefore focus on vulnerable species with unique combinations of functional traits and unique evolutionary history.
Keywords: Marine mammals, climate change, vulnerability

5.4 ⚡ Assessing plant species ranges against the degree of human impact

Elina Aletrari[1], Mark Mulligan[2], Neil Brummitt[3]
[1] King's College London / Natural History Museum London
[2] King's College London
[3] Natural History Museum London
Contact: elina.aletrari@kcl.ac.uk

The continuing increase in human population, in conjunction with rising per-capita consumption rates, is placing unprecedented pressure on natural ecosystems, threatening to push many species into extinction. The aim of this project is to develop an automated procedure to assess and re-assess plant species' conservation status pan-tropically. The project focuses on improving the methodology for calculating species ranges using the available IUCN Sampled Red List Index plant data and producing the Extent of Suitable Habitat for each species and a global species richness map. The species Extent of Suitable Habitat maps are being produced based on information of the appropriate ecology for the species as well as land cover and environmental information, both within the convex hull defining the species' Extent of Occurrence. These ranges are then assessed against the degree of human impact using the human pressure layer from the Co$ting Nature conservation prioritisation tool as well as information on progressive land cover change. By using land cover change as a proxy for local extinction risk we should be able to provide more dynamic and spatially detailed Red List Index updates.

5.5 ⚡ Mediterranean wood pastures for biodiversity – making the lynx

Harriet Allen[1], William Simonson[2], Erin Parham[3], Paul Hotham[3], Eduardo Santos[4]
[1] Department of Geography, University of Cambridge, UK
[2] Department of Plant Sciences, University of Cambridge, UK
[3] Fauna & Flora International, Cambridge, UK
[4] Liga para a Protecção da Natureza, Lisbon, Portugal
Contact: hda1@cam.ac.uk

Using a 25-year time series of satellite imagery, we are seeking to understand patterns of land use/land cover (LULC) change in the emblematic wood pasture landscapes of southern Portugal. In the past these were home to a number of critically endangered species, such as the Iberian lynx (*Lynx pardinus*). Ecological evidence and field survey data of wild plants, butterflies and birds have allowed us to create habitat preference maps for these groups. Combining these with the LULC change maps and using modelling approaches we have attempted to predict past (and future) levels of biodiversity. Using Change Vector Analysis and Morphological Spatial Pattern Analysis, our initial results show habitat connectivity changes to the core areas and corridors linking different wood pasture habitats, on a continuum from open to more closed, shrub-dominated communities. The dynamic nature of agricultural land cover changes is also apparent. The aim of this research is to produce robust evidence-based outputs and frameworks that can help land managers and planners maintain wood pasture biodiversity; to integrate landscape level impacts and achieve smarter targeting of agri-environment funding.
Keywords: Land use/land cover change; Mediterranean wood pasture; Change Vector Analysis; Morphological Spatial Pattern Analysis; Habitat conservation

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5.6 Plant invasion hotspots in the contiguous United States

Jenica Allen[1], Adrienne Keller[2], Bethany Bradley[1]
[1] Dept. Environmental Conservation, University of Massachusetts
[2] Dept. Biology, Indiana University
Contact: jenicaa@eco.umass.edu

Invasive plants can alter population dynamics, community composition, and ecosystem function in affected systems. Resources for early detection and management programs are limited, yet are key to preventing or mitigating the effect of invasives. Identifying areas with greatest potential invasive load may help in effective allocation of conservation resources. We developed an occurrence database of over 1300 species listed as invasive or noxious at the federal or state level to determine the location and intensity of invasive plant hotspots in the contiguous United States. We identified hotspots of invasion risk based on an ensemble of individual species distribution models created using MaxEnt. Hotspots of invasion risk were identified based on both potential establishment (using all available data) and potential impact (using data geographically associated with states where species are listed as invasive). The spatial extents of invasion hotspots under current and future climate conditions can identify areas under constant threat over time, candidate areas in high need for early detection monitoring, and areas at low risk of invasion.

Keywords: invasive species; species distribution modeling; climate change

5.7 Advancing biodiversity modelling using geodiversity information

Joseph Bailey[1], Richard Field[1], Doreen Boyd[1], Jan Hjort[2], Helena Tukiainen[2], Janne Alahuhta[2]
[1] University of Nottingham, UK
[2] University of Oulu, Finland
Contact: joseph.bailey@outlook.com

The concept of geodiversity, the diversity of earth surface materials, forms and processes, has much potential for modelling and mapping biodiversity, and highlighting areas capable of supporting high biodiversity into the future. As part of the GEOBIO project, we aim to develop geodiversity as a concept and develop the means by which we can quantify it for incorporation into biodiversity models. We study biodiversity–geodiversity relationships across scales (1x1km and 10x10km grids) for vascular plants (alien and native) in Great Britain and Finland using existing national species databases. Geodiversity data are compiled from primary sources and use both manual methods based on expert knowledge and automated extraction of landform data using recently developed geomorphometric techniques. Preliminary results suggest notable relationships between biodiversity and geodiversity. This research aims to progress thinking towards a more holistic approach to nature in which biodiversity and geodiversity are considered in parallel. Such understanding can contribute to the establishment of cost-effective methods for targeting conservation actions, as well as progressing biogeographic theory.

Keywords: biodiversity, biodiversity modelling, geodiversity, vegetation, vascular plants, conservation

5.8 Consequences of tropical land use for multitrophic biodiversity and ecosystem functioning

Andrew Barnes[1], Malte Jochum[1], Steffen Mumme[1], Noor Farikhah Haneda[2], Achmad Farajallah[3], Tri Heru Widarto[3], Ulrich Brose[1]
[1] Systemic Conservation Biology, University of Goettingen
[2] Faculty of Forestry, Bogor Agricultural University
[3] Department of Biology, Bogor Agricultural University
Contact: abarnes@gwdg.de

Our knowledge about land-use impacts on biodiversity and ecosystem functioning is mostly limited to single trophic levels, leaving us uncertain about whole community biodiversity-ecosystem functioning relationships. We analyse consequences of the globally important land-use transformation from tropical forests to oil-palm plantations. Species diversity, density, and biomass of invertebrate communities suffer at least 45 % decreases from rainforest to oil palm. Combining metabolic and food-web theory, we calculate annual energy fluxes to model impacts of land-use intensification on multitrophic ecosystem functioning. We demonstrate a 51% reduction in energy fluxes from forest

to oil-palm communities. Species loss clearly explains variation in energy fluxes, but this relationship depends on land-use systems and functional feeding guilds, whereby predators are the most heavily affected. Biodiversity decline from forest to oil palm is thus accompanied by even stronger reductions in functionality, threatening to severely limit the functional resilience of communities to cope with future global changes.

Keywords: Land-use intensification; species diversity; metabolic theory of ecology; ecosystem functioning; ecosystem energy flux; ecological networks; Sumatra, Indonesia

5.9 Effects of anthropogenic and environmental factors on the range contraction of North American bird and mammal species

Patrice Betz[1], Rob Channell[1]
[1] Department of Biology, Fort Hays State University
Contact: pmbetz@mail.fhsu.edu

The largest contributor to biodiversity loss is habitat destruction caused by human encroachment into areas used by species. Little research has been done to establish the contribution of separate anthropogenic and environmental variables on the persistence of species that have experienced range contraction. Our objective was to determine the relative contribution of several variables on the range contraction of bird and mammal species in North America. Anthropogenic variables we examined include land cover conversion, human population size, and urbanization. The environmental variables examined were elevation, mean annual precipitation, and mean annual temperature. Species were examined separately to determine which variables had the greatest influence on how the ranges have contracted. The findings of this study could potentially assist with future endeavors to conserve biodiversity, such as predicting where a declining species will eventually persist or determining the best locations to establish wildlife reserves to conserve North American species.

Keywords: Range contraction, extinction, human, environment, anthropogenic

5.10 ⚡ Potential European bison habitat in the Caucasus

Benjamin Bleyhl[1], Taras Sipko[2], Eugenia Bragina[3], Aurel Heidelberg[4], Pedro J. Leitão[1], Rustam Pshegusov[5], Volker C. Radeloff[3], Sergej Trepet[6], Pavel Weinberg[7], Tobias Kuemmerle[1]
[1] Geography Department, Humboldt-Universität zu Berlin, Germany
[2] A. N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia
[3] Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, USA
[4] WWF-Germany, Berlin, Germany
[5] Tembotov Institute of Ecology of Mountain Territories, Kabardino-Balkarian Scientific Centre, Russia
[6] Caucasian State Biosphere Reserve, Maikop, Russia
[7] North-Ossetian State Nature Reserve, RSO-Alania, Russia
Contact: benjamin.bleyhl@geo.hu-berlin.de

Large mammal populations in many parts of the world are small and isolated, and identifying potential reintroduction sites to enlarge and connect existing populations is key for safeguarding such species. European bison (*Bison bonasus*) are a classic example of a large mammal species reduced to a fraction of its former range. Our goal here was to identify potential European bison habitat in the Caucasus, one of its last strongholds. We used seasonal occurrence data from all Caucasian populations to (1) map habitat suitability for summer and winter separately, (2) identify potential habitat patches for future herds, and (3) assess habitat connectivity among existing and potential future herds. We found that potential habitat is widespread, especially in Russia and Georgia, yet much of this potential habitat has considerable risk of conflict with people or land use. We also identified 69 potential habitat patches for reintroductions (together 10,200 km²) with low risk of human-wildlife conflict. Our results show that the Caucasus may contain sufficient habitat to sustain a large metapopulation of European bison, which would be a milestone for preserving the species.

Keywords: habitat suitability, human-wildlife conflict, large herbivores, Maxent, species distribution modeling, wisent

5.11 ⚡ The Pseudoscorpions of Montenegro - An overview and conservation status

Nina Curcic[1], Rajko Dimitrijevic[2], Bozidar Curcic[2]
[1] Geographical Institute "Jovan Cvijic" of the Serbian Academy of Sciences and Arts
[2] Institute of Zoology, Faculty of Biology, University of Belgrade
Contact: nina.b.curcic@gmail.com

The territory of Montenegro is home to 53 pseudoscorpion species belonging to 8 genera (*Neobisium, Chthonius, Roncus, Cheiridium, Allochernes, Withius, Hysterochelifer, Rhacochelifer*) and five families (Neobisiidae, Chthoniidae, Cheiridiidae, Chernetidae, Cheliferidae). The most abundant genera are *Neobisium* (with 27 species or 50.94%), *Chthonius* (with 11 species or 20.75%) and *Roncus* (with 10 species or 18.87%). According to the present distribution, the established 53 species are grouped in four zoogeographical complexes: cosmopolitans, widely distributed species, European species, and endemics. Of 53 species, 32 (60.38%) are endemics of Montenegro, that mostly belong to the family Neobisiidae (with 23 species or 62.16% within family). The current conservation status is analyzed and discussed.

Keywords: Arachnida, Balkan Peninsula, distribution, endemism, protection

5.12 Energy crops, neglected players in the 'land sparing vs. land sharing' debate

Jens Dauber[1]
[1] Thünen Institute of Biodiversity
Contact: jens.dauber@ti.bund.de

Debates on land sparing vs. land sharing often miss out a land-use type of increasing importance: energy crops. They interfere with both concepts on a range of spatial scales. Energy crops could be segregated from food crops at coarse spatial scales by determining whole regions or farms for energy crop production, e.g. based on the productivity of the land. In contrast, at a fine-scale, strips or patches of energy crops could be positioned in the landscape for improving biodiversity and ecosystem services within the food crops (combined food and energy systems). Additionally, as a land sharing option, energy crops could become part of the food crop rotation cycle. Both fine-scale approaches would require informed land-use and landscape planning. For this, a better knowledge about the most efficient combinations of energy crops (1st generation or 2nd generation; annual or perennial) and food crops is required. In the present paper, I present scenarios of sparing or sharing food and energy production on either productive or marginal land and discuss their potential impacts on biodiversity and ecosystem services within the respective systems.

Keywords: bioenergy biodiversity agricultural landscapes nature conservation land-use scenarios

5.13 An empirical investigation of why species-area relationships overestimate species losses

Rafael De Camargo[1], David Currie[1]
[1] Department of Biology, University of Ottawa
Contact: rafael.x.camargo@gmail.com

It is generally assumed that, when natural habitat (NH) is converted to human-dominated (HD) land cover, such habitat is "lost" to its native species. Species richness should vary as a function of remaining NH, following the classic species-area relationship (SAR). SARs have consistently over-estimated species losses resulting from habitat loss. Moreover, richness is sometimes a peaked function of NH. Modified SARs have been proposed based on species' utilization of multiple habitat types, yet none accounts for a peaked SAR. Here we evaluate the responses of Total Bird Richness (TBR), Forest Bird Richness (FBR), and open-habitat bird richness (OHBR) to land cover within 991 quadrats, each 100 km^2, in Ontario, Canada. TBR peaks at roughly 50% NH cover. FBR varies as a classic power function of forested area. In contrast, OHBR does not increase monotonically with either NH or HD land cover. OHBR can be predicted when we partition HD land cover into an "available HD" component and "lost" habitat. Distinguishing three land cover types (natural, HD, and lost) can thus permit accurate predictions of species richness in landscapes with differing levels of natural habitat conversion.

Keywords: Species-area relationship, Endemic-area relationship, Bird species richness, Forest cover, Human-dominated land cover, Southern Ontario, countryside model, Lost-Habitat model

5.14 Setting the stage for common hippo (*Hippopotamu amphibius*) conservation: rationale and priorities

Kristen Denninger Snyder[1]
[1] University of California - Davis
Contact: kldenninger@ucdavis.edu

The common hippo is listed as vulnerable by the IUCN and is susceptible to habitat loss and poaching. Populations have undergone marked declines that are projected to worsen. Despite this state of affairs, the species has been largely overlooked in the conservation world and systematic conservation efforts are notably absent. This study seeks to elucidate a rationale for the conservation of the common hippo based upon its ecological importance and value in conservation planning, to determine priority areas for conservation across Africa, and to outline primary directions for future research and conservation efforts. The feasibility and usefulness of the common hippo as an indicator species for the conservation planning of other threatened species is explored in a GIS using species range data. The suitability of protected areas in providing quality habitat for the common hippo is assessed under future climate scenarios using species distribution models in combination with land use projections.

Keywords: Africa, common hippo, GIS, indicator species, systematic conservation planning

5.15 ⚡ The role of species by family shares in biogeographical and conservation patterns in old versus new biotas

Felipe Domínguez Lozano[1]
[1] Biología Vegetal I, University Complutense of Madrid
Contact: felipe.dominguez@bio.ucm.es

Uneven species distributions in families across the systematic structure provide a way to find out biogeographic and conservation trends in different Biotas. We use Gini index as a measure to explore the species distribution across families in California, Iberia and Southwestern Australia floras. Data come from Jepson Manual project , Anthos and FloraBase databases. Results indicate that the three regions follow similar patterns of endangerment and biota homogenization, although Gini index is always higher in SWA. Differences are found when floras are explored in biogeographical portions. Thus, the endemic portion of SWA is extremely uneven whereas the non-native portion of the Iberian flora is very even. Family sizes play different roles in the three floras. Small families (low species numbers) account for Iberian differences and SWA hold the largest unevenness in the largest families. Californian plants produce the highest imbalance of the three floras for medium size families. These findings are discussed in the light of age and speciation rates in these territories.

5.16 Transferability of species distribution models: the case of *Phytophthora cinnamomi* in southwest Spain and southwest Australia

Joaquin Duque Lazo[1], Hein van Gils[2], Thomas Groen[2], Rafael Maria Navarro-Cerrillo[3]
[1] Institute of Biology. Systematic botany and Functional biodiversity., University of Leipzig
[2] Department of Natural Resources, Faculty of Geo-information Science and Earth Observation (ITC), University of Twente
[3] Department of Forestry, School of Agriculture and Forestry, University of Córdoba
Contact: joaquin.duque_lazo@uni-leipzig.de

Studies comparing SDM transferability (training in one area and applying to another) and the influence of number of variables on their performance, remain scarce. We compared the predictive power and transferability of the 10 SDM techniques using *Phytophthora cinnamomi* point locations. *P. cinnamomi* Rands is an oomycete associated with Oak Decline in SW Spain and Jarrah Dieback in SW Australia. The environmental similarity between the two areas was assessed by the Mahalanobis distance. Model performance was evaluated by AUC and complemented with sensitivity and specificity analysis. The spatial distribution of *P. cinnamomi* was predicted accurately by nine modelling techniques. Further, the machine-learning methods showed high predictive power in the training areas but low transferability, while linear models achieved reasonable accuracy within the training area but better transferability performance. Model techniques presented diverse responses to a decrease in number of variables. The most desirable combination of model performance and transferability was demonstrated by GAM and GLM, while MaxEnt presented a robust response throughout the number of variables used

Keywords: Jarrah Dieback, Mahalanobis distance, Oak Decline, Phytophthora cinnamomi, species distribution models, transferability

5.17 How does UV-B radiation perform in predicting alien reptile invasions?

Katharina J. Filz[1], Stefan Lötters[2]
[1] Museum of Natural History of Dortmund
[2] Biogeography, Trier University
Contact: loetters@uni-trier.de

Correlative Species Distribution Models (SDMs) are common tools applied to predict invasions of alien species. We use the recent global UV-B radiation dataset (glUV) to study SDM performance in UV-B sensitive animals, i.e. 14 (invasive) alien reptiles. We processed different variable combinations (i.e. out of bioclim 1-19, partly combined with glUV's UV-B variables), employing Support Vector Machines. The predictive power of SDMs built on native records only and different variable combinations was compared in regions of known introductions. Bioclim-only models and those incorporating UV-B variables revealed largely similar results. Regions only predicted suitable by either one approache occurred (commonly smaller than the mutal model overlap). SDMs with UV-B tended to predict larger areas of suitability and better explained alien occurrences. Also in both modelling approaches accurate reflections and failure in predicting known alien distributions were found. Results acknowledge glUV being valuable in SDM building. However, when predicting aliens' invasive potentials in geographic space, their incorporation does not necessarily result in better predictions than bioclim-only models.

Keywords: Bioclim, glUV, model performance, species distribution model, Support Vector Machines, variable choice

5.18 Spatial modeling of tree species diversity in eastern North America using geographically weighted regression

David Goldblum[1], Adam Bauer[1]
[1] Department of Geography, Northern Illinois University
Contact: dgoldblum@niu.edu

Understanding the environmental drivers of biodiversity is crucial for conservation. Many spatial predictive models of biodiversity fail to account for spatial heterogeneity (non-spatial stationarity), resulting in under- and over-estimations (Ex. Ordinary Least Squares [OLS]) across geographic space. Using Geographically Weighted Regression (GWR), which accounts for spatial heterogeneity, we examine the environmental variables driving North American tree species diversity. Our results from landscape-level GWR analysis across the eastern United States indicate a high degree of predictability in many environments, with precipitation, temperature, and soil moisture being the most important environmental variables. The model under-predicts diversity in several physiographic provinces (Ozarks plateau, Appalachian ridge, Southeastern coastal plain) and over-predicts diversity in southern Florida, northern New England, and lower Mississippi valley. At all spatial sampling densities, GWR yielded higher R^2 values than OLS. Although GWR's predictability was low in a subset of environments, it still out-performed OLS and should be considered an effective modeling alternative.

Keywords: diversity, GWR, geographically weighted regression

5.19 ⚡ Maintaining current forests would still lead to reduced landscape conditions for eastern titi monkeys following climate change

Sidney Gouveia[1], João Pedro Souza-Alves[1], Raone Beltrão-Mendes[2], Ricardo Dobrovolski[3], Ludmila Rattis[4], Leandro Jerusalinsky[5], Stephen Ferrari[1]
[1] Department of Ecology, Federal University of Sergipe, Brazil
[2] Graduate Program in Biological Sciences, Federal University of Paraiba, Brazil
[3] Department of Zoology, Federal University of Bahia, Brazil
[4] Graduate Program in Ecology, University of Campinas, Brazil
[5] National Center for Research and Conservation of Brazilian Primates - CPB, Ministry of Environment, Brazil
Contact: sgouveia@ufs.br

The effects of climate change and land use have serious implications for the inhabitants of tropical forests, such as the five titi monkey species from eastern Brazil (*Callicebus personatus* group). We combined species distribution

modeling of titi populations with a map of existing forest to test whether predicted changes in distribution, provoked by climate change, would interact with landscape parameters, i.e. habitat cover, mean patch size and connectivity. We built MAXENT models for current and future (2070) conditions, based on three global circulation models and two contrasting scenarios of greenhouse gas concentrations. We downscaled the models using habitat remnants and compared landscape descriptors among predicted species' distributions assuming forest maintenance. While species' habitats with increased connectivity had reduced patch size (9–61%), one with increased mean patch size had decreased connectivity. Total remnant cover reduced for all species (4–83%) under most climate scenarios. In general, even if forest is conserved, landscape condition for most species would deteriorate, emphasizing the need for habitat recuperation to impede further loss of populations.

Keywords: Brazil, Callicebus, habitat fragmentation, Maxent, species distribution modeling

5.20 ⚡ Tsunami impact on the population development of a critically endangered bird species in a island ecosystem

Ingo Hahn[1], Pablo Vergara[2], Uwe Römer[3], Julia Baumeister[4]
[1] Faculty for Geo-information, University of Munich (HM)
[2] Dep. Geographical Engineering; USACH - Univ. Santiago de Chile
[3] Dep. Biogeography; Univ. Trier
[4] Stockdorf, Gauting, Bavaria
Contact: ingo.hahn@hm.edu

For more than a century now it is a question in biogeography how natural catastrophes like tsunamis can influence wild populations of animals and plants. Tsunami events can have a devastating impact on island ecosystems, extensively effecting habitats located below the sea flood level, but very limited pre- and post-event data are available. Most of the population of the Cabbage Tree (*Dendroseris litoralis*) from Robinson Crusoe Island was removed by 2010 Chilean tsunami. Based on pre- and post-tsunami data we determined if the Cabbage Tree loss was related to a decline in the population of its principal pollen disperser and nectar feeder, the critically endangered Juan Fernández Firecrown (*Sephanoides fernandensis*). After the tsunami, the abundance of firecrowns severely declined in human settlement areas, and this reduction in abundance was positively correlated to the loss of Cabbage Trees. We detected a decline in firecrown abundance of the overall population. We suggest that the loss of Cabbage Trees may lead to a further decline in the firecrown population as the Cabbage Trees previously represented an important food source during the nectar bottleneck in autumn for the entire island hummingbird population.

Keywords: Tsunami • Sephanoides fernandensis • Dendroseris litoralis • Robinson Crusoe • population decline • island endemics • endangered hummingbird - natural catastrophes

5.21 ⚡ Predicting the potential distribution of the critically endangered *Medemia argun* using remotely sensed data

Marwa Halmy[1], Manal Ahmed[1], Arege Yehia[1]
[1] Alexandria University
Contact: marwawaseem@yahoo.com

Medemia argun is a rare fan palm of tribe Borasseae. Knowledge about the species was first based on the discovery of its fruits in many ancient Egyptian tombs. Since the discovery of *M. argun* living in northern Sudan in 1837, then in Egypt in Nakhila Oasis in 1901 and in Dungul Oasis in 1963; no more records were reported for decades either in Egypt or Sudan and it was almost considered globally extinct. However, it was found living in new locations in northern Sudan in 1995, and in 1996. Other records in Egypt were later reported in tributaries of Wadi Allaqi in 2006. The ambiguity about the status of this species stimulated the current study aiming at predicting the potential distribution of *M. argun* using remotely sensed data. Spectral variables derived from Landsat 8 data and land-surface parameters were used for building the prediction model by applying both GLMs and random forests techniques. The results showed that random forests provided more accurate prediction of the species distribution which is confined to the Nubian Desert. It is hoped that the outcomes form the current study would help in providing more protection to the sites where the species exists.

Keywords: Medemia argun, endangered species, remote sensing, potential distribution, Egypt

5.22 Phylogenetic diversity of regional beetle faunas at high latitudes: geographical patterns and ecological drivers

Jani Heino[1], Janne Alahuhta[2]
[1] Finnish Environment Institute
[2] University of Oulu, Department of Geography
Contact: jani.heino@environment.fi

Phylogenetic diversity of regional biotas is driven by evolutionary, historical and environmental factors, but their relative roles remain elusive. We examined the drivers of phylogenetic diversity in provincial beetle faunas at high latitudes (54°N - 71°N) in Northern Europe. Our study area was colonized by plants and animals in the last 12,000 years, implying that differences in the phylogenetic diversity among provincial faunas are principally caused by historical and ecological rather than evolutionary factors. We found that variation in beetle species richness was strongly associated with mean annual temperature, but variation in our proxy measures of phylogenetic diversity was more closely driven by maximum annual temperature. Furthermore, while species richness showed a clear latitudinal gradient, phylogenetic diversity showed at best weak relationships with latitude. Phylogenetic diversity may hence be determined by factors different from those of species richness even in a relatively small geographical area. Those discrepancies in the drivers of different facets of biodiversity may have wider implications for conservation decisions in the face of global change.

Keywords: Beetles, Biodiversity, Phylogenetic diversity, high latitudes

5.23 ⚡ Analysis of mangrove forest distribution change using remote sensing and GIS from 1986-2006 in Akwa Ibom State, Nigeria

Marcellinus Hula[1]
[1] Geography, Benue State University
Contact: akamas3@yahoo.com

The mangrove forest is known to be rich in both aquatic and terrestrial biodiversity as such a major source of rural life sustenance in Akwa Ibom State. Unfortunately, the mangrove in recent times has been subjected to the effects of a growing population,rapid urbanization, agricultural expansion and industrialization. The mangrove forest is not under any known form of protection or strategies of biological conservation in Nigeria. Even in areas where they seem to exist, they have alienated the knowledge systems and practices of the local people. This paper therefore examines the change mangrove forests have undergone in Akwa Ibom State using GIS and remote sensing. Landsat images of 1986 and 2006 of the study area were used while change detection and analysis were done using Erdas Imagine 9.2 and ArcGis 9.2. The result of the analysis revealed that mangrove forests have changed from 114103.8ha (17.2%) in 1986 to 107669.7ha (15.3%) in 2006. This change resulted in the loss of 96434.1ha of mangrove forest in the area. Thus, the study concludes that forest reserves should be established where mangrove is still luxuriant with integrated sustainable forest management.

Keywords: Mangrove, forest, remote sensing, GIS, AkwaIbom

5.24 ⚡ Mapping reindeer calving grounds across the Russian Arctic

Tobias Kuemmerle[1], Leonid Baskin[2], Leitao Pedro[1], Prishchepov Alexander[3], Thonicke Kirsten[4], Radeloff Volker[5]
[1] Geography Department, Humboldt-University Berlin
[2] Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences
[3] Leibniz Institute for Agricultural Development in Central and Eastern Europe (IAMO)
[4] Potsdam Institute for Climate Impact Research (PIK)
[5] Department of Forest and Wildlife Ecology, University of Wisconsin-Madison
Contact: tobias.kuemmerle@geo.hu-berlin.de

Drivers of biodiversity loss are increasingly broad in scale, requiring conservation planning to move towards range-wide assessments. This is challenging for migratory species, which use only a small portion of their range at a given point in time, yet for which some portions are critical. Our aim was to identify potential calving ground habitat of wild tundra reindeer (*Rangifer tarandus*) in Russia, using known calving locations and species distribution models. As predictors, we used a range of MODIS-variables, including vegetation productivity and composition, and snow cover.

We found wide areas suitable for calving throughout the Russian Arctic, including for some reindeer populations where calving grounds were unknown. Comparing our calving ground map with threat indicators showed that oil and gas development impacts calving grounds especially in the Barents Sea region and in southwestern Siberia, whereas climate change may affect calving grounds on Taymyr, Chukotka, and Kamchatka. Given the potentially strong impact and high spatial heterogeneity of threats, conservation networks that would aid Arctic biodiversity in general to move freely in time and space are needed.

5.25 Spatial mismatches between biodiversity hotspots and protected area in Japan: process-based assessment of biases in conservation planning

Buntarou Kusumoto[1], Takayuki Shiono[2], Yasuhiro Kubota[2], Masashi Konoshima[2], Atsushi Yoshimoto[1]
[1] The Institute of Statistical Mathematics
[2] University of the Ryukyus
Contact: kusumoto.buntarou@gmail.com

Systematic conservation planning of protected area is a promising approach for enhancing effectiveness of biodiversity conservation. Protected area that restricts economic activity is regarded as social cost. Therefore, it is essential to maximize biodiversity in protected area while minimizing its area that surrogates the costs. Evaluation actions based on their cost effectiveness provides an algorithm that can solve the minimum set coverage. In this study, we compiled spatial data of plant diversity and protected area (e.g. national park) in Japan, and examined the minimum set of protected area for conserving plant species richness. Our results demonstrated the current status of protected area and its spatial mismatches with biodiversity hotspots.

5.26 A bio-geographical approach to species selection for restoration projects in the grasslands of the Atlantic and alpine bioregions of Europe

Emma Ladouceur[1], Costantino Bonomi[2], Borja Jiménez-Alfaro[3], Pietro Ianetta[4]
[1] Museo delle Scienze, University of Pavia, Italy
[2] Museo delle Scienze, Italy
[3] Masaryk University, Czech Republic
[4] James Hutton Institute, Scotland
Contact: emmala@gmail.com

The grasslands of the Atlantic and alpine bioregions have extreme ecological value, are heavily impacted by human degradation, thus restoration of degraded grasslands is becoming an important option for supporting ecosystem function and biodiversity. Restoration practitioners cannot gain the practical or scientific information they need from existing habitat classification systems. Specific selected taxa are most appropriate for restoration which are suitable for wild seed collection, storage, large-scale reproduction and field seed survival to maximize success. The aim of this study is to select taxa representative of key characteristic habitat types suitable for the restoration of functional diversity, plant biodiversity, and ecosystem services in these degraded grasslands to maximize and facilitate desired outcomes. A critical review of habitat classification, functional trait and distribution of community character species, germination tests, and field trials will be carried out. Expected results include a simplified classification system, a guide to best-performing seed lots and a decision tree for species selection for restoration within target bio-geographical regions.

Keywords: dry grasslands; bioregions; Europe; restoration; practical; seeds; nasstec

Continued next page

5.27 The WetVegEurope project: a formalized vegetation-based typology of European aquatic and wetland habitats as a tool for biogeography and nature conservation

Flavia Landucci[1], Kateřina Šumberová[2], Milan Chytrý[1], Liene Aunina[3], Claudia Bita-Nicolae[4], Aleksandr Bobrov[5], Lyubov Borsukevych[6], Andraž Čarni[7], Csiky Csiky[8], Els De Bie[9], Dmytro Dubyna[10], Panayotis Dimopoulos[11], Tetiana Dziuba[10], Úna Fitzpatrick[12], Xavier Font Castell[13], Daniela Gigante[14], Valentin Golub[15], Stephan Hennekens[16], Richard Hrivnák[17], Lorenzo Lastrucci[18], Svitlana Iemelianova[10], Ute Jandt[19], Florian Jansen[20], Zygmunt Kącki[21], Konrád Lájer[22], Dalytė Matulevičiutė[23], Attila Mesterházy[24], José Antonio Molina[25], Jaanus Paal[26], Eva Papastergiadou[27], Alessandro Properzi[14], Vladimir Ranđelović[28], Marcela Řezníčková[1], John Rodwell[29], Joop Schaminée[16], Urban Šilc[7], Zofija Sinkevicienė[23], Aleksei Sorokin[15], Zvjezdana Stančić[30], Jazep Stepanovič[31], Boris Teteryuk[32], Rossen Tzonev[33], Roberto Venanzoni[14], Lynda Weekes[12], Wolfgang Willner[34], Igor Zelnik[34]

[1] Department of Botany and Zoology, Masaryk University
[2] Institute of Botany, Academy of Sciences of the Czech Republic
[3] Laboratory of Geobotany, Institute of Biology of University of Latvia
[4] Department of Ecology and Nature Conservatio, Institute of Biology, Romanian Academy
[5] Institute for biology of inland waters, Russian Academy of Sciences
[6] Botanical Garden, Ivan Franco National University of Lviv
[7] Institute of Biology, Scientific Research Center of the Slovenian Academy of Sciences and Arts
[8] Department of Ecology, University of Pécs
[9] Unit Environment and Climate, Research Institute for Nature and Forest
[10] Department of Geobotany and Ecology, M. G. Kholodny Institute of Botany NAS of Ukraine
[11] Laboratory of Ecology and Biodiversity Conservation, University of Patras
[12] National Biodiversity Data Centre, Carriganore WIT West Campus
[13] Department of Plant Biology, University of Barcelona
[14] Department of Chemistry, Biology and Biotechnology, University of Perugia
[15] Institute of Ecology of the Volga River Basin Russian Academy of Sciences
[16] Alterra, Wageningen UR
[17] Institute of Botany, Slovak Academy of Sciences
[18] Department of Biology, Laboratory of Plant Systematics and Phytogeography, University of Florence
[19] Institute of Biology, Geobotany and Botanical Garden, Halle
[20] Institute of Botany and Landscape Ecology, University of Greifswald
[21] Department of Botany, University of Wrocław
[22] Department of Environmental Engineering, Óbuda University
[23] Institute of Botany, Nature Research Centre
[24] Institute of Botany and Nature Conservation, University of West-Hungary
[25] Department of Plant Biology II, Complutense University
[26] Institute of Ecology and Earth Sciences, University of Tartu
[27] Department of Biology, School of Natural Sciences, University of Patras
[28] Department of Biology and Ecology , University of Niš
[29] Ecological consultant, Lancaster
[30] Faculty of Geotechnical Engineering, University of Zagreb
[31] V. F. Kuprevič Institute of Experimental Botany, National Academy of Sciences of Belarus
[32] Department of Flora and Vegetation of North, Institute of Biology, Academy of Sciences of Russia
[33] Department of Ecology and Environmental protection, Sofia University
[34] Vienna Institute for Nature Conservation and Analyses
Contact: flavia.landucci@gmail.com

WetVegEurope is a project scientifically supported by the European Vegetation Survey (EVS) Working Group. It started in 2013 with the purpose to introduce consistent vegetation-based typology of freshwater aquatic and wetland habitats of Europe as a tool for ecological and biogeographical research and nature conservation. Specific aims of the project are (1) to provide a synthesis and formalized classification of freshwater aquatic vegetation and marsh vegetation to the level of phytosociological associations sharable by most European countries and (2) to characterize each classification unit in terms of ecology, distribution and nature conservation status. The project involves more than 40 people including data contributors and experts. The data collected until now are constituted by more than 150,000 already digitalized vegetation plots from 26 European countries, including 333 aquatic and wetland associations of the 480 ones recorded in Europe so far. These are used for formalization of the classification units, which is currently in progress. The project will find applications in the refinement of the EUNIS classification system of European habitats and in the project “Red List of European Habitat Types”.

Keywords: Aquatic and wetland habitats, Classification, Databases, Nature conservation

5.28 How well can catchment productivity be used as a proxy of stream biodiversity at high latitudes?

Kirsti Leinonen[1], Jaakko Erkinaro[2], Grönroos Mira[1], Hjort Jan[3], Karjalainen Satu Maaria[1], Kärnä Olli-Matti[3], Luoto Miska[4], Manninen Marja[3], Nokela Tiina[1], Soininen Janne[4], Tokola Laura[3], Heino Jani[1]
[1] Finnish Environment Institute, Oulu
[2] Finnish Game and Fisheries Research Institute
[3] University of Oulu, Department of Geography
[4] University of Helsinki, Department of Geosciences and Geography
Contact: kirsti.leinonen@ymparisto.fi

Species diversity typically increases with increasing productivity, but different sources of productivity may have different effects on various organismal groups. Abundant vegetation in a catchment may indicate high species diversity, whereas scarce vegetation in a catchment may suggest low species diversity in a stream draining that particular catchment. Our aim was to examine the relative effects of stream-level, catchment-level, climatic and spatial variables on species diversity of bacteria, algae and invertebrates in high-latitude streams (70oN). Partial regression and subsequent variation partitioning were used to examine the relationships between variation in species diversity and those four predictor variable groups. Normalized Difference Vegetation Index (NDVI), climatic and spatial variables explained 25 % of the variation in invertebrate diversity, but other predictor variables were more important for bacteria and algae. Using stream, catchment, climatic and spatial variables helps us understand drivers of stream biodiversity at high latitudes, which are currently severely threatened by climatic change and other anthropogenic drivers.

Keywords: biodiversity, climate, NDVI, bacteria, diatoms, macroinvertebrates.

5.29 Distribution patterns of Anisophyllous *Sabicea* (Sabiceeae, Rubiaceae) in Continental Africa

Zemagho Mbouzang Lise Arlette[1], Meve Ulrich[1], Sonké Bonaventure[2], Dessein Steven[3], Liede-Schumann Sigrid[1]
[1] Departement of Plant Systematics, University of Bayreuth
[2] Plant Systematic and Ecology Laboratory, Department of Biology, Higher Teachers' Training College, University of Yaoundé I
[3] Botanic Garden of Belgium, Meise, Belgium
Contact: lisemez@yahoo.fr

The genus *Sabicea* which presents a tropical Africa-tropical America disjunctions is by this fact, an ideal system to investigate the role of geography, historical events with the central importance in delimiting species. It includes in continental Africa, 96 species growing mostly in open areas under a variety of environemental conditions.

In recent phylogenetic studies, some species of *Sabicea* form a well supported clade which corresponds to those species with anisophylly at nodes and glomerulate inflorescence. Comprehensive herbarium material of this clade was consulted. Specimen data were databased and exported for georeferencing and mapping in order to determine areas of high endemism and species richness. Today 13 species are recognized. The most species-rich area is the Guineo-Congolian Region housing 10 species, in which 8 species are in the Lower Guinea Domain. Only three species occur in Lake Victoria Regional Mosaic. This pattern of species richness centred in the Lower Guinea Domain widely conforms to the patterns found in many groups of angiosperms of Tropical Africa.

Keywords: Lower Guinea Domain, Rubiaceae, Sabicea.

Continued next page

5.30 The role of Amur honeysuckle encroachment in the white oak regeneration and recruitment gap: Modeling seasonal carbon gain in a midwest tall-grass oak savanna restoration at Nachusa Grasslands, Illinois, USA

Shannon McCarragher[1], Lesley Rigg[1], David Goldblum[1]
[1] Geography Department, Northern Illinois University
Contact: smccarragher@gmail.com

White oak, an important Midwest savanna tree, requires an abundant amount of light to facilitate successful reproduction and recruitment to the canopy. Encroachment of exotic species, like Amur honeysuckle, has altered the understory light environments of Midwest oak savannas. Very few studies have assessed how these encroached present day understory environments influence white oak seedling photosynthetic efficiency and seasonal carbon gains. This research bridges that scholarly gap by: quantifying *in situ* light environments, monitoring seasonal leaf phenology, measuring *in situ* leaf-level photosynthesis, and modeling carbon gains of white oak seedlings and Amur honeysuckle shrubs for three growing seasons in an oak savanna restoration at Nachusa Grasslands in Illinois, USA. Spring was identified as crucial to white oak seedling seasonal carbon balances, which were marginally positive under the restoration’s dense tree canopy, but became negative when Amur honeysuckle encroachment was taken into account. Findings from this research can inform pragmatic management strategies for targeted *in situ* invasive shrub removal intended to stimulate white oak regeneration and recruitment.

Keywords: Invasive species, Amur honeysuckle, Carbon assimilation, White oak, Restoration

5.31 ⚡ Global determinants of species distribution knowledge across taxa and spatial scales

Carsten Meyer[1], Susanne Fritz[2], Robert Guralnick[3], Holger Kreft[1], Walter Jetz[4]
[1] University of Göttingen, Germany
[2] Biodiversity & Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung, Germany
[3] University of Florida, Gainesville USA
[4] Yale University, USA
Contact: cmeyer2@uni-goettingen.de

Detailed species distribution knowledge is vital for ecological research and conservation, but knowledge extent and gaps in global distribution data remain little quantified. We integrated ~200M accessible occurrence records with ~20,000 vertebrate range maps to analyze knowledge patterns and drivers across taxa, spatial grains and extents. Outside a few well-sampled regions e.g., in North America, distribution knowledge is coarse, spatially and taxonomically highly biased, and without careful consideration of these limitations unsuited for most research and conservation applications. Large emerging economies are particularly underrepresented, even more so than species-rich, developing countries in the tropics. Assemblage-level inventory completeness is mainly limited by distance to researchers, national research funding, and political cooperation. These socio-economic factors also determine species-level record number and range coverage, which are additionally constrained by range geometry (size and shape) but not by traits related to detectability such as body size. Our analyses highlight the need for targeted data integration and intensified cooperation to more effectively address biodiversity knowledge needs.

Keywords: Species distributions, Wallacean shortfall, primary biodiversity data, sampling bias, inventory completeness

5.32 ⚡ Visitation of the energy plant *Silphium perfoliatum* L. (Asteraceae) by hoverflies (Diptera: Syrphidae) in landscapes of different farming intensity

Anna Lena Müller[1], Jens Dauber[1]
[1] Thünen Institute of Biodiversity
Contact: anna-lena.mueller@ti.bund.de

Cultivation of energy crops is an important driver of land use change in Central Europe. In some regions of Germany, maize for biogas is becoming increasingly dominant and is criticized for negative effects on biodiversity and the

environment. In that context, *Silphium perfoliatum* is discussed as a promising alternative crop due to its lower input requirements and provision of floral resources for pollinators. In 2012, we collected hoverflies with pan traps in 15 study areas (3000m radius) in Lower Saxony/Germany, showing a gradient in landscape structure and diversity of agricultural crops. For comparison, we examined *Silphium* fields, maize fields and grassy linear habitats outside the farmland. In total we found 49 species belonging to different larval feeding groups. While the abundance of aquatic-saprophagous hoverflies in *Silphium* was comparable to that in the other landscape elements, abundance of aphidophagous species was lower. One reason is the little overlap between their activity period and the flowering of *Silphium*. Abundance and richness of aquatic-saprophagous species was influenced positively by seminatural habitats in the surrounding.

Keywords: bioenergy, biodiversity, pollinators, landscape structure

5.33 ⚡ Biogeographical interactions of ecologically related species using fuzzy logic: is the endangered Egyptian Vulture being affected by the abundant Griffon Vulture?

Antonio Roman Muñoz[1], Ana Luz Marquez[1], Raimundo Real[1]
[1] Universidad de Malaga
Contact: roman@uma.es

The study of species distributions can facilitate the application of biogeographical principles to problems regarding biodiversity conservation. In conservation biogeography species distributions models are frequently used to study relationships between species and their environment, and also to assess biogeographical relationships between very different taxa. In this sense, when one species affects the survival of another species population dynamics may be altered, and this process is particularly important when it involves an endangered species. We have explored the biogeographical interactions of two ecologically related vultures, in an area that holds the largest populations of both species in the western Palearctic. The Spanish population of Egyptian Vultures has decreased in recent years, and it is considered endangered, while the population of Griffon Vulture has undergone a sharp increase. We modelled the environmental favourability for both species and estimated using fuzzy logic the vulnerability of Egyptian Vulture. We used the overlapped favourability models to map the areas of conflict between the two species and to identify areas of high conservation concern.

Keywords: conservation, interspecific relationships, vultures

5.34 ⚡ Analysis of the biogeographic distribution patterns of the scarab beetle tribe Phanaeini in Colombia (Coleoptera: Scarabaeinae)

Jorge Ari Noriega[1], Joaquin Hortal[1], Ana Margarida Coelho dos Santos[1], Isaac Pozo[2]
[1] Departamento de Biogeografía y Cambio global, Museo Nacional de Ciencias Naturales (CSIC)
[2] Geoimagine S.L.
Contact: jnorieg@hotmail.com

Dung beetles are an ideal group for biodiversity research and conservation planning. Within the Scarabaeinae subfamily, the Phanaeini are the best-known tribe, containing 12 genera and 160 species. However, the knowledge about phanaeines in Colombia is limited. Based on fieldworks, review of 26 national entomological collections and literature, the biogeographical patterns of Phanaeini were synthesized. 43 species in 9 genera are recorded in 224 georeferenced localities with 130 new departmental records. Biogeographic pattern for each species and genus is presented. A significant correlation exists between species and collecting localities. Amazonia is the richest ecoregion. The fauna presents a higher diversity in low lands and a strong elevation gradient; species richness decreases strongly at 1500 masl. Few species are endemic and most of them present a widespread pattern related with habitat type and elevation, causing a complementarity arrangement amongst the biogeographic provinces. Priority areas for future collecting and for establishing new conservation programs are proposed including the Choco -Pacific belt region, which is essential to protect biodiversity in Colombia.

Keywords: Biogeographic provinces, Conservation areas, Choco region, Diversity, Endemicity, Scarabaeidae.

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5.35 Species distribution modeling of snub-nosed monkey

Jonas Nüchel[1], Peder Klith Bøcher[1], Jens-Christian Svenning[1]
[1] Section for Ecoinformatics and Biodiversity, Department of Bioscience, Aarhus University
Contact: j.nuchel@bios.au.dk

According to the IUCN red list are around 22% of mammals species threatened with extinction. Among the mammal taxa with many threatened species are the primates, with 60% of species threatened with extinction. In this study we focus on one group of threatened primates, the snub-nosed moneys (Rhinopithecus), a temperate-subtropical East Asian genus. We use species distribution modeling to assess the following question of key relevancy for conservation management of snub-nosed monkeys; 1. Which factors determine their present distribution? 2. To which extent do snub-nosed monkeys live in non-optimal refuge habitats due to exclusion by human activities? 3. When considering climate and habitat availability to which areas could snub-nosed monkeys be reintroduced?
Keywords: biodiversity, biogeography, conservation, China, snub-nosed monkey, primates, species distribution modeling

5.36 Extensive and rapid hybridization between *Crocodylus moreletii* and *C. acutus* throughout their distribution along the Gulf of Mexico and the Caribbean

Gualberto Pacheco-Sierra[1], Ella Vázquez-Domínguez[1], Jerónimo Domínguez-Laso[2], Zachariah Gompert[3]
[1] Ecología de la Biodiversidad, Instituto de Ecología, UNAM
[2] COMAFFAS
[3] Utah State University
Contact: evazquez@ecologia.unam.mx

Natural interspecific hybridization plays an important role in evolutionary and conservation biology, that may contribute to the formation of new hybrid taxa, whereas introgression may promote adaptive divergence and facilitate speciation. *Crocodylus moreletti* and *Crocodylus acutus* are known to be historically sympatric in a region along the northern Yucatan peninsula. Our study is the first that has rigorously evaluated the existence, level and extent of hybridization between them. We sampled 300 crocodiles along the Gulf of Mexico and the Caribbean, amplified 12 microsatellites and applied Bayesian and maximum-likelihood statistical analyses to evaluate hybridization, introgression and genetic isolation. We confirm our hypotheses: hybridization process is not recent, occurring for several generations and significantly extended throughout most of their evaluated range; evidence of isolation by distance and of expansion of admixed individuals; 'pure' populations are significantly reduced. Our results reveal the relationship of ecological and behavioural features in hybrids, point to evaluate loci under selection and adaptation of hybrids, and are key for conservation (CITES)
Keywords: reptiles, Crocodylia, introgression, conservation, Mexico

5.37 ⚡ Plant Richness and Composition of Urban Domestic Gardens are Strongly Related to Socioeconomic and Demographic Characteristics of their Owners in Touristic Residential Areas of the Costa Brava (SPAIN)

Josep Padullés[1]
[1] University of Girona
Contact: josep.padulles@udg.edu

Domestic gardens collectively represent large areas within cities and play a relevant role in supporting ecosystem functioning and urban biodiversity. We recorded the plant species composition, garden cover types, and demographic, socioeconomic and cultural characteristics of 258 households in urban areas along the Costa Brava (Spain). The distribution of the 635 species in these gardens were the input to a cluster analysis, in which wild gardens, vegetable gardens, lawn gardens and ornamental gardens formed strong floristic groups. A Non-metric Multidimensional Scaling (NMDS) analysis showed that the main floristic gradients in the garden vegetation were correlated to the occupancy rate of the house, birthplace, income and the percentage of people not working in the household. Results from a stepwise multiple regression showed all plant biodiversity parameters (Shannon diversity index, overall plant richness and exotic and native plant richness) strongly related to garden area, the occupancy rate of the house and other different socio-economic and cognitive characteristics of household members.

Keywords: Gardens, plant composition, exotic species, urban sprawl, Costa Brava.

5.38 Eurasian temperate grasslands: A consistent soil pH optimum for fine-scale species richness across biogeographical regions

Salza Palpurina[1], Viktoria Wagner[1], Milan Chytrý[1], Henrik von Wehrden[2], Annika Brinkert[3], Jiři Danihelka[1], Norbert Hölzel[3], Johannes Kamp[3], Pavel Lustik[1], Kristina Merunková[1], Zdenka Preislerová[1], Karsten Wesche[1]
[1] Department of Botany and Zoology, Masaryk University, Brno, Czech Republic
[2] Leuphana University Lüneburg, Centre of Methods & Institute of Ecology, Germany
[3] Institute of Landscape Ecology, University of Münster, Germany
Contact: salza.palpurina@gmail.com

The relationship between soil pH and fine-scale species richness of vascular plants changes across climatic regions. In most European temperate grasslands, richness peaks at pH between 6 and 7. However, little is known about the richness–pH relationship in more arid parts of Eurasia. Here, we report the first large-extent study on richness-pH relationships in Eurasian temperate grasslands. Study regions span a large precipitation gradient in Eurasia, from the Czech Republic to Mongolia and Yakutia. We asked whether richness–pH relationships changed across regions. Data on soil pH and species richness of vascular plants was collected in 10×10 m plots; modelled mean annual precipitation (MAP) was obtained at the scale of ca. 1×1 km. Poisson regressions revealed unimodal richness–pH relationships in regions of both high and low MAP, with a consistent peak at pH of ca. 7. However, across regions, MAP (a proxy for water availability) appeared as the main control of local richness in temperate grasslands. Results are discussed in reference to the species pool hypothesis, and potential ecological factors confounding high–pH soils are outlined.

5.39 New insights in European pteridophyte distribution patterns

Luciano Pataro[1], Santiago Pajarón[2], Miguel Ángel Rodríguez[3], Juan Carlos Moreno-Saiz[1]
[1] Universidad Autónoma de Madrid
[2] Universidad Complutense de Madrid
[3] Universidad de Alcalá
Contact: luciano.pataro@gmail.com

Pteridophytes are capable to disperse to long distances due to their small-sized, wind-dispersed spores, and also to inhabit a range of habitats possibly due to their variable ploidy levels. We investigated Pteridophyte richness patterns in Europe by updating the Atlas Florae Europaeae and compiling published data to differentiate between diploid and polyploid species (96 and 75, respectively), and between monolete and trilete spore species (108 and 63, respectively). Higher richness occurred in and around mountain ranges, primarily the Alps and Cantabrian-Pyrenaean mountains, and in north-western coastal areas, possibly favored by the North Atlantic Current. Also, the Dinaric Alps harbored the highest densities of European endemics. Richness of polyploids was higher than that of diploids in northern areas, suggesting a connection between polyploidy and resistance to harsh environments. Species with trilete spores were widely distributed, while those with monolete spores clustered in the Mediterranean Basin. These patterns were discussed according to past and present climate conditions and the role of coastal regions and Mediterranean mountain ranges as Pleistocene refugia.

Keywords: polyploidy, ferns, lycopods, spores, Europe

5.40 Projecting the spread of a large carnivorous reptile

Hannah Perkins[1], David Jenkins[1]
[1] Biology, University of Central Florida
Contact: hperkins@knights.ucf.edu

The Nile monitor lizard (*Varanus niloticus*) is a large generalist carnivore that is native to sub-Saharan Africa and the Nile River. Nile monitors burrow, swim, and climb trees. Gut content analyses show they prey on many different invertebrate and vertebrate animals. It has been established in North America (Florida, USA) since ~1990 as a result of the pet trade and is a potential invasive threat though not widely recognized. Given its wide range in Africa (Nile

delta to Cape Town, South Africa), it may spread into many other habitats. We modeled the potential global range of the Nile monitor using ensemble modeling (Biomod2 in R), based on ~506 geo-referenced reported observations across Africa. Preliminary projections based on current climate indicate this predator will spread into subtropical and tropical regions consistent with its African range. Further model refinements will be presented, including future climate models. If the Nile monitor spreads further by natural dispersal, human transport, or both, it could cause important declines in many vulnerable prey species in tropical and subtropical regions.

Keywords: Invasive species, ensemble modeling, Biomod2,reptile, America, Africa, pet trade, projections.

5.41 ⚡ Exploring policy options to curb future deforestation in the Argentine Chaco

Maria Piquer-Rodriguez[1], Van Butsic[2], Ignacio Gasparri[3], Sebastian Torrella[4], Gregorio Gavier[5], Jose Volante[6], Ruben Ginzburg[4], Tobias Kuemmerle[1]
[1] Humboldt Universität zu Berlin, Germany
[2] University of California, Berkley, USA
[3] University of Tucuman, Argentina
[4] University of Buenos Aires, Argentina
[5] INTA, Buenos Aires. Argentina
[6] INTA, Cerrillos. Argentina
Contact: maria.piquer-rodriguez@geo.hu-berlin.de

The South American Chaco has among the highest rates of dry forest loss in the world, mainly due to the expansion of soybean production and cattle ranching. Argentina recently implemented a national zoning plan (i.e., the Forest Law) to limit forest loss. However, it is unclear how its implementation will interact with other policy options to influence future deforestation trajectories. Here, we use a comprehensive set of socioeconomic and environmental variables to model deforestation in the Argentine Chaco in order to explore a range of policy options to curb future deforestation. If the Forest Law would be implemented as planned, forest area would continue to decline drastically. However, implementing environmental payments, such as REDD+, would aid in preserving forests. The inclusion of economic incentives in national policies, such as fertilizer subsidies or reducing current export taxes, would translate into increased deforestation. Understanding the relative power and complementarity of policy interventions to curb deforestation are thus important for land-use and conservation planning, and in general, in debates about sustainable resource use in the Chaco and elsewhere.

Keywords: scenarios, cropland, dry forest, economic incentives, environmental payments, Forest Law, grazing, REDD+, returns.

5.42 Measuring range-wide carrying capacity and connectivity within species' geographic distribution providing their conservation status diagnosis

Ludmila Rattis[1], Ricardo Dobrovolski[2], Maurício Talebi[3], Loyola Rafael[4]
[1] Ecology, Campinas State University, Campinas, São Paulo, Brazil
[2] Zoology, Bahia Federal University, Salvador, Bahia, Brazil
[3] Biology, São Paulo Federal University, Diadema, São Paulo, Brazil
[4] Ecology, Goiás Federal Unversity, Goiânia, Goiás, Brazil
Contact: ludmilarattis@gmail.com

Ecologists have traditionally measured species and population conservation status at the landscape scale. However, as the species occur in different landscapes, their population conservation status might vary widely across their geographic distribution. We evaluated the area and isolation of the remaining habitat found within the entire geographic distribution of species, and compared these evaluations with measures taken at the landscape scale to test if the diagnosis of specie's landscape conservation status changes according to the employed scale. Our models were successful in predicting species' occurrence to four of five species. Going from 5km-wide landscapes to the range-wide landscape increased connectivity, which was clearly different among scales. We did not observe the same for carrying capacity, suggesting that species' response to landscape connectivity was more dependent on the scale of assessment rather than on the ecological profile of

species. Our approach can lead to lower risks of incurring in commission errors arising from landscape-scale underestimation of species' occurrences by assessing species' range-wide landscape conservation status.

Keywords: Conservation Biogeography; Deductive Habitat Suitability Models; Functional Connectivity; Landscape Metrics; Movement Ecology; Scale Dependency.

5.43 ⚡ The geography of bushmeat hunting sustainability in central Africa: Integrating biodiversity protection and human nutrition

Raimundo Real[1], J.E. Fa[1], J. Olivero[1], J.M. Farfán[1], A.L. Márquez[1], J.M. Vargas[1], R Nasi[2]
[1] Departamento de Biología Animal, Universidad de Málaga
[2] Consultative Group on International Agricultural Research (CGIAR), CIFOR Headquarters, Jalan CIFOR, Situ Gede, Bogor 16115, Indonesia
Contact: rrgimenez@uma.es

Wild animals are a primary source of protein for people living in tropical forests. Ideally, the effect of bushmeat harvests should be monitored by making estimates of offtake rate and size of stock available for exploitation, which is highly effort and time-demanding. As alternative, we use environmental favorability models for terrestrial mammals in Central Africa to map areas of high species richness and hunting susceptibility. We develop an index for assessing Potential Hunting Sustainability (*PHS*) of each species based on their ecological traits. Using the favorability values of all species, and their *PHS* values, we finally identify weak spots, defined as high diversity regions of especial hunting vulnerability for wildlife, as well as strong spots, defined as high diversity areas of high hunting sustainability potential. We thus chart the geography of where species are more or less likely to be at risk of extinction from hunting. We finally use the distribution of weak spots and strong spots, and inferred extraction levels of hunted mammals, to relate bushmeat sustainability and stunting in children, as a measure of malnutrition.

Keywords: Congo Basin, natural resources, wildlife conservation, diversity hotspots, favourability funtion, fuzzy logic

5.44 ⚡ Urban flora of São Paulo city, Brazil: Data from an education project

Yuri Rocha[1], Patricia Oliveira[1]
[1] Department of Geography, University of São Paulo
Contact: yuritr@usp.br

São Paulo (Brazil) is one of the largest cities in the world and the center of the largest metropolitan area in South America. This city growth in the Atlantic Rainforest region. Since 2010, an educational project was initiated with undergraduate students the of course "Biogeography" (Geography degree/University of São Paulo) in order to train the identification of species of plants found in your neighborhood and mapping of individuals by Google Maps. Data collected by the students are systematized in order to have a diagnosis of urban flora species. During four years (2010-2013), this educational project have been identified 162 flora species (trees, shrubs, epiphytes) from 63 families; 57% are alien species (from various parts of the world) and 43% are Brazilian species (from various natural regions). The results have been very productive because the students showed great interest, devotion and excellent learning about urban flora. This project constitutes a simple educational proposal, but totally viable in terms of time and financial support, and more important, to produce rich information about surviving urban flora species in metropolitan areas.

Keywords: Urban Biogeography, teaching resource, São Paulo, mapping, urban flora

5.45 Does rarity leave a footprint in herbarium material? A case study in Bavaria

Alexander Rockinger[1], Susanne S. Renner[1]
[1] Systematic Botany and Mycology, University of Munich (LMU)
Contact: a.rockinger@gmail.com

Herbaria provide many kinds of data and are essential to research in plant systematics. Through their preserved specimens they may also document changes in occupied range or abundance as long as collecting effort can be

accounted for. We are testing the extent to which changes in a flora can be tracked through herbarium material in Bavaria, using material in the Munich herbaria, with 3 million specimens, a significant number of them from Bavaria. With ~70,500 sq. km, including the Alps in its south, Bavaria has a great diversity of habitats and species (vascular plant species ~3500). So far we have quantified collections for 10 common and 10 rare species in 40-year bins between 1780 and 2014 to test how collection number has changed over time. So far, for all species, peak collecting occurred between 1901 and 1980 and decreased towards the present. We are still enlarging our species sampling, however. To detect range change signal in the herbarium we are focusing on (i) invasive species and (ii) local extinctions in endangered low nutrient environments. Because of the decrease in collecting since 1981, neither invasions nor local extinctions appear to be well documented.

Keywords: Herbarium material, herbaria, collections, flora, Bavaria, rarity, extinction, invasive species

5.46 ⚡ Plant extinctions and colonizations in European grasslands due to loss of habitat area and quality: a meta-analysis

Liina Saar[1], Krista Takkis[2], Aveliina Helm[1]
[1] Department of botany, University of Tartu
[2] Department of Geography, University of the Aegean
Contact: liina.saar@ut.ee

During last centuries, species rich grasslands in Europe have faced vast area and quality loss due to cessation of traditional management, agricultural intensification, eutrophication, urbanization etc. Loss of habitat area and quality can lead to local extinctions of plant species, as conditions become unsuitable for populations. Despite the intensive research, we still lack thorough knowledge of which species are most threatened by the changes in area and quality of European grasslands. We compiled data from 17 studies to describe changes in plant community composition in European grasslands. Information about species extinction and colonization during the past 30 to 300 years allows us to reveal the changes in grassland community composition and in species abundances as well as identify driving factors behind the changes. Our results can be applied to define the species most prone to future extinctions in less degraded grasslands. Knowledge about species that increased their abundance or colonized the grasslands recently enables to predict future changes in European grasslands and take proper conservation actions.

Keywords: Species resurvey, European-scale vegetation shifts, climate change, habitat isolation, habitat preference, life-history traits.

5.47 Conservation areas in private properties, Paraná State, Brazil

Gustavo Schacht[1], Yuri Rocha[1]
[1] Department of Geography, University of São Paulo
Contact: yuritr@usp.br

The Private Reserve of Nature Patrimony (RPPN) is a category of Brazilian conservation area, in which a private property, in partnership with the government, becomes part of the country protected areas. Conservation on private property in Brazil is quite old and comes along with the first forestry law, the Federal Decree 23.793 of January 23, 1934, then being referred to as Protective Forest. Only in 1990, with the Federal Decree 98.914 of January 31 of that year, was officially established in Brazil called RPPN. In a pioneering way, the Paraná State sanctioned the State Decree 4.262 on November 21, 1994, starting in the state creating these important conservation areas. With the enactment of Law 9.985 of July 18, 2000, the National System of Conservation Nature Units was created, which is integrant to RPPN, the group of units of sustainable use. Currently, Paraná State has 228 private reserves that are an effective way to increase protected areas, forming ecological corridors, buffer zones, and protecting different ecosystems of the Paraná State.

Keywords: Conservation area; private property RPPN; Brazil

5.48 ⚡ Effects of recent and past climatic shifts on the range dynamics and genetic structure of the high mountain Yellow-spotted ringlet butterfly (Lepidoptera, Satyrinae): a conservation problem

Thomas Schmitt[1], Jan Habel[2], Dennis Rödder[3], Dirk Louy[4]
[1] Senckenberg German Entomological Institute
[2] Technical University München
[3] Museum Koenig Bonn
[4] Trier University
Contact: thomas.schmitt@senckenberg.de

Mountain species evolved genetic differentiation due to past climatic fluctuations. We analysed allozyme polymorphisms of the mountain butterfly *Erebia manto* and perform Species Distribution Models (SDMs). We obtained six most likely genetic clusters: (i) Pyrenees + Massif Central, (ii) Vosges, (iii-v) Alps including Slovakian Carpathians, (vi) southern Carpathians. The Vosges showed the strongest split followed by Pyrenees-Massif Central and southern Carpathians. These groups most likely survived more than one glacial-interglacial cycle close to their actual distributions with up-hill and down-slope shifts. The three groups present in the Alps show shallower genetic structures and a more recent origin. SDM projections predict rising temperatures strongly impacting the species' distribution. Although populations in the Alps will shrink, survival of the three Alpine lineages is not at risk. However, all models predict the extinction of the Vosges lineage, and also the southern Carpathians and Pyrenees-Massif Central lineages are at high risk. Albeit global warming will not threaten *E. manto* as a species, a major proportion of the species' intraspecific uniqueness might be lost.
Keywords: Key-words: Climatic oscillations, global warming, global change, glacial refugia, postglacial colonisation, mountain archipelagos, genetic structure, allozyme electrophoresis, Species Distribution Models

5.49 Elucidating patterns of diversity and phylogenetic structure in the Eastern Himalayas.

Stephanie Shooner[1], Jonathan Davies[2], Selvadurai Dayanandan[1]
[1] Biology, Concordia University
[2] Biology, McGill University
Contact: svshooner@gmail.com

Analyses across environmental gradients are one of many ways ecologists have attempted to address the question of why species occur where they do and why they do not occur elsewhere. The Himalayan region of Arunachal Pradesh, India, provides not only one of the most extensive elevational gradients in the world, but also hosts an unusually rich diversity of flora and fauna. However, relatively little is known about the diversity of forest communities in this region. Using abundance data and a regional phylogeny, we investigated the phylogenetic relatedness of tree species in 337 plots distributed along the mountainside, and evaluated the relationship between elevation and phylogenetic community structure. We found that the most clustered plots were located at high altitudes while the most over-dispersed plots were distributed at lower elevations. Interestingly, however, we found that there was no overall elevational trend in phylogenetic structure, suggesting that factors other than elevation are influencing patterns of species relatedness in the region. This study is one of the first to look at diversity and phylogenetic structure in the unique flora of this region.
Keywords: Phylogenetics, commmunity ecology, elevational gradient, diversity, species richness

5.50 ⚡ Effects of post-Soviet land-use change on large mammals‘ habitat in European Russia

Anika Sieber[1], Tobias Kuemmerle[1], Nikolai Uvarov[2], Alexey Pankov[2], Leonid Baskin[3], Volker Radeloff[4]
[1] Geography Department, Biogeography and Conservation Biology, Humboldt-Universität zu Berlin
[2] Oksky State Nature Reserve, Russia
[3] A. N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Russia
[4] Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, USA
Contact: anika.sieber@geo.hu-berlin.de

Land-use change can strongly affect wildlife populations, either via habitat loss where land use expands, or via increasing habitat availability where land use contracts. Large mammals are particularly challenging to protect in human-dominated landscapes, in part because they often critically depend on habitat surrounding protected areas. Here, we use the breakdown of the Soviet Union and the widespread land-use changes it triggered as a natural experiment to study how land change outside Oksky State Nature Reserve (OSNR) in European Russia influences wildlife. To do so, we mapped land-use change between 1987 and 2007 from Landsat TM/ETM+ images, and used a unique, long-term data set of field observations of wild boar (*Sus scrofa*), moose (*Alces alces*), and wolf (*Canis lupus*) from the same period in a time-calibrated species distribution modelling approach. Our results show that the proportion of suitable habitat outside of OSNR increased markedly (up to 25%) due to post-Soviet farmland abandonment and also changed within those protection zones permitting land use. Thus, this study provides valuable insights into the complex interrelations between land-use change and biodiversity.

Keywords: Habitat, land-use change, protected areas, zone of interaction, long-term data, species distribution models, large mammals, Russia

5.51 ⚡ Mapping the occurrence of small cats in India: co-occurrence in *Prionailurus* spp.

Andre Silva[1], Mats Björklund[1], Carlos Fernandes[2], Shomita Mukherjee[3]
[1] Dept of Animal Ecology, Evolutionary Biology Centre, Uppsala, Sweden
[2] Centro de Biologia Ambiental, Universidade de Lisboa, Lisboa, Portugal
[3] Sálim Ali Centre for Ornithology and Natural History, Tamil Nadu, India
Contact: andre.silva@ebc.uu.se

Four species of small cats belonging to the genus *Prionailurus* occur worldwide. Leopard cat, fishing cat, and rusty-spotted cat occur in India where their distribution is poorly known. Recent occurrence records for the rusty-spotted cat suggest the species may have a wider range than previously described, which translates to possible co-occurrence with other members of the *Prionailurus* genus.

Here we use bibliographic and new occurrence records to estimate potential occurrence of the three *Prionailurus* species occurring in India through ecological niche models. We then evaluate the importance of climate, land cover and human disturbance to explain *Prionailurus* spp. occurrence at the national scale.

Consensus models show higher probability of rusty-spotted cat in three main biogeographic regions, the Western Ghats, Deccan south and the Himalayan foothills. These new predictions suggest that the landscapes of the Himalayan foothills and Deccan south may be inhabited by all three species. We show that the importance of climate differ in explaining the species ecological niche and discuss these results in the light of climate-change.

Keywords: Prionailurus bengalensis, Prionailurus viverrinus, Prionailurus rubiginosus, climate, Asia

5.52 ⚡ Biogeography and conservation of sloth bear (*Melursus ursinus*): Modelling ecological niches for detecting conservation gaps areas in India

Randeep Singh[1]
[1] Animal Ecology and Conservation Biology, Wildlife Institute of India
Contact: randeep04@rediffmail.com

The sloth bear is endemic (*Melursus ursinus*) to the Indian-subcontinent and its population is continuing to decline, but information available about the species geographic distribution is sparse. We used Maxent modelling tool to predict geographical distribution range and protected area connectivity of species across the distribution range to aid in conservation planning. We overlapped the forest cover and land use map and boundaries of protected areas to define low, medium, and high risk areas and pinpoint priority areas. We found a high degree of fragmentation gap, mainly dominated by anthropogenic activities. Over 49 % of the potential habitat was found to be unprotected. A total 73 out of 174 protected areas were identified across the study region need to be high priorities sloth bear conservation area. We urge creation or restoration of forest corridors between these protected areas for functional movement, which helps in dispersal and gene flow and leads to structuring the meta-population. Our results suggest that the biogeographic distribution pattern of species and identifying the high suitability habitats can be foundations for planning conservation areas and species recovery initiatives.

Keywords: Ecology, India, maximum entropy, predictive distribution, protected area, Sloth bear

5.53 Assessment of the diversity and distribution of the lizards of Iran at different geographic and taxonomic scales

Jiri Smid[1], Jindrich Brejcha[2], Sara Varela[3]
[1] Department of Zoology, National Museum in Prague
[2] Department of Philosophy and History of Science, Charles University in Prague
[3] Department of Ecology, Charles University in Prague
Contact: jirismd@gmail.com

The lizard fauna of Iran is extremely rich and diverse. It currently consists of 144 species in 11 families and the number is growing gradually with new species being described each year. Precise distribution data for all the species have been recently assembled and show that most of the country has been surveyed to some extent. The only exceptions are the deserts on the central Iranian Plateau. However, regardless of how well covered the area of Iran may seem when all species are pooled together, the knowledge of the distribution is more patchy when it comes to individual families (or other equally ranked higher taxa). For instance, we believe that the knowledge about the diversity of geckos - small, nocturnal, cryptic – should be lower than the knowledge of the diversity of agamids - large, diurnal, and conspicuous. Our aim here is to quantify the completeness of the Iranian species list at different geographic scales by calculating species accumulation curves. Our objectives are 1) to identify which families are well sampled and which families need more sampling effort, 2) construct a map of the completeness of the species lists in Iran at a local scale, to identify the areas that need more field work.

Keywords: Iran, lizards, diversity, species accumulation curve, families

5.54 Drivers of extinction: The case of Azorean beetles

Sofia Terzopoulou[1], Francois Rigal[2], Robert J. Whittaker[3], Paulo A.V. Borges[2], Kostas A. Triantis[1]
[1] Department of Ecology and Taxonomy, Faculty of Biology, National and Kapodistrian University of Athens, Greece
[2] Azorean Biodiversity Group, Centre for Ecology, Evolution and Environmental Changes, and Platform for Enhancing Ecological Research & Sustainability, Departamento de Ciências Agrárias, Universidade dos Açores, Azores, Portugal
[3] School of Geography and the Environment, University of Oxford, UK.
Contact: island.biogeography@gmail.com

Habitat destruction is the main threat to biodiversity in the current years. Of the recorded species extinctions worldwide, oceanic islands have suffered the vast majority. Two of the main factors known to influence species proneness to extinction are their geographical distribution and body size.

In this study, we focus on the endemic beetles of the archipelago of the Azores and we ask whether the extinct species differ from the extant regarding their degree of isolation and body size. Azores is among the most isolated archipelagoes of the world and has suffered a major destruction of its natural forest. We tested for differences in body size between extinct and extant species considering i) all endemic species and ii) only single-island endemic species (SIE) separately. We further compartmentalize these groups into species strictly present in native forest or not. Analyses were performed using GLMM in a phylogenetic framework. Extinct species were significantly bigger than the extant when strict native forest, SIE and SIE strictly in native forest were considered. Our results confirm that extreme isolation and large body size could increase species susceptibility to extinction.

5.55 ⚡ Terrain features shaping the spatial distribution patterns of *Polylepis* forest stands in the high Andes of southern Peru

Johanna Toivonen[1], Carlos Gonzales-Inca, Kalle Ruokolainen, Michael Kessler
[1] Department of Biology, University of Turku
Contact: jomito@utu.fi

High Andean *Polylepis* forests grow in sparely distributed stands forming one of the highest alpine treelines worldwide. However, natural factors determining the forest distribution are poorly known. In this study, we studied the associations between the distribution of *Polylepis* stands and topography. We conducted a detailed mapping of *Polylepis* stands in the Cordillera Urubamba, southeast Peru, using a high-resolution aerial photograph with an extensive ground truthing. We overlapped the mapped polygons with a high-resolution digital terrain model and derived 10 ecologically relevant terrain features to compare between *Polylepis* forest stands and landscape. We

found that at low and mid-elevations (3800-4600 m), *Polylepis* stands were located in more humid and sheltered sites than the landscape mean, whereas at high elevations (>4600 m) they were located in drier and sunnier sites. This indicates that that terrain features play an important role shaping the spatial pattern of *Polylepis* forest distribution presumably by providing refugia from human activities at lower elevations and thermically favorable micro-climatic conditions at high elevations.

Keywords: Mountain forests, topography, species distribution, environmental niche, human impact

5.56 Deconstructing trait patterns of stream macroinvertebrate communities at high latitudes

Katri Tolonen[1], Jaakko Erkinaro[2], Mira Grönroos[1], Jan Hjort[3], Olli-Matti Kärnä[3], Laura Tokola[3], Jani Heino[1]
[1] Finnish Environment Institute, Oulu
[2] Finnish Game and Research Institute
[3] University of Oulu/ Department of Geography
Contact: katri.e.tolonen@ymparisto.fi

Ecological research based on species traits has increased rapidly recently because trait-based approaches help us to understand the mechanisms structuring ecological communities. However, finding all influential environmental filters at different spatial scales is challenging. Using variation partitioning in constrained ordination, we deconstructed variation in the trait structure of benthic macroinvertebrate communities in subarctic headwater streams in northernmost Finland (latitude: 70°N) and used predictor variables measured at four spatial scales. Our aim was to unravel the effects of different variables on the taxonomic and functional trait structure of macroinvertebrate communities. We expected species-by-sites matrices to be more strongly associated with the spatial location of the site and traits-by-site matrices to be more strongly associated with environmental variation across the sites. We found that variables measured at different spatial scales were different for species composition and trait composition, and that the deconstruction of the trait matrix into its components yielded increased understanding of community organization in high-latitude streams.

Keywords: catchment, community structure, environmental filters, invertebrates, species traits, streams

5.57 ⚡ Monitoring of biodiversity in the Italian Alps: a multi-taxa approach

Ramona Viterbi[1], Emanuel Rocchia[2], Cristina Movalli[3], Luca Pedrotti[4], Enrico Vettorazzo[5], Cristiana Cerrato[6], Antonello Provenzale[6]
[1] Gran Paradiso National Park
[2] Department Environmental Sciences and Territory, University of Milano Bicocca, Milan
[3] Val Grande National Park, Italy
[4] Stelvio National Park, Italy
[5] Dolomiti Bellunesi National Park, Italy
[6] Institute of Atmospheric Sciences and Climate, National Research Council, Torino, Italy
Contact: ema.rocchia@gmail.com

Altitudinal gradients are natural laboratories to study ecosystem dynamics, biodiversity and species' distribution response to climate gradients. In this framework, in 2012-2014, 6 Italian Parks (4 National Parks and 2 Regional Parks), distributed along the Alps, from west to east, shared a common protocol for studying animal biodiversity in mountain ecosystems. Along 24 altitudinal transects, involving 132 sampling stations, seven taxonomic groups have been sampled (Coleoptera Carabidae, Coleoptera Staphylinidae, Araneae, Orthoptera, Lepidoptera Rhopalocera, Aves), using semi-quantitative sampling techniques, that are easy to apply, cheap, and standardized. Such monitoring program allows to recognize common points and differences between geographic areas and altitudinal zones and represents a way to identify actual and future vulnerability. This shared protocol represents an important step of a monitoring effort that will be repeated every five years to highlight the response of alpine biodiversity to climate and land-use changes.

5.58 ⚡ Dispersal capability is a major determinant of the genetic population structure of two wetland insects

Jessica Weyer[1], Ortwin Elle[2], Michael Veith[2], Thomas Schmitt[3], Axel Hochkirch[2], Joe Chipperfield[4]
[1] Ecology, Senckenberg German Entomological Institute
[2] Biogeography, University of Trier
[3] Senckenberg, German Entomological Institute
[4] University of Bergen
Contact: jessica.weyer@senckenberg.de

Landscape fragmentation due to anthropogenic activities is a major threat for a wide range of species. Wetlands are among the most vulnerable terrestrial habitat types and have become fragmented in Central Europe. We studied the genetic population structure of two wetland insect species differing in dispersal capability. We sampled 14 populations of *C. montanus* and nine population of *B. ino* in SW Germany and genotyped them with different polymorphic microsatellite loci. The populations of the poor disperser, *C. montanus*, were highly fragmented; strong connectivity existed among populations of the mobile butterfly. Using a novel Bayesian Landscape Genetics approach, we revealed that covered areas and forests provide substantial barriers to gene flow among populations of both species. Our study underlines the importance of improving the habitat connectivity for wetland species via conserving small wetland patches, which may serve as stepping stones hereby creating new corridors for such species. The current habitat connectivity program focuses on forest habitats, and may thus create new barriers to threatened open-land species.

Keywords: Microsatellites, conservation genetics, landscape genetics, habitat fragmentation, connectivity, landscape conversion

5.59 ⚡ Assessing the genetic diversity, distribution, and population status of American ginseng (*Panax quinquefolius*) in the eastern U.S.

John Young[1], Tim King[1], David Smith[1]
[1] Leetown Science Center, US Geological Survey
Contact: jyoung@usgs.gov

American ginseng (*Panax quinquefolius*) is a North American native medicinal plant that is widely distributed but thought to be locally scarce because of legal and illegal harvest to supply international market demand. In an effort to better understand the distribution, diversity, and abundance of American ginseng, we conducted an extensive regional survey of suspected wild and known cultivated populations on public and private lands across 13 U.S. states. We developed a set of microsatellite DNA markers for genetic analysis and conducted a variety of population structure, diversity, and phylogeographic analyses. Our analysis shows that, while relatively diverse, American ginseng populations are small and heavily structured in natural settings, making them more vulnerable to extinction. We detected a strong phylogeographic signal in the regional data, but with significant translocation and admixture of suspected cultivated material, even on public lands. In order to better inform management on four U.S. National Forests, we recently initiated a more intensive follow-on survey to assess threats to distribution, diversity, and population viability under current harvest regimes.

Keywords: ginseng, genetics, population, diversity, distribution

P6 Modelling species and ecosystems

6.1 ⚡ sdm: an extendable R framework for species distribution modelling

Miguel Araújo[1], Babak Naimi[1]
[1] Department of Life Science, Imperial College London
Contact: b.naimi@utwente.nl

Species distribution models (SDMs) explore relationships between species occurrences and corresponding environmental variables and become important in a numerous range of applications. Many models are now available for this purpose, although they may yield different results, even when calibrated with the same response and predictor variables. However, it is not usually easy to explore these differences, especially for taking the new models into account, because different models are scatter and implemented in various environments following different standards. sdm in an extendable R framework to develop species distributions models using individual and community-based approaches, generate ensembles of models, evaluate the models, and predict species potential distributions in space and time. Unlike the existing software, sdm is not limited to a few algorithms, but can be extended by users to support new algorithms or the existing ones with a new setting. The design of the package has been benefited from object oriented programming, followed by a graphical user interface, and supports high performance computing to enhance the computational performance.

Keywords: species distribution modelling, R programming

6.2 Quantification of uncertainty of ecological niche models

Edith Calixto-Perez[1], Miguel Nakamura[2], Enrique Martínez-Meyer[1], Carlos Díaz-Avalos[3], Héctor Arita[4]
[1] Instituto de Biología, UNAM
[2] Centro de Investigación en Matemáticas, A.C.
[3] Insituto de Investigación en Matemáticas Aplicadas y en Sistemas, UNAM
[4] Centro de Investigación en Ecosistemas, UNAM
Contact: edith.calixto@st.ib.unam.mx

Ecological niche models (ENM) are an important tool in research and to support make decisions of conservation, public health, and others. However, there are different uncertainty sources both data input and modeling process. Different options have been proposed to reduce them, but there is not a method to quantify this uncertainty. Virtual species are useful to analyze this problem because we can know their fundamental and realized niche, which is difficult to know for real species. Here we show that uncertainty from input data can be quantified using inference statistics tools, and virtual species. We built virtual species based on probability distribution model which describes its physiology, considering that the fitness of the species increases toward medium values of environmental variables. Knowing the ecological niche and geographic range of the virtual specie, we induced intentional bias in different subsets of records, and use them like input data for ENM. Using a bootstrap method we quantified the variability in each pixel and generated an uncertainty map. These results could allow us to make best decisions using EMN results.

Keywords: Uncertainty, Ecological niche models, Virtual species, Inference statistics tools

6.3 ⚡ The effects of scale, data type and sample size on occurrence-based characterization of species environmental niches

Ben Carlson[1]
[1] Ecology and Evolutionary Biology, Yale
Contact: ben.s.carlson@gmail.com

The characterization of a species' realized environmental niche has a long history in ecology and biogeography. Species distribution modeling (SDM) is a popular method used to support geographic range estimates, macroecological analyses and conservation decisions. At the core of these methods is a characterization of the environmental conditions where a species is found or absent. Here we explore how the outcome of this characterization, and downstream SDM results, depend strongly on factors such as the spatial and temporal grain of the environmental and species data, the data type used for representing species presence and absence (incidental, survey or expert data), as well as sample size and bias. We investigate the magnitude and consequences of these issues for a variety of taxa using a range of data sources and new niche characterization tools implemented in the Map of Life infrastructure. Based on these results we provide guidelines on how to evaluate potential limitations of

occurrence-based niche characterizations, assess their sensitivity and report metadata that facilitate subsequent interpretation.

Keywords: Niche, Species Distribution Modeling

6.4 ⚡ Evaluation of SDM with a biological approach: How realistic or how ecologically meaningful is the model?

Valeria Di Cola[1], Antoine Guisan[2]
[1] DEE, University of Lausanne
[2] DEE & IDYST, University of Lausanne and
Contact: valeriadicola@gmail.com

In species distribution models (SDMs) model evaluation is the search for a parsimonious model that can adequately approximate the data considered, providing a measure for its accuracy/generalizability and its usefulness. Model evaluation includes many different aspects, going from uncertainty analysis, to sensitivity analysis, to evaluation of the ecological/biological meaning, to accuracy/generalizability. Usually, the evaluation performed is at the level of mismatch between predictions and observations, which is measured using one of the many available evaluation metrics. Our framework will be based on the idea of model evaluation by assessing the ecological realism of the models as a procedure that consists in assessing the realism of a model in terms of its adequacy with biological theory, for example, shape of response curves, causality of environmental predictors and its ability to reproduce natural ecological patterns (e.g. biodiversity patterns from single species predictions). Here we present an integrated practical framework for SDMs evaluation, focusing mainly on ecological evaluation. Hence, we do not deal with sensitivity and uncertainty analysis.

Keywords: Species distribution model, model evaluation, ecological realism

6.5 ⚡ ecospat: a miscellaneous R package for spatial analyses and modelling of species niches and distributions

Antoine Guisan[1], Valeria Di Cola[2]
[1] DEE & IDYST, University of Lausanne
[2] DEE, University of Lausanne
Contact: antoine.guisan@unil.ch

The ‘ecospat’ package brings together tools and methods to complement various existing analyses in spatial ecology, with a particular focus on pre- and post-analyses of species distribution models, niche quantification and community assembly. The package is written in the R language. It offers the possibility to perform pre-modelling analyses, such as spatial autocorrelation, MESS (multivariate environmental similarity surfaces), phylogenetic diversity, niche quantifications and comparisons, and species co-occurrence. It also provides functions to complement the ‘biomod2’ package in preparing the data, calibrating, evaluating (e.g. presence-only evaluation) and projecting the models. Post-modelling analysis, based on model predictions (e.g. co-occurrences analyses), are also provided. A major feature of the ecospat package is the niche quantification and overlap functions to compare niches between distinct ranges or time periods. ecospat can also be complemented with the MigClim R package, developed by the same research group. With this package we hope to strengthen the development and use of comprehensive and interdisciplinary approaches in spatial ecology.

Keywords: R package, Modelling, Community Ecology, Diversity, Niche overlap

6.6 ⚡ Implications for conservation decisions of modeling populations versus species under climate change

Maria Hällfors[1], Jishan Liao[2], Jason Dzurisin[2], Ralph Grundel[3], Kevin Towle[2], Marko Hyvärinen[1], Grace Wu[2], Jessica Hellmann[2]
[1] Botany unit, Finnish Museum of Natural History, University of Helsinki
[2] Dept. of Biological Sci., University of Notre Dame, USA
[3] U.S. Geological Survey
Contact: maria.hallfors@helsinki.fi

Species distribution models (SDMs) have been criticized for making assumptions that ignore many factors that dictate species distributions, such as dispersal ability and biotic interactions. One aspect that has not been widely explored is the effect and relevance of accounting for disjunct populations and the possibility for local adaptation. A common approach in ecological studies, including SDMs, is to treat a species as a single entity although populations may occupy different environments and vary in their tolerances. This could lead to erroneous management decisions, if the populations are locally adapted. We explore this in the context of climate change using two species that have spatially separated populations and thus may be locally adapted: the Karner blue butterfly (*Lycaeides melissa samuelis*) and the Siberian primrose (*Primula nutans* ssp. *finmarchica*). We build SDMs based on occurrences of 1) the whole species and 2) its distinct populations. Our results show different predicted suitable areas using the two approaches. We explore the magnitude of difference and discuss the conservation implications and repercussions of making a type I or II error in this context.

Keywords: niche models, local adaptation, conservation, climate change, species distribution models,

6.7 ⚡ On the universality of plant-climate relationships

Norbert Kühl[1], Christian Ohlwein[1]
[1] University of Bonn
Contact: kuehl@uni-bonn.de

The close relationship of plant species distributions to climatic conditions is frequently used to infer climate of the past as well as to predict species occurrence under changed environmental conditions or in new habitats. However, for predictions as well as hindcasts it is essential that the underlying estimated plant climate relationship is universal, i.e. stable and transferable over time. This prerequisite is generally assumed as being fulfilled, but is rarely tested.

Here we demonstrate and discuss violations of this assumption and show potential solutions. For example, we demonstrate the effect of uneven frequency of specific climatic values on the estimation of probabilistic plant-climate relationships and quantify the effect of a weighing procedure. Nevertheless, tests using independent training versus test sets of distribution areas of individual taxa show that the type of combination of important climate parameters - usually a thermal and moisture component - has great influence on the results. The results highlight that considering data-inherent specifics may improve transferability of plant climate relationships for hindcasts and prediction.

6.8 ⚡ Testing species distribution modelling techniques and hypotheses with virtual species: the 'virtualspecies' R package

Boris Leroy[1], Christine Meynard[2], Céline Bellard[3], Franck Courchamp[4]
[1] UMR Biologie des Organismes et Ecosystèmes Aquatiques, Muséum National d'Histoire Naturelle
[2] Virginia Institute of Marine Science, College of William & Mary, USA
[3] Centre for Biodiversity and Environment Research, Department of Genetics, Evolution and Environment, University College London, London, UK.
[4] Ecologie, Systématique & Evolution, UMR CNRS 8079, Univ. Paris-Sud, France
Contact: leroy.boris@gmail.com

The generation of virtual species distributions has been proposed as a robust approach to evaluate different aspects of species distribution models: protocols, techniques, or underlying hypotheses. In this talk we will introduce the freely available R package 'virtualspecies', designed to generate virtual species distributions. This package provides a framework for integrating the existing methodological approaches, to generate virtual species distributions with increased ecological realism. The package includes generating virtual species' suitability from a spatial set of environmental conditions, with two different approaches; converting the environmental suitability into presence-absence with a probabilistic approach; introducing dispersal limitations in the realised virtual species distributions and sampling occurrences with different biases in the sampling procedure. The package was designed to be extremely flexible, to provide a fine control over every simulation parameter. We will present an example showing how virtual species can be used to assess the true predictive performance of species distribution models in future climate conditions.

Keywords: Climate change; ecological niche models; species range change

6.9 ⚡ Data uncertainty confuse richness patterns and ecological gradient drivers

Xueyan Li[1], Babak Naimi[1], Miguel Araujo[1]
[1] Imperial College London
Contact: x.li14@imperial.ac.uk

Nowadays, more and more species distribution data are available for mapping richness patterns and exploring macro -scale ecological gradients, but the discrepancy among different sources of data and its potential impact remain unclear. We aim to investigate to what extent data uncertainty exists and how it will influence our understandings about richness pattern determinants. We gathered four sources of species distribution data of China, including citizen-based database, global museum and survey dataset, regional checklist and global range maps. Four widely used species distribution models were used to predict richness patterns. We explored the impact of data uncertainty by measuring discrepancy in richness patterns as well as the disagreement in what we can potentially understand as the main driving force for the patterns. Our results showed different data sources generated different richness patterns. Distinct inconsistency of variable importance cross data sources indicated different potential ecological determinants of richness patterns. Our findings suggest that data uncertainty would bias our understandings about main driver of large-scale ecological gradient.

Keywords: Data uncertainty, species distribution models (SDM), richness patterns, environmental determinants

6.10 ⚡ Community level models outperform traditional species distribution models in no-analog climatic and ecological regimes

Kaitlin Clare Maguire[1], Diego Nieto-Lugilde[2], Jessica Blois[1], Matthew Fitzpatrick[2], John Williams[3]
[1] University of California, Merced
[2] Appalachian Laboratory, University of Maryland Center for Environmental Science
[3] University of Wisconsin, Madison
Contact: kmaguire@ucmerced.edu

Species distribution models (SDM) utilize species-environment relationships to predict species response to climatic changes; however, a species response is also influenced by biotic interactions. Recently developed community level models (CLMs) incorporate species associations (i.e. biotic interactions) into models of species responses by using co-occurrence matrices. It is unclear from previous work whether CLMs outperform SDMs when building and projecting models in climatically similar scenarios and it is unknown how the two compare when projected to climatically novel regimes. Here we compare the performance of five SDMs and their CLM equivalents across spatial and temporal scales by capitalizing on the rich fossil pollen record of the Eastern United States through the last 21,000 years. Model performance of both SDMs and CLMs decreases when projected to climatically and ecologically distant time periods but CLMs outperform SDMs in these instances. These results indicate the importance of including biotic interactions into models that predict how species will respond to the novel climatic regimes of the future.

Keywords: biotic interactions, paleoecology, paleobiogeography, pollen

6.11 ⚡ Combining knowledge on intraspecific variation of thermal niches to species distribution models in geographical projections under climate change

Brezo Martínez[1], Francisco Arenas[2], Christine Maggs[3], Olivier De Clerck[4], Galice Hoarau[5], Alexander Jueterbock[5]
[1] Biodiversity and Conservation Group, Rey Juan Carlos University
[2] CIIMAR, Porto University
[3] School of Biological Sciences, Queen's University, Belfast
[4] Phycology Research Group, Ghent University
[5] Faculty of Biosciences and Aquaculture, Nordland University
Contact: brezo.martinez@urjc.es

Predictions of species distribution are based on projections of the current niches to future climates. Niche stability is assumed, though may result in unrealistic predictions for species that have shifted their niches along their evolution. Although the concept of niche is linked to physiological tolerance, the paradigm of niche conservatism has been seldom considered in Physiology. Under niche conservatism, we may expect individuals from populations of different genetic lineages to show similar tolerance. We empirically investigated the survival and growth thresholds to temperature of two macroalgae from border and central populations. Northern populations of Fucus serratus are genetically diverse, having recolonized after the LGM from southern UK and Ireland. In contrast, Ascophyllum nodosum was affected less by the LGM and more by contemporary climate, showing less genetic diversity. We also developed Species Distribution Models and compared the projections with the two approaches. This hybrid approach based on intraspecific mechanistic knowledge and correlative modelling resulted in robust predictions of distributional contractions of both species to Global Warming.

Keywords: Fundamental niche conservatism, adaptation, physiological thresholds, predictions, Climate Change

6.12 ⚡ The importance of absences in species distribution modelling

Aidin Niamir[1]
[1] Senckenberg
Contact: niamir@gmail.com

The importance of sampled but not observed locations, so called absences is often neglected in species distribution modelling (SDM). We evaluated the performance of distribution models using absence-only occurrence data. To do this, we obtained absence information from the Atlas of Amphibians and Reptiles of Spain. We incorporated different types of pseudo-presence to create different sets of training data that account for lack of observation at the species, the family, the order, and the class level. We explored the effect of using different kinds of datasets on SDM results. We used these datasets to calibrate SDMs with GLM and BRT as modelling technique and bioclimatic variables as predictors, and compared these results with the distribution of the species created using presence-only occurrence data independently. We assess the discrimination capacity and calibration of the models, also examined the omission and commission errors to provide better understanding of the reliability of SDM results. Our results confirm the importance of absences in modelling practices, certainly for geographically widespread species.

6.13 ⚡ Improving species distribution model transferability by incorporating co-occurrence patterns and the fossil record

Diego Nieto-Lugilde[1], Kaitlin C. Maguire[2], Matthew C. Fitzpatrick[1], Jessica L. Blois[2], John W. Williams[3]
[1] Appalachian Laboratory, University of Maryland Center for Environmental Science
[2] School of Natural Sciences, University of California, Merced
[3] Nelson Center for Climatic Research and Department of Geography, University of Wisconsin
Contact: dnieto@al.umces.edu

Two contrasting strategies, among others, have been proposed to improve the reliability of species distribution models (SDMs): 1) the fossil record can be used to calculate a pooled-niche (PN) —the full range of climate conditions in which the species has occurred through time—, approximating the fundamental niche, and 2) community level models (CLMs) can be used to account for co-occurrence patterns (and implicitly biotic interactions), approximating the realized niche. Using observed changes in plant distributions (as recorded in fossil pollen at 500-year intervals from 21 ka BP to the present) in eastern North America and independent paleoclimate simulations, we tested and integrated these ideas by comparing the ability of CLMs and SDMs based on the PN and data at independent time periods to forecast species distributions across time. We also assessed which time periods provide the most distinct information for describing the PN. Models fit with the PN strategy outperformed models fit at independent time periods, however to avoid biasing the models it is important to use only time periods that provide unique information (e.g., the transition between the LGM and the Holocene).

Keywords: Paleoecology, paleobiogeography, pollen, species distribution models, community level models, fundamental niche, realize niche, biotic interactions

6.14 ⚡ From population dynamics to biogeography: a mechanistic model unifying ecological, evolutionary and environmental processes

Juliano Sarmento Cabral[1], Kerstin Wiegand[2], Holger Kreft[1]
[1] Biodiversity, Macroecology and Conservation Biogeography, University of Göttingen
[2] Ecosystem Modeling, University of Göttingen
Contact: jsarmen@uni-goettingen.de

How organisms are distributed in space and time has been of long-standing interest in biogeography and requires considering ecological, evolutionary and environmental drivers. However, disentangling the effects of these drivers remains a challenge. To tackle this, mechanistic models and pattern-oriented modelling can provide powerful insights into theoretical concepts about biodiversity distribution. We present a mechanistic niche-based model for plant species that incorporates key ecological processes at the population level (i.e. metabolic, demographic and interaction constraints) combined with evolutionary processes and environmental dynamics. We applied the model to oceanic islands. From island biogeography, a large theoretical framework is available to validate model results. Emergent population dynamics, species ranges, community composition and biogeographical dynamics proved to be realistic upon contrast with empirical data and theoretical expectations. Additionally, exploratory simulations switching off processes (e.g. speciation) confirmed the necessity of mechanistic complexity to generate realistic patterns at multiple ecological levels.

Keywords: Process-based model, island flora, ecological niche, population dynamics, species ranges, community ecology, species richness, biogeographical rates, speciation, adaptive radiation

6.15 ⚡ Are seasonal niches in migratory birds conservative or divergent? Niche evolution in Nearctic *Oreothlypis* warblers

Darius Stiels[1], Jan O. Engler[2], Kathrin Schidelko[1], Dennis Rödder[3], Dieter Thomas Tietze[4]
[1] Section of Ornithology, Zoological Research Museum Alexander Koenig
[2] Section of Herpetology, Zoological Research Museum Alexander Koenig; Department of Wildlife Sciences, University of Göttingen
[3] Section of Hereptology, Zoological Research Museum Alexander Koenig
[4] Institute of Pharmacy and Molecular Biotechnology, University of Heidelberg
Contact: d.stiels@zfmk.de

In recent years, ecological niche models and phylogenetic analyses have greatly enhanced our understanding of environmental niche evolution. However, for species inhabiting different geographical ranges within their life span, analyses based on correlative models might be more complex. Among such species, migratory birds are a typical example as they are confronted with at least two potentially different environmental conditions in the respective breeding and wintering ranges. Over evolutionary time scales, these seasonal niches might evolve in different directions. To assess whether seasonal niche evolution shifts into more conservative or divergent directions, we study a monophyletic group of six North American wood-warblers within the genus *Oreothlypis* (Parulidae) including breeding birds of high boreal latitudes as well as species which breed in the south-western US and Mexico. In order to get insight into the evolution of seasonal environmental niches, we apply a procedure based on a dated multigene phylogeny in combination with species-specific environmental niche models based on predictors representing (1) seasonal and (2) year-round climate data.

Keywords: ecological niche model, ancestral niches, Maxent, Phyloclim, Parulidae

6.16 ⚡ A global remote sensing-based characterization of terrestrial habitat heterogeneity for biodiversity and ecosystem modeling

Mao-Ning Tuanmu[1], Walter Jetz[1]
[1] Department of Ecology and Evolutionary Biology, Yale University
Contact: mao-ning.tuanmu@yale.edu

Habitat heterogeneity has long been recognized as a key determinant of biodiversity patterns and ecosystem functioning. A lack of global, high-resolution, and temporally updatable heterogeneity information based on direct

habitat measurements hinders our full understanding of diversity-heterogeneity relationships and effective biodiversity conservation. To address this information gap, we developed a suite of global 1-km data layers of habitat heterogeneity based on the textural features of the Enhanced Vegetation Index imagery from the Moderate Resolution Imaging Spectroradiometer. We demonstrate that the newly derived metrics and associated layers successfully and consistently capture fine-grain habitat heterogeneity both among and within land cover types over global extent. They also outperform conventional heterogeneity metrics (derived from topography or categorical land cover data) in modeling two bird community attributes across the conterminous United States. The standardized collection of data supporting this information based on ongoing remote sensing provides an array of different uses, ranging from basic inference to monitoring of biodiversity and ecosystems.

Keywords: heterogeneity–diversity relationship, species richness, functional diversity, image texture, vegetation index, MODIS

6.17 ⚡ Environmental niche trackers and niche adapters revealed through fine scale phenological niche modeling

Matthew H. Van Dam[1], Andrew J. Rominger[1], Michael S. Brewer[1]
[1] Entomology, Zoologische Staatssammlung München, Germany
Contact: matthewhvandam@gmail.com

Phenology, the relationship between biological traits and the climate, is a crucial behavioral trait shared among life on earth. How species adapt their phenologies to climate change is poorly understood, but critical in understanding how species will respond to future change. Here we explore a novel approach for taxa with constrained phenologies to accurately model their environmental niche. We compared the results with WorldClim data that is partitioned by month or quarter to examine what effect using more precise data has on capturing a species environmental niche. We then examine what phylogenetic signal in phenotypic traits and climate tolerances can tell us about how species adapt. The findings show that Bioclim variables fail to capture the real climate space that our focal taxon occupies. Finally, we identify how species adapt to different climate niches through phenological or morphological adaptation using a phylogenetic approach.

Keywords: Environmental niche modeling, niche adaptation, phenology, Maxent, phyloclim, Rhaphiomidas, Daymet, North American Deserts

6.18 letsR: a new R package for data handling and analysis in macroecology

Bruno Vilela[1], Fabricio Villalobos[1]
[1] Departamento de Ecologia, Instituto de Ciências Biológicas, Universidade Federal de Goiás, Goiânia, Goiás, Brazil
Contact: brunovilelasilva@hotmail.com

We present a new R package, ‘letsR’, for handling and analyzing macroecological data, mainly species' geographic distributions and environmental variables, as well as retrieving species' description information and conservation status as provided by the IUCN's RedList database. Our package includes functions to create presence-absence matrices based on species distributions and user-defined grid systems, from which other functions can be applied to generate, for example, species richness rasters, geographical midpoints of species, and species- and site-based attributes. The package can also provide spatial correlograms of variables. As an example, we applied the package’s functions to evaluate if the description year of anuran species globally is related to geographic range sizes or areas with high human activity. The results indicated that both aspects influenced the anurans’ description year, although only 20% of the variance was explained altogether. All data preparation and analyses were made using the functions of ‘letsR’, illustrating its potential for conducting macroecological analyses under a single computer platform, saving time and effort throughout them.

Keywords: Macroecology; Software; Biogeographic data; Spatial analyses; Geographic biodiversity patterns

6.19 ⚡ Comparing single-species, co-occurrence and joint species distribution model predictions for invasive pollinators and plants

Jennifer Weaver[1], George K. Roderick[2]
[1] Berkeley Initiative in Global Change Biology, UC Berkeley, Berkeley, CA, U.S.
[2] Environmental Science, Policy and Management, UC Berkeley, Berkeley, CA, U.S.A.
Contact: jennweaver@berkeley.edu

The field of species distribution modelling has become increasingly complex as models have advanced from modelling single species to incorporating interactions between species within a single model. Here, we compare species distribution models of increasing complexity that specifically incorporate interactions between competing native and invasive pollinator species and their invasive host plant. We utilize generalized linear models and MaxEnt for the basic single-species and co-occurrence models. We then employ joint species distribution models to determine current distributions. Models which incorporate co-occurring species perform better than those that do not. All of these models are calibrated on current environmental variables and then used to predict future species distributions. As a case study, we model the invasive yellow star-thistle (Centaurea solstitialis), native bumble bees (Bombus occidentalis and Bombus vosnesenskii) and invasive honey bee (Apis mellifera) species in North America, where there has been a recent decline in the native bumble bee population.

6.20 ⚡ Variation in species composition explained by spatially autocorrelated environmental variables

David Zelený[1], Li-Wan Chang[2], Chang-Fu Hsieh[3]
[1] Department of Botany and Zoology, Masaryk University, Czech Republic
[2] Technical Service Division, Taiwan Forestry Research Institute, Taiwan
[3] Institute of Ecology and Evolutionary Biology, National Taiwan University, Taiwan
Contact: zeleny@sci.muni.cz

Variation explained by environmental variables in multivariate methods such as constrained ordination is often used to quantify the link between environment and species composition (concept of R^2 and adjusted R^2). In the presence of spatial autocorrelation, explained variation is biased toward higher values (the more the variable is autocorrelated, the more variation it explains). Here, we introduce concept of explained variation adjusted for the effect of spatial autocorrelation. We define it as the amount of variation explained by one or several real spatially autocorrelated variables additionally to the variation explained by the same number of randomly generated variables with the same level of spatial autocorrelation. Using artificial data, we compare performance of several methods generating random variables with certain level of spatial autocorrelation (such as toroidal shift, dual-tree complex wavelet transform). Using vegetation dataset from 25 ha subtropical forest dynamics plot in Taiwan as a case study, we study the relationship between species composition and environmental variables, quantified by explained variation adjusted for the effect of spatial autocorrelation.

Keywords: constrained ordination, forest dynamics plot, R2, random spatially autocorrelation variables

P7 Phylogeography

7.1 ⚡ Spectacular radiation of Mycalesina butterflies in the old world tropics

Kwaku Aduse-Poku[1]
[1] Zoology, University of Cambridge
Contact: ka374@cam.ac.uk

The radiation of the species rich (*ca.* 300 species) butterfly group, mycalesine in the Old World tropics is not only spectacular but also presents an excellent platform for investigation in detail the pattern and processes of adaptive radiation. Using DNA sequences of nine gene regions of over 300 exemplar taxa, we have reconstructed a phylogeny and historical biogeographic hypothesis for the mycalesine butterflies. We identified Asia as the ultimate origin of the subtribe in the early Oligocene (~38 MYA). Africa is believed to have been colonized at least twice by Asian mycalesines between 24-22 MYA. The Mycalesina radiations which responded to or exploited new ecological opportunities, following dispersal into new regions (i.e.*Bicyclus* in Africa, *Heteropsis* in Madagascar and *Mydosama* in Indo-Australia) had been rapid, similar to an early burst of evolutionary diversification. It is interesting all these rapid radiations are dated between 20 and 10 MYA, coinciding with the period of warmer climatic conditions and major grassland expansion in the old world tropics, thereby implicating climate and host plants shifts as a possible drivers of Mycalesina diversification

Keywords: butterflies, Mycalesines, Asia, Africa, Madagascar, radiation, historical biogeography

7.2 ⚡ Phylogeography of two closely related skink species with different climatic niche breadth in Australia

Ana Catarina A. Silva[1], Jason Bragg[2], Sally Potter[2], Dan Rosauer[2], Carlos Fernandes[3], Maria Manuela Coelho[3], Craig Moritz[2]
[1] University of Lisbon and Australian National University
[2] Australian National University
[3] University of Lisbon
Contact: ana.silva@anu.edu.au

Climatically restricted specialists may be more prone to cryptic divergence than widespread species because they are prone to isolation in current and past climates. Using genomic datasets, we explore the phylogeographic patterns of two closely related skink species from northwest Australia: the widespread *Carlia triacantha* and the tropically restricted *C. johnstonei*. We sequenced the ND4 mtDNA gene and applied a customized exon capture system to identify independently evolving lineages. This method generated a high quality phylogenomic dataset (more than 2000 loci) as is needed for coalescent-based analyses of demographic and divergence histories. Initial results identify two new species within *C. triacantha-johnstonei* clade. Importantly, the more climatically restricted species, *C. johnstonei*, shows more cryptic divergence than the widespread *C. triacantha*. Paleoclimate models for *C. jonhstonei* in LGM suggests severe conditions for this species in the Kimberley, indicating that fine topographic effects that may have allowed persistence of this species in different *refugia*.

Our results show how a species' climatic niche breadth translates to survival while enduring climatic change.

Keywords: Carlia johnstonei, Carlia triacantha, Kimberley, exon capture, mtDNA, climatic niche breadth

7.3 ⚡ Phylogeographic patterns in Africa and high resolution delineation of genetic clades in the African lion

Laura Bertola[1], Klaas Vrieling[2], Hans de Iongh[1]
[1] Institute of Environmental Sciences, Leiden University
[2] Institute of Biology, Leiden University
Contact: laura.bertola@gmail.com

Numerous large African savannah mammals show congruent patterns in their taxonomy and phylogeny, in which populations from West/Central Africa are distinct from East/Southern Africa. However, for the lion, all African populations are considered to belong to a single subspecies. The Asiatic lion is constricted to a single population in India. Phylogenetic trees based on data throughout the complete geographic range of the lion show six monophyletic clades. The most basal split makes a distinction between populations from the northern part of the range, including the Asiatic subspecies, and populations from the southern part. Temporal expansion of the African rain forest or the Sahara desert may have led to contractions of populations to local refugia. The results illustrate that the genetic diversity in the lion is greater than the taxonomy implies. The validity of the subspecies status of the Asiatic lion is challenged, due to the nested position of this population in the African clade. Recognizing a northern subspecies, including the Asiatic lion, and a southern subspecies, is more in line with the evolutionary history of the lion, and a revision of the taxonomy is warranted.

Keywords: phylogeography, lion (Panthera leo), Africa, historic climate, savannah mammals

7.4 Combining phylogeny and niche models to unravel the biogeographic history of the shovel-footed squeaker

Gabriela Bittencourt-Silva[1], David Blackburn[2], Michele Menegon[3], Peter Nagel[1], Simon Loader[1]
[1] Department of Biogeography, University of Basel
[2] Herpetology, California Academy of Sciences
[3] Tropical Biodiversity Section, Museo delle Scienze di Trento
Contact: gabrielabitt.ufrrj@gmail.com

The shovel-footed squeaker, *Arthroleptis stenodactylus* Pfeffer 1893, is a small, direct-developing frog that lives in leaf litter. This species occurs from the east African coastal forests of Tanzania and Mozambique to the central African plateau, in Congo and Angola where it can be found in forests, savannah woodlands, thickets and suburban areas. Both its wide geographical distribution and its highly varied habitats are unusual for amphibians. A report in the literature based on mating calls suggests that there are at least two cryptic species, a forest form and a savannah form, and a recent molecular phylogeny of *Arthroleptis* split the six specimens of *A. stenodactylus* that it included into two well-supported clades. We present the first investigation of the phylogeographic history of this 'species'. We used molecular markers to infer relationships among 126 specimens from throughout its range and the Bayesian general mixed Yule-coalescent model to delimit taxonomic units (TU). Additionally, we built ecological niche models for each TU to investigate the degree of niche overlap and further test alternative explanations of current diversity and distribution.

Keywords: Africa; Amphibia; Anura; Arthroleptis; Phylogeography; Distribution

7.5 ⚡ Biogeographic patterns underlying the increasing specialization or loss of symbiotic association between ant and plants

Guillaume Chomicki[1], Susanne Renner
[1] Biology, University of Munich (LMU)
Contact: guillaume.chomicki@gmail.com

Symbioses between ants and plants, where plants provide housing to ants in exchange for defence or trophic payback, involve a mix of obligate and facultative mutualisms. The biogeographic context for the evolution or loss of these mutualisms is poorly understood. We used the largest clade of ant plants, the Hydnophytinae, some 98 species in Australasia associated with four species of *Philidris*, to address the role of spatial barriers in this system. A densely sampled phylogeny of the Hydnophytinae revealed multiple losses of the symbioses, always associated with niche shifts to higher altitudes, outside ants' ranges. We then studied specialization in the Fijian clade, which has seven species, including a species new to science collected by GC. Field ecology and phylogeny reveal a transition from facultative to obligate symbiosis across a North–East gradient in the Fijian archipelago. The transition involves a switch from morphologically unspecialized, non-rewarding plants with low occupancy rates that host three unspecialized ant species to symbioses with a number of co-evolved traits such as entrance holes matching the ant partner's body size, a novel type of food bodies, ant-dispersed seeds, and specialized domatium structure.

Keywords: Symbiosis Mutualism Ant/plant interaction

Continued next page

7.6 ⚡ The Mediterranean peninsulas and central Asia were both post-glacial colonization sources for the widespread European species of water beetles

David Garcia Vazquez[1], Ignacio Ribera Galan[1]
[1] Institute of Evolutionary Biology (IBE-CSIC)
Contact: deivizzz@hotmail.com

In this work we study the temporal and geographic origin of some central and northern European diving beetles of the genera *Deronectes*, *Platambus*, *Oreodytes* and *Hydraena* to understand the effect of Pleistocene glaciations in their diversification. All of them include both widespread European and narrowly distributed species, usually in southern peninsulas and islands. We used probabilistic methods with molecular data of six different genes (four mitochondrial and two nuclear) to produce calibrated phylogenies/phylogeographies, which were used to estimate the geographic origin of the species and populations. According to our results, in the genus *Hydraena* a recent range expansion from the Iberian Peninsula resulted in the widespread *H. gracilis*, genetically homogeneous through its range. Of the four species groups of *Deronectes* with widespread European species, Turkey was the origin of the *D. latus* group, the Balkans of the *D. platynotus* group, the Iberian Peninsula of the *D. aubei* group and the area between Iberian Peninsula, Maghreb and Corsica and Sardinia of the *D. moestus* group. Preliminary results suggest an eastern, Asiatic origin for the species of *Platambus* and *Oreodytes*.

7.7 A phylogeographic synthesis for Sub-Saharan Africa

Paolo Gratton[1], Gaelle Bocksberger[1], Hjalmar Kuehl[1]
[1] Primatology, Max Planck Institute for Evolutionary Anthropology
Contact: paolo_gratton@eva.mpg.de

The Afrotropical region hosted the evolution of hominins, harbours the last remains of the mammalian megafauna and presents some of the most significant challenges for biodiversity conservation. Retraction of organisms ranges as a response to Pleistocene climate cycles (refugia model) is regarded as a main determinant of the current distribution of African biodiversity, and a precise knowledge of the refugial history of African biomes is essential to understand the evolution of humans and their closest relatives. However, a statistical analysis of how much the available phylogeographic data support the existence of biome-level refugia is still lacking. As a part of the wide-scope PanAf project, we are systematically bringing together published DNA sequence data for African terrestrial vertebrates and we are integrating the relevant geodata in order to: i) produce a continental-scale map of genetic diversity in Sub-Saharan Africa; ii) statistically evaluate the spatial clustering of phylogeographic patterns to identify biome-level refugia; iii) build up a consistent data-set of phylogeographic information that will help testing a diverese set of biogeographic hypotheses.
Keywords: Phylogeography, Refugia, Africa, Biodiversity, Pleistocene

7.8 ⚡ Distribution models and a dated phylogeny for the Louisiana irises

Jennafer Hamlin[1], Tyler Simmonds[1], Michael Arnold[1]
[1] Genetics, University of Georgia
Contact: jhamlin@uga.edu

Spatial and temporal environmental variation influences evolutionary processes such as genetic divergence among populations and speciation. Furthermore, solving relationships of recently diverged taxa, poses a challenge due to shared polymorphisms and potentially weak reproductive barriers. Multiple lines of evidence are needed to identify independently evolving lineages and clarify the impact of ecology on speciation within those lineages. Here, we seek to address what role ecology played in the speciation of the Louisiana irises as well as understanding the timing of divergence within these species. We combined chloroplast and nuclear markers with environmental information to clarify relationships and ecological niches of the Louisiana iris species complex. A species phylogeny was constructed for the Louisiana irises using *BEAST. Species DistributionModels were constructed for present day distributions, in order to better understand environmental factors, which contribute to species divergence. Furthermore, ecological niches were compared to test how significant ecological divergence is among species.
Keywords: Divergence dating, Louisiana irises, southeastern United States, species distribution models

7.9 ⚡ Holocene re-colonisation, central-marginal-distribution and habitat specialisation shape population genetic patterns within an Atlantic European grass species

David Harter[1], Anke Jentsch[2], Walter Durka[3]
[1] Department of Biogeography, BayCEER, University of Bayreuth
[2] Department of Disturbance Ecology, BayCEER, University of Bayreuth
[3] Department of Community Ecology, Helmholtz-Centre for Environmental Research UFZ
Contact: david.harter@uni-bayreuth.de

Corynephorus canescens is a short-lived grass species, specialised on scattered and disturbance-dependent sandy habitats. Its distribution includes Atlantic regions of Western and Central Europe, but not the two other classical European glacial refuge regions (Appenine and Balkan Peninsulas). Decreasing genetic diversity from SW to NE and distinct gene pool clustering (AFLP variation among 49 populations) imply glacial refugia on the Iberian Peninsula and in western France and post-glacial range expansion towards NE Europe. High genetic diversity within and moderate differentiation among populations, and a significant isolation-by-distance pattern indicate a gene flow-drift-equilibrium within *C. canescens*, probably due to its restriction to scattered and dynamic habitats and limited dispersal distances. These features and the re-colonisation history significantly affected genetic diversity gradients from central to marginal populations, emphasizing the need for including the specific ecology and species histories into such analyses. To account for discontinuous distributions, new indices of marginality were tested for their suitability for studies of centre-periphery gradients.
Keywords: abundance-centre hypothesis, degree of peripherality, metapopulation dynamics, phylogeography, Poaceae, psammophyte pioneer species

7.10 The British-Irish Ice Sheet at the end of the LGM: Tabula rasa? Perhaps not

Emma Howard-Williams[1], Xiao-Dong Dang[2], Colin Kelleher[2], Pablo Vargas[3], Kevin Walker[4], Conor Meade[1]
[1] Biology, Maynooth University, Ireland
[2] National Botanic Gardens, Glasnevin, Dublin 9, Ireland
[3] Real Jardín Botánico de Madrid, Spain
[4] Botanical Society of Britain and Ireland, UK
Contact: conor.v.meade@nuim.ie

Glacial models infer the existence of total ice-sheet cover in Ireland and northern Britain at the height of the LGM c. 20,000 years bp, precluding the existence of dry-land refugia, and affirming postglacial immigration as the sole driver of new ecosystem assembly. Here we present phylogeographic analysis of two disjunct arctic-alpine species (*Arenaria ciliata* and *A. norvegica*) with known ecological tolerance for Ice-age conditions, and find strong evidence for in-situ refugial survival in Ireland through the Pleistocene-Holocene transition. Bayesian MRCA, Population Mismatch Analysis and SAMOVA all infer that Holocene genetic identities arose via multiple haplotype lineage expansion events in the European metapopulation during the late Pleistocene. Stronger geographic structuring in the nuclear genetic signal suggests subsequent pollen-mediated homogenization among disparate immigrant types. Population groups may have been isolated more than once during this period in Northwestern Europe, implying the possible existence of mobile eco-climatic refugia that skirted the margins of constantly changing ice-sheets until the beginning of climate amelioration in the early Holocene.
Keywords: High Resolution Melting Analysis; AFLP; DNA; Angiosperm; Phylogeography

7.11 ⚡ Museum archives revisited: Biogeographic discoveries in brain-teasing high elevation *Hyles* (Lepidoptera: Sphingidae)

Anna K. Hundsdoerfer[1], Martin Päckert[1], Christian Kehlmaier[1], Ian J. Kitching[2]
[1] Museum of Zoology, DNA-laboratory, Senckenberg Dresden, Germany
[2] Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, U.K.
Contact: anna.hundsdoerfer@senckenberg.de

Species sampling in the hawkmoth genus *Hyles* (~ 30 species) has been increased to over 80% allowing cladistic biogeographic ancestral state analyses. With the assumption of colonisation routes via Fiji and Antarctica, *Hyles* is

corroborated as being of Neotropical origin, radiating to North America, Madagascar and Australia. The ancestral range of the Palaearctic species remains equivocal. Ancient DNA techniques were implemented for three mitochondrial gene sequences and applied to museum specimens (including holo- and paratypes) of three high elevation *Hyles* species to elucidate their much debated phylogenetic relationships. The Afghan endemic, *Hyles salangensis*, is only known from 15 males caught in the 1960s. The species status of the Nepal endemic *Hyles renneri* is corroborated and its known distribution extended by over a thousand kilometres eastwards. Sequences of *H. nepalensis* indicate no genetic differentiation between specimens from Nepal and low elevation Palaearctic *H. gallii*. Surprisingly samples from the NW-Himalaya are recovered in a monophyletic group that also includes samples from North America. This complex biogeographical history requires further study.

Keywords: cladistic biogeographic ancestral state analyses, phylogeny, moths, aDNA, Central Asia, taxonomy.

7.12 ⚡ Implications of phylogeography and population genetics for the taxonomy of grass snakes (*Natrix natrix*)

Carolin Kindler[1], Wolfgang Böhme[2], Claudia Corti[3], Václav Gvoždík[4], Daniel Jablonski[5], David Jandzik[5], Margarita Metallinou[6], Pavel Široký[7], Uwe Fritz[1]
[1] Phylogeography, Museum of Zoology, Senckenberg Dresden
[2] Zoologisches Forschungsinstitut und Museum Alexander Koenig
[3] Museo di Storia Naturale dell'Università di Firenze
[4] National Museum Prague
[5] Comenius University Bratislava
[6] Institut de Biologia Evolutiva, Barcelona
[7] University of Veterinary and Pharmaceutical Sciences, Brno
Contact: carolin.kindler@senckenberg.de

Grass snakes (*Natrix natrix*) represent one of the most widely distributed snake species of the Palaearctic region. Within *N. natrix*, up to 14 distinct subspecies are regarded as valid. In addition, some authors recognize big-headed grass snakes from western Transcaucasia as a distinct species, *N. megalocephala*. Based on phylogenetic analyses of a 1984-bp-long alignment of mtDNA sequences (cyt b, ND4+tRNAs) of 410 grass snakes, a nearly range-wide phylogeography is presented for both species. Within *N. natrix*, 16 terminal mitochondrial clades were identified, most of which conflict with morphologically defined subspecies. Hypotheses regarding glacial refugia and postglacial range expansions are presented. In Central Europe, there are two contact zones of three distinct mitochondrial clades, one of these contact zones was theretofore completely unknown. In agreement with previous studies using morphological characters and allozymes, there is no evidence for the distinctiveness of *N. megalocephala*. Therefore, *N. megalocephala* is synonymized with *N. natrix*. In addition, first preliminary results of 14 tested microsatellite loci are presented as an outlook on future work.

Keywords: Reptilia, grass snake, taxonomy, species delimitation, phylogeography

7.13 Performance of steppe plants in Central Europe – a comparative analysis of four steppe species based on fruit set and germination data

Matthias Kropf[1], Katharina Bardy[1], Kristina Plenk[1]
[1] Institut für Integrative Naturschutzforschung, Universität für Bodenkultur Vienna, Austria
Contact: matthias.kropf@boku.ac.at

A transect towards the (north-)westernmost distribution limit of rare and endangered Central European steppe species was not only used for studying genetic structure and diversity patterns at the absolute periphery of the species' distributions (see respective contribution by Kristina Plenk), but also for analyses of plant performance in the field and germination success. We hypothesised decreased performance values and lower germination rates, i.e. reduced overall fitness, towards the absolute distribution limit within our core project taxa *Carex supina* (Cyperaceae), *Inula germanica* (Asteraceae), *Oxytropis pilosa* (Fabaceae), and *Poa badensis* (Poaceae) based on four representative populations within each of the three study regions (i.e. Central Hungary, Eastern Austria, Western Germany). To a small extent, the results show expected patterns in fruit set, weight of fruits, and germination (rates). But in general, most findings are more species-specific, and notably, strongly influenced by species' ability for vegetative propagation as well as by varying population sizes.

Keywords: steppe species, range edge, phylogeography, plant performance, germination, relict populations

7.14 Genetic variation reveals large-scale population expansion and migration during the expansion of Bantu-speaking peoples

Sen Li[1], Carina Schlebusch[2], Mattias Jakobsson[3]
[1] Natural History Museum of Denmark, University of Copenhagen
[2] Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University
[3] Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University & Science for Life Laboratory
Contact: sen.li@snm.ku.dk

The current distribution of Bantu-speaking populations (sub-Saharan Africans) has been found to largely be a consequence of the movement of people rather than a diffusion of language alone. We re-analysed microsatellite markers typed for large number of African populations that capture signatures of recent population history. We confirm the spread of west African people and estimated the expansion of Bantu-speaking groups, using a Bayesian approach, to around 5600 years ago. We tested four different divergence models for Bantu-speaking populations with a distribution comprising three geographical regions in Africa. We found the most likely model for the movement of the eastern branch involves migration of Bantu-speaking groups to the east followed by migration to the south. This model, however, is only marginally more likely than other models, which might indicate direct movement from the west and/or significant gene flow with the western branch. Our study use multi-loci genetic data to explicitly investigate the timing and mode of the Bantu expansion and it demonstrates that west African groups rapidly expanded both in numbers and over a large geographical area.

Keywords: Africa Approximate Bayesian computation Bantu-speakers Migration Population expansion

7.15 ⚡ Going West – a subtropical lineage (*Vincetoxicum*, Apocynaceae: Asclepiadoideae) expanding into Europe

Sigrid Liede-Schumann[1], Riwana Khanum[2], Abdul Samed Mumtaz[2], Iulian Ghergel[3], Amirhossein Pahlevani[4]
[1] Dept. of Plant Systematics, University of Bayreuth
[2] Pakistan Museum of Natural History, Islamabad
[3] Department of Zoology, Oklahoma State University
[4] Department of Botany, Iranian Research Institute of Plant Protection
Contact: sigrid.liede@uni-bayreuth.de

Using a dataset of combined nuclear and cpDNA sequences, the phylogeny of *Vincetoxicum* sensu lato was investigated with Bayesian and Maximum Likelihood tools. Using S-DIVA, the biogeographical history of the genus was explored and ecological niche modelling using Maxent was conducted on selected subclades. *Vincetoxicum* is a tropical lineage comprising two clades that have reached high latitudes. One of the temperate clades is restricted to the Far East, the other one extends into Europe along the Asian mountains. The latter clade includes the native *V. hirundinarium* as well as *V. rossicum* and *V. nigrum*, both invasive in North America. Capacity for autogamy and the possession of phenanthroindolizidine alkaloids is restricted to this clade and its subtropical sister clade. Climatic niche modelling revealed different climatic preferences of the nine species sampled, except for the common exposure to at least one month of subfreezing temperatures. We hypothesize that the adaptation to cold climates in combination with the possession of toxic alkaloids and the capacity for autogamy is linked to the successful colonization of Europe and for the invasive potential of several species.

Keywords: Apocynaceae, Asclepiadoideae, Biogeography, Climatic Niches, Invasive species, Maxent, Molecular phylogeny, Subzero temperatures, Tylophora, Vincetoxicum

7.16 ⚡ Climate change, phylogeography and the future of genetic diversity

Katharine Marske[1], Mirnesa Rizvanovic[1]
[1] Center for Macroecology, Evolution and Climate, Natural History Museum of Denmark
Contact: kamarske@snm.ku.dk

One potential response of species to climate change is to shift their distributions. Species distribution models have thus emerged as an important scientific and conservation tool, but deploying these models at the species level may fail to detect important intraspecific variation related to local environmental adaptation or that will provide the raw materials for future evolution. We estimated how much existing genetic diversity is likely to remain by the end of this century, and

which aspects of a species' phylogeographic history this represents, for New Zealand forest beetles under different climate change scenarios. Each species' phylogeny was pruned to include just those haplotypes currently present in areas predicted by ecological niche models to remain climatically suitable. Trees resulting from these future haplotype pools were compared against a series of random draws from the full haplotype pool to determine whether genetic diversity will be lost in a random or nonrandom fashion. This provides the opportunity to calculate not just projected loss of genetic diversity, but the extent to which this loss obscures a species' evolutionary history.
Keywords: Phylogeography Species distribution models

7.17 ⚡ Phylogeography and evolution of the Australian marsupial genus Antechinus

Thomas Mutton[1], Andrew Baker[1], Susan Fuller[1]
[1] Queensland University of Technology
Contact: thomas.mutton@connect.qut.edu.au

The marsupial genus *Antechinus*, like many mammalian fauna, has a chequered taxonomic history, with multiple revisions occurring since its establishment by Macleay in 1841. Today, generic placement of *Antechinus* within the Family Dasyuridae is well-resolved, thanks to several genetic studies over recent decades that included nominal representation of most species. Building on this foundational work, we aimed to provide the first detailed molecular systematic and phylogeographic study across the entire geographic range of all recognised species in the genus, which collectively encompass thousands of kilometers across the length and breadth of Australia. Our work led to the discovery of multiple new species of *Antechinus*, representing a 50% increase in known diversity, and a clearer understanding of the phylogeographic factors which may over time have influenced evolution in this genus.
Keywords: Phylogeography, Molecular Systematics, Mammal, Australia, Antechinus

7.18 Biogeographic and phylogenetic analysis of the tree fern family Dicksoniaceae (Cyatheales)

Sarah Noben[1], Anna Weigand[1], Michael Krug[2], Michael Kessler[1], Dietmar Quandt[2], Marcus Lehnert[2]
[1] Systematic Botany, University of Zurich
[2] Nees Institute for Biodiversity of Plants, University of Bonn
Contact: sarah.noben@uzh.ch

Tree ferns of the family Dicksoniaceae (Cyatheales) are among the most impressing ferns in forests of the southern hemisphere. Although this genus has attracted a huge interest because of its primitive appearance, old age and relict distribution, it has never been in the focus of an exhaustive phylogenetic, taxonomic and biogeographic analysis. Thus we performed a global phylogenetic study of all morphologically distinguishable taxa to clarify species limits, to outline character evolution and to investigate species migration patterns, with the scope to better understand the evolution of this genus. Our results using four non-coding plastid markers (*rpl16, trnL-F, trnG-R* & *matK*) support the monophyly of the Dicksoniaceae as well as the morphologically recognized genera *Dicksonia, Lophosoria* and *Calochlaena*. The genus *Lophosoria* is sister to *Dicksonia*; together forming the sister group to *Calochlaena*. Within *Dicksonia* three monophyletic groups of 38-12 Ma in age can be recognized: A "Pacific" clade, an "Antarctic" clade and a "Palaeotropic" clade. It is likely that the current distribution of these groups reflect their origin on the former continent Gondwana followed by vicariance.

7.19 ⚡ Genetic variation of steppe plants in Central Europe – a comparative analysis of four steppe species based on AFLPs and cpDNA sequence data

Kristina Plenk[1], Katharina Bardy[1], Maria Höhn[2], Mike Thiv[3], Matthias Kropf[1]
[1] Institute for Integrative Nature Conservation Research, University of Natural Resources and Life Sciences, Vienna
[2] Faculty of Horticultural Science, Corvinus University of Budapest, Hungary
[3] Botany Department, Stuttgart State Museum of Natural History, Germany
Contact: kristina.plenk@boku.ac.at

A transect towards the (north-)westernmost distribution limit of rare and endangered Central European steppe species was used to study genetic structure and diversity patterns at the absolute periphery of species' distributions. All study species show a more wide-spread continuous occurrence in the Pannonian Basin (Hungary), compared to the western range edge of their continuous distribution range (Eastern Austria) and the (north-)westernmost isolated exclave in western Germany (mainly Rhineland-Palatinate). We assumed an increasing population differentiation and a decreasing within population diversity towards the (north-)westernmost absolute distribution limit. AFLP-fingerprints and cpDNA sequence analyses were carried out for our core project taxa *Carex supina* (Cyperaceae), *Oxytropis pilosa* (Fabaceae) and *Poa badensis* (Poaceae), and additionally, for *Linum flavum* (Linaceae) based on four representative populations per study region and species. The results partially show the expected patterns, but generally the findings are more species-specific. Nonetheless, the outcomes provide some evidence for the relict status of the populations in western Germany.

Keywords: steppe species, range edge, phylogeography, genetic diversity, relict populations

7.20 Investigating the phylogeography and population structure of *Podarcis tauricus* group

Nikolaos Psonis[1], Aglaia Antoniou[3], Oleg V. Kukushkin[4], Boyan Petrov[5], Jelca Crnobrnja - Isailović[6,7], Iulian Gherghel[8], Daniel Jablonski[9], Petros Lymberakis[1], Nikos Poulakakis[2]
[1] Natural History Museum of Crete, University of Crete, Irakleio, Greece
[2] Department of Biology, University of Crete, Irakleio, Greece
[3] Institute of Marine Biology and Genetics & Aquaculture, Hellenic Center for Marine Research, Irakleio, Greece
[4] Karadagh Nature Reserve of Ukrainian National Academy of Sciences, Republic of the Crimea, Ukraine
[5] National Museum of Natural History, Sofia, Bulgaria
[6] Department of Biology and Ecology, Faculty of Sciences and Mathematics, University of Niš, Serbia
[7] Department of Evolutionary Biology, Institute for Biological Research "Siniša Stanković", Beograd, Serbia
[8] Department of Zoology, Oklahoma State University, Stillwater, USA
[9] Department of Zoology, Faculty of Natural Sciences Comenius University, Bratislava, Slovakia
Contact: nikos.psonis@gmail.com

Wall lizards of the genus *Podarcis* comprise 21 currently recognized species in southern Europe. In the Balkans *Podarcis* are divided in two subgroups: the subgroup of *P. tauricus* and the subgroup of *P. erhardii*. Here, we explored the evolutionary history of *tauricu*s group by employing phylogenetic and phylogeographic approaches and using both mitochondrial and nuclear markers. The phylogenetic relationships and the genetic distances retrieved, supported the monophyly of *Podarcis tauricus* group and suggest that *P. gaigeae, P. milensis* and *P. tauricus* form a clade, which thereinafter connects to *P. melisellensis*. However, *P. tauricus* is subdivided into two major lineages that are phylogenetically and geographically distinct, leaving insinuations whether it is a single species or a species complex. The phylogeographical scenario suggests that the present distribution of this group was determined by a combination of dispersal and vicariance events in the Balkan Peninsula dating back to Miocene and continuing up to Pleistocene. Thus, our data stress the need for a reconsideration of the evolutionary history of *Podarcis taurícus* group.

Keywords: dispersal, microsatellites, mtDNA,nuDNA, vicariance

7.21 ⚡ Deep and wide valleys drive nested phylogeographic impacts across an entire montane bird community

V.V. Robin[1], C.K Vishnudas[1], Pooja Gupta[1], Uma Ramakrishnan[1]
[1] National Centre for Biological Science
Contact: robinvijayan@gmail.com

Montane species distributions interrupted by valleys can lead to range fragmentation, differentiation and speciation. Paleoclimatic fluctuations may accentuate or reduce such diversification and may affect species differentially. We used genetic data from 24 species to examine how an entire montane bird community responds to topographic (and habitat) valleys in the Western Ghats. We examined if species reveal spatial concordance in population differentiation, and whether the timing of these divergences correlate with climatic events. Our results reveal a nested effect of valleys, with several species (10) demonstrating the oldest divergence associated with the widest and deepest valley in the mountain range, the Palghat Gap. A subset of these 10 species revealed younger divergences across shallower, narrower valleys. Divergence times for most valley-affected montane birds dated to the Pleistocene, highlighting the role of climatic fluctuations in driving species evolution. We also explore species traits that correlate with genetic divergence. Studying the entire community allowed us to uncover a range of species responses, some generalizable and other unpredicted patterns.

Keywords: sky islands, montane, bird, Western Ghats, paleo-climate

7.22 Repeatability of patterns of hybridization after post-glacial contact of *Myodes rutilus* and *M. gapperi*

Amy Runck[1], Marjorie Matocq[2], Joseph Cook[3]
[1] Biology Department, Winona State University, Winona, Minnesota
[2] Department Of Natural Resources and Environmental Science, University of Nevada, Reno, Nevada
[3] Biology Department and Museum of Southwestern Biology, University of New Mexico, Albuquerque, New Mexico
Contact: arunck@winona.edu

A post-glacial contact zone between northern red-backed voles (*Myodes rutilus*) and southern red-backed voles (*M. gapperi*) extends across Alaska and Canada. Three diagnostic characters (nuclear intron, cytochrome *b* gene, and morphology) were examined from latitudinal transects in southeast Alaska (SE), British Columbia (BC), and Northwest Territories (NT) to determine the timing of contact and to test for concordance of hybridization patterns. Voles were genotyped to test for contemporary gene flow among the parental species and hybrids. Because deglaciation occurred at distinct times in each transect, different stages of the hybridization process are revealed. Timing of expansion was estimated through coalescent and cline analyses. The two oldest transects, BC and SE, converged on a similar stable introgressant. In contrast, the NT transect had a variety of mixed ancestry backcrosses that may be due to recent contact in this transect and we hypothesize that a favorable recombinant type should eventually emerge in this younger point of contact. Alternatively, differences we document across these transects may be related to differential environmental selective pressures.

7.23 Correlates of gene flow in terrestrial and marine environments

Lauren M. Schiebelhut[1], Michael N Dawson[1]
[1] University of California, Merced
Contact: lschiebelhut@ucmerced.edu

Theory predicts that differences in phylogeographic structure between species should be caused by differences in life-history, environment, and evolutionary time. Contrasts of life-history traits and gene flow between synchronously diverging co-distributed (SDC) taxa control for effects of environment and time, offering opportunity to test whether traits favoring greater dispersal potential lead to higher gene flow. To explore the generality of this prediction we did a meta-analysis using pairs of SDC taxa in marine and terrestrial settings. We tested whether increased gene flow is proportional to traits including fecundity (F), census population size (N_c), and others linked to dispersal. In both terrestrial and marine settings we find a strong relationship between gene flow and F, N_c, and other dispersal-linked traits. SDC taxa with similar dispersal potential show similar gene flow, and those with higher dispersal potential have higher gene flow, consistent with predictions. While we recognize many factors influence population genetic structure, contrasts in gene flow can be explained largely by contrasts in F, N_c, other dispersal-linked traits and/or their co-correlates.

Keywords: FST

7.24 The role of ecogeographic isolation in the diversification of alpine *Androsace* (Primulaceae)

Gerald M. Schneeweiss[1], Peter Schönswetter[2]
[1] Botany and Biodiversity Research, University of Vienna
[2] Botany, University of Innsbruck
Contact: gerald.schneeweiss@univie.ac.at

Alpine habitats, i.e., habitats above the tree-line, are biodiversity hotspots. This renders alpine organisms well suited systems to study biogeographic and ecological aspects of diversification and speciation. A model group for diversification in the central and southern European mountain system is the *Aretia* clade of *Androsace* (Primulaceae). Although its species can readily hybridize, they are generally reproductively isolated via non-overlapping distribution areas and/or distinct habitat preferences, suggesting that ecogeographic isolation is the main force behind speciation in this group. Little is, however, known about the relative importance of geographic differentiation versus ecological (habitat) differentiation. Here, we test the hypothesis that habitat differentiation will be more frequent in cases of sympatric speciation (i.e., speciation within the same discrete geographic region) than in cases of allopatric speciation. To this end, we use a time-calibrated species phylogeny of the *Aretia* clade derived from plastid sequence data and employ a dispersal-extinction-cladogenesis model of habitat and geographic evolution allowing for founder-event speciation.

Keywords: Alpine plants; ecogeographic differentiation; sympatry; allopatry; Dispersal-Extinction-Cladogenesis Analysis

7.25 ⚡ Spatiotemporal diversification of Balkan biota

Peter Schönswetter[1], Bozo Frajman[1]
[1] Institute of Botany, University of Innsbruck
Contact: peter.schoenswetter@uibk.ac.at

Due to strong spatial heterogeneity and limited Pleistocene glaciation, the Balkan Peninsula is a major European biodiversity hotspot. Surprisingly little, however, is known about patterns and processes of intraspecific diversification. My contribution will summarise unpublished and published phylogeographic work on plants and animals of both, Balkan endemics or more widespread, southern European biota in order to attempt a first review of the emergent patterns of spatiotemporal diversification. Although examples will cover all altitudinal life zones, I will focus on the hitherto largely neglected high altitude species. Alongside the intra-peninsular patterns, I will also explore connections between the Balkans and adjacent areas, such as the Carpathians and the Apennine Peninsula. Evidently, the topographically highly complex and during the last glacial maximum only locally glaciated Balkan Peninsula is not only a hotspot of species richness and endemism but also a sanctuary of intraspecific genetic diversity, even if the underlying causes remain insufficiently understood.

Keywords: phylogeography; Balkan Peninsula; Pleistocene refugium; barriers; long-distance dispersal

7.26 Connecting environmental, genetic and geographical distances: A case study of maritime pine

M.J. Serra Varela[1], D. Grivet[2], L. Vincenot[2], O. Broennimann[3], J. Gonzalo-Jiménez[1], N.E. Zimmerman[4]
[1] University of Valladolid, Department of Plant Production and Forest Resources, Palencia, Spain
[2] INIA, Forest Research Centre, Department of Forest Ecology and Genetics, Madrid, Spain
[3] University of Lausanne, Department of Ecology and Evolution, Lausanne
[4] Landscape Dynamics, Swiss Federal Research Institute WSL, Birmensdorf, Switzerland
Contact: majes85@hotmail.com

Phylogenetics combined with Species Distribution Models (SDMs) provide insights into species´ histories on one hand and the possibility to model environmental requirements in a spatially explicit framework on the other. Thereby, they enable to better understand past populations´ dynamics which can be a fundamental tool to guide conservation agenda in the face of climate change. Here, we combined both tools to provide with a novel approach to test for the influence of environment in modeling genetic structure patterns using *Pinus pinaster* Ait as a model species. We analyzed separately genetic and climatic niche distances among the eight clades of *P. pinaster* and obtained consistent results from both. Although the major phylogenetic pattern of maritime pine can be explained by its demographic history, our results support that local environmental adaptation also played an important role in shaping its lower order phylogeographic distribution patterns. We also compared niche overlap among clades revealing a large niche differentiation thus pointing to niche dynamism. Finally, this work enabled us to show an improvement in the predictions of SDMs when including molecular information.

Keywords: Species distribution model (SDM), niche conservatism, climate change, conservation, infraspecies, genetics

7.27 ⚡ Cryptic diversification on widespread species in Madagascar

Lynika Strozier[1], Sushma Reddy[1], Steve Goodman[2], Marie Jeanne Raherilalao[3]
[1] Loyola University Chicago
[2] The Field Museum of Natural History,Association Vahatra, Madagascar
[3] Association Vahatra, Madagascar
Contact: lstrozier@luc.edu

Madagascar is known for its rich biodiversity and high level of endemic species that are found nowhere else. Despite the overall species diversity, there are fewer bird species than one would predict on Madagascar given the size of the island. Cryptic diversification, when genetically distinct species are hard to detect because they are morphologically undifferentiated, has been hypothesized to occur in some groups on Madagascar. Currently it is unclear to what extent this occurs in birds because only a few studies have been conducted. This study aims to understand the phylogenetic and phylogeographic patterns within members of a Madagascar endemic songbird genus, *Newtonia*. We conducted a phylogenetic analysis using multiple molecular markers in order to examine the evolutionary

relationships and diversification patterns among these species. We further examined phylogeographic structure within two widespread species to assess the potential for cryptic species. Preliminary evidence shows substantial genetic differentiation both within and among species of *Newtonia*. We conducted additional analyses to determine whether distinct lineages are associated with habitat type or geographic area.

7.28 Biogeography of the genus *Acanthodactylus* Fitzinger, 1834

Karin Tamar[1], Salvador Carranza[2], Roberto Sindaco[3], Jiří Moravec[4], Jean-François Trape[5], Shai Meiri[1]
[1] Department of Zoology, Tel Aviv University
[2] Institute of Evolutionary Biology (CSIC-UPF), Barcelona, Spain
[3] Museo Civico de Storia Naturale, Carmagnola, Italy
[4] Department of Zoology, National Museum, Prague 9, Czech Republic
[5] Laboratoire de paludologie et zoologie médicale, Institut de Recherche pour le Développement, Dakar, Senegal
Contact: karintmr@gmail.com

Acanthodactylus lizards are among the most diverse, abundant and widespread reptiles in the arid areas of northern Africa to southwest Asia. It is the most species rich genus in the family Lacertidae, currently with over 40 recognized species. We sampled 302 individuals representing 36 species and most subspecies from across the distributional range of the genus. We sequenced all specimens for two mitochondrial (12S, Cytb) and three nuclear (MC1R, ACM4, c-*mos*) markers, reconstructing the first large scale calibrated molecular phylogeny of *Acanthodactylus* to gain insights into its historical biogeography. The onset of *Acanthodactylus* cladogenesis is estimated to have occurred due to vicariance and dispersal processes with the separation into three clades: the Western and the *scutellatus* clades mostly distributed in northern Africa, and the Eastern clade from the Middle-East, Arabia and southwestern Asia. Most *Acanthodactylus* species diverged during the Miocene corresponding to regional tectonic movements and climate change.

Keywords: Acanthodactylus, Reptiles, Biogeography, Phylogeny, Diversification

7.29 ⚡ Differences in gene flow in a twofold secondary contact zone of pond turtles in southern Italy (Testudines: Emydidae: *Emys orbicularis galloitalica*, *E. o. hellenica*, *E. trinacris*)

Melita Vamberger[1], Heiko Stuckas[1], Francesco Sacco[2], Stefania D'Angelo[3], Marco Arculeo[2], Marc Cheylan[4], Claudia Corti[5], Federico Marrone[2], Michael Wink[6], Uwe Fritz[1]
[1] Pyhlogeography, Senckenberg Dresden
[2] Dipartimento di Scienze e Tecnologie Biologiche
[3] WWF Nature Reserve 'Lago Preola e Gorghi Tondi'
[4] Centre d'Ecologie Fonctionnelle & Evolutive (CNRS)
[5] Museo di Storia Naturale dell'Università di Firenze
[6] Universität Heidelberg
Contact: melita.vamberger@senckenberg.de

Using virtually range-wide sampling for three pond turtle taxa (*Emys orbicularis galloitalica*, *E. o. hellenica*, *E. trinacris*), we analyse gene flow across the southern Italian contact zone, where the ranges of all three taxa abut. Based on population genetic analyses of 15 highly polymorphic microsatellite loci and a mitochondrial marker, we show that the general genetic pattern matches well with the current taxon delimitation. Cline analyses reveal that the major genetic break between *E. o. galloitalica* and *E. o. hellenica* corresponds well with the currently accepted intergradation zone in southern Italy. However, introgression is largely unidirectional from *E. o. galloitalica* into *E. o. hellenica*. Gene flow between *E. orbicularis* and *E. trinacris* is negligible, with the Strait of Messina matching well with the narrow cline centre between the two species. The differences between the two taxon-pairs *E. orbicularis/E. trinacris* and *E. o. galloitalica/E. o. hellenica* support their current taxonomic classification and make them attractive objects for follow-up studies to elucidate the underlying mechanisms of speciation by comparing their properties.

7.30 ⚡ How to survive past climate changes - lessons from *Lyciasalamandra*

Michael Veith[1], Sarah Kieren[1], Bayram Göçmen[2], Konstantinos Sotiropoulos[3], Stefan Lötters[1]
[1] Department of Biogeography, Trier University
[2] Zoology Section, Biology Department, Ege University Izmir, Turkey
[3] Department of Biological Applications and Technologies University of Ioannina Greece
Contact: veith@uni-trier.de

The ten species of the viviparous salamander genus *Lyciasalamandra* are endemic to the Taurus Mountains and to some Aegean island. We reconstruct the range histories of all species using genetic data and species distribution modelling. A phylogenetic analysis (five mitochondrial genes, 4,500 bp) set a temporal framework of species evolution. Seven lineages evolved almost synchronously at Messinian times ca. 5.5 mya, with some of them showing a significant substructuring, presumably triggered by Quaternary climatic alterations. Within species, population genetic and phylogeographic patterns (based on two mtDNA markers, 1,000 bp) indicate repeated range expansions and contractions. Species distribution models using paleoclimatic data of the Eastern Mediterranean indicate that during periods of cold climate, suitable conditions for the species were met at low elevations, from where higher elevations could be re-colonised during warmer periods. Hence, *Lyciasalamandra* serves as a model for long-term survival of a highly specialised amphibian almost on the spot, with repeated small-scale range shifts allowing to survive periods of unfavourable climatic conditions.

Keywords: Phylogeography, species distribution modelling, paleoclimate, molecular clock, range shift

7.31 ⚡ Phylogeography and speciation of the brown algal genus *Lobophora* (Dictyotales, Phaeophyceae)

Christophe Vieira[1], Olga Camacho[2], Zhongmin Sun[3], Suzanne Fredericq[2], Claude Payri[1], Olivier De Clerck[4]
[1] U227 “Biocomplexité des écosystèmes coralliens”, Institut de Recherche pour le Développement, Nouvelle-Calédonie, France
[2] Department of Biology, University of Louisiana at Lafayette, USA
[3] Kobe University Research Center for Inland Seas, Rokkodai, Japan
[4] Phycology Research Group and Center for Molecular Phylogenetics and Evolution, Ghent University, Belgium
Contact: cvcarp@gmail.com

The combination of global sampling with the use of molecular techniques is giving a good idea of global patterns of diversity and offers a proper background for speciation studies. Recent molecular studies substantially fueled species identification of the cosmopolitan brown algal genus *Lobophora* (Dictyotales, Phaeophyceae). Here we use a global scale dataset containing over 500 DNA verified specimen records belonging to the genus *Lobophora* to elucidate the mechanisms that drove the high level of speciation of this brown algal genus, which contains over 50 MOTUs. The focus is on tropical and warm temperate environments. We characterize the phylodiversity at various spatial scales (between ocean basins to individual localities) and examine the predictions of various geographic (allopatric, sympatric, and peripatric) models of speciation, using patterns of range overlap and range size symmetry between sister clades. Results from geographic speciation models and adaptation to specific environments at a local scale are combined to draw conclusions on the relative roles of adaptive and non-adaptive processes on diversification of marine algae.

Keywords: Phylogeography, marine speciation, Lobophora, algae, global-scale

Continued next page

7.32 *Orthotrichum shevockii*, another moss species displaying the rare biogeographic disjunction California-Macaronesia?

Beatriz Vigalondo[1], Isabel Draper[1], Ricardo Garilleti[2], Vicente Mazimpaka[1], Jairo Patiño[3], James Shevock[4], Ana Losada-Lima[5], Juana María González-Mancebo[5], Francisco Lara[1]
[1] Departamento de Biología (Botánica), Facultad de Ciencias, Universidad Autónoma de Madrid, Spain
[2] Departamento de Botánica, Facultad de Farmacia, Universidad de Valencia, Spain
[3] Department of Biology, Ecology and Evolution, University of Liège, Belgium
[4] Department of Botany, California Academy of Sciences, San Francisco, USA
[5] Departamento de Biología Vegetal (Botánica), Universidad de La Laguna, Tenerife, Spain
Contact: beatriz.vigalondo@uam.es

Orthotrichum shevockii Lewinsky-Haapasaari & Norris is a saxicolous moss described from the mountains of southern California. Recent field surveys had defined the distribution range of the species throughout California and neighboring regions of western Nevada, mainly in dry mountain areas, but also in some localities at low altitude or with relatively humid climates. More recently, putative populations of this species have been found in the Northeastern Atlantic region, specifically at high altitudes in the Canary Islands. In the present study, an integrative approach combining morphological and molecular analyses enable the confirmation of the new populations from the Canary Islands as *O. shevockii.* Specimens from both sides of the disjunction share characteristic morphological traits and show comparable levels of variation among them. We also use an explicit time-calibrated, molecular-based phylogenetic approach to infer the historical biogeography of this singular disjunction. In conclusion, we present a new case for the California–Macaronesia disjunction, rare among bryophytes and only known in this genus for the sister species *O. underwoodii* and *O. handiense*.

Keywords: biogeography, disjunction, phylogeny, integrative taxonomy, Orthotrichum, bryophytes

P8 Quaternary and cultural legacies

8.1 ⚡ Natural species distribution inferred from pollen-based quantitative land-cover reconstruction

Vojtěch Abraham[1], Libor Petr[2], Helena Svitavská-Svobodová[3], Radka Kozáková[4], Eva Jamrichová[5], Petr Pokorný[6], Petr Kuneš[5], Markéta Gabriela Švarcová[5]
[1] Departmet of Botany, Faculty of Science, Charles University in Prague & Department of Botany, Faculty of Science, University of South Bohemia
[2] Department of Botany and Zoology, Faculty of Science, Masaryk University
[3] Institute of Botany of the Academy of Sciences of the Czech Republic
[4] Institute of Archaeology of the Academy of Sciences of the Czech Republic
[5] Department of Botany, Faculty of Science, Charles University in Prague & Institute of Botany of the Academy of Sciences of the Czech Republic
[6] Center for Theoretical Study, Charles University in Prague
Contact: vojtech.abraham@gmail.com

The aim of the contribution is to find the difference between the natural distribution of selected taxa inferred from quantitative reconstruction and from Potential Natural Vegetation (PNV). We calculated regional vegetation estimates (60 km radius) by REVEALS model in nine regions in the Czech and Slovak Republics. The post-glacial vegetation development can be clustered into three general phases: Early, Middle and Late Holocene. Mid Holocene spruce phase (spruce >32%) in middle altitudes contrasts with most of the previous palynological interpretations, which describe it as mixed oak woodland. Quantities of individual taxa from REVEALS estimates at 750 AD and PNV composition substantially differ due to methodological biases of the PNV. Spruce forests host poor herb layer and always were considered as artificial introduction, thus the natural distribution of spruce is underestimated by PNV. The continual presence of landscape openness (Poaceae >9%) and pioneer trees (pine >7%) in lowlands highlights the important role of additional natural drivers allowing their permanent abundance, be it herbivores, dry climate or fire activity.

Keywords: quantitative interpretation of pollen analysis, PNV, Central Europe, Holocene vegetation

8.2 ⚡ Asymmetrical responses of woodrats (*Neotoma sp.*) across their range to late Quaternary climate

Meghan Balk[1], Felisa Smith[1], Stephen Jackson[2], Julio Betancourt[3]
[1] Biology, University of New Mexico
[2] University of Wyoming
[3] USGS
Contact: mabalk04@unm.edu

The consequences of anthropogenic climate change for species currently drives scientific research. Studies show that species can shift geographic ranges or become locally extirpated. Adaptation is often disregarded, as anthropogenic global warming is thought to be too rapid. We use the fine-scale paleomidden record from the western US of the bushy-tailed woodrat, *Neotoma cinerea* to quantify the ability to adapt to climatic shifts over the last 25,000 years. The ability for woodrats to shift mean population body size over space and time has been demonstrated in previous studies, suggesting the ability to adapt *in situ*. We assess (1) whether the presence and absence of *N. cinerea* paleomidden records are biased towards a particular temperature regime, and (2) whether the ability to adapt varies across latitudes. Findings: *N. cinerea* are capable of tolerating climate changes of up to 4ºC within a 100-year interval; extirpations are limited and are restricted to geographic range boundaries. The scientific community may be underestimating the ability of species to adapt *in situ* over relatively short time scales.

Keywords: Paleomidden, woodrat, climate change, Bergmann's Rule

8.3 Reconstructing the environment and climate of NE-Africa in the Holocene based on records of animals in ancient Egyptian art

Carl Beierkuhnlein[1], Josephine Beuter[1], Reinhold Stahlmann[1]
[1] Biogeography, BayCEER, University of Bayreuth
Contact: carl.beierkuhnlein@uni-bayreuth.de

Knowledge from other disciplines and especially arts and humanities is mostly ignored in natural sciences. Also, information on environmental conditions during the Holocene in NE Africa is scarce. Here, we present a trans-disciplinary approach to detect past climate and environmental changes. Hunting scenes in tombs are of high

precision. They reflect the wildlife in the vicinity of river Nile. We analyse records of mammals in paintings and other precisely dated artefacts. Data were retrieved from screening literature, analysing digital documents, visiting museums and collections, exhibitions, and travelling to Egypt. In addition, bone finds are considered. 691 records contribute to the data set. 64 mammals with sufficient frequency are considered. Current ecology and distribution of mammals is well documented, allowing SDM and the analysis of historical analogues. Based on current distribution, climatic niches were identified. These were applied to records between 4500 and 500 BC to reconstruct the environmental and climatic history of NE Africa. Furthermore, we analyse trends in trophic levels and mammal biodiversity, including regional and global extinction of species.

Keywords: Proxies, Mammals, Hunting, Extinction, Bioindication, Bioclimatic Envelopes

8.4 ⚡ Reconstructing the geographic distribution and ecological niche of Neanderthals during Oxygen Isotope Stage 5e (~125 ka BP)

Blas M. Benito[1], Trine Kellberg Nielsen[2], Jens C. Svenning[3], Felix Riede[2], Brody S. Sandel[3], Peter C. Jkaergaard[2]
[1] Centre for Biocultural History / Ecoinformatics and Biodiversity (Aarhus University)
[2] Department of Culture and Society / Centre for Biocultural History (Aarhus University)
[3] Ecoinformatics and Biodiversity / Centre for Biocultural History, Aarhus University
Contact: blas.benito@biology.au.dk

Neanderthals have attracted much attention from different scientific disciplines. As a consequence, we know a great deal about their diet, hunting strategies, technology and genetic diversity. Decisive knowledge of their spatial ecological niche, however, remains elusive. We address this gap by studying the geographical distribution and topo-climatic niche of Neanderthals during Oxygen Isotope Stage (OIS) 5e (~125 ka BP). We have compiled a database of OIS 5e Neanderthal occurrence records and a set of six environmental factors representing topography, water availability and temperature. We used this data to calibrate a state-of-the-art species distribution model based on an ensemble of Generalized Linear Models. Our model helps to understand the environmental determinants of the distribution of Neanderthals at both broad and local scales as well as provides a description of the potential occurrence patterns of this hominin during OIS 5e. By projecting the model into the Last Glacial, it also helps us understand the Neanderthal range contraction during this period. We discuss our results in the light of the archaeological evidence and ecological niche theory.

Keywords: Neanderthal, paleo-distribution, ecological niche, species distribution modeling

8.5 Holocene vegetation dynamics in the island of Gran Canaria: new palaeoecological evidences

Lea de Nascimento[1], Michela Mariani[2], Cesare Ravazzi[3], Constantino Criado[1], Sandra Nogué[4], Francisco Perez-Torrado[5], Robert J. Whittaker[4], Kathy J. Willis[4], José María Fernández-Palacios[1]
[1] University of La Laguna
[2] University of Milano
[3] Consiglio Nazionale delle Ricerche
[4] University of Oxford
[5] University of Las Palmas de Gran Canaria
Contact: jmferpal@gmail.com

We provide the first pollen and charcoal analysis from the island of Gran Canaria (Canary Islands). The pollen record spans the last *c.* 4500 cal. years BP covering the period of human colonization of the island and provides a pre-human baseline. At the earliest period forested vegetation covered the area suggesting a wider distribution of some communities in the past. Close in time to the earliest archaeological evidence of human presence in the island (*c.* 2000 cal. years BP) vegetation began to change. These change involved the clearance of forests and the spread of grasses and shrubs. The charcoal record shows an increased frequency of fires at that time while pollen from cultivated cereals became significant indicating that humans were transforming vegetation. In the following centuries the open vegetation persisted and there is no evidence of forest recovery. This analysis provides new data to advance in the reconstruction of the Holocene vegetation history of the Canary Islands.

Keywords: Palaeoecology Canary Islands forest dynamic human impact fire

8.6 ⚡ Historic and prehistoric extinctions have reshaped global mammal diversity patterns

Søren Faurby[1], Svenning Jens-Christian[1]
[1] Aarhus University
Contact: soren.faurby@biology.au.dk

In this presentation we will compare species, phylogenetic, and functional diversity of all late Quaternary mammals for current and potential natural distributions, i.e., in the absence of past and present human-linked range modifications in order to estimate the extent to which current diversity patterns have been reshaped by anthropogenetic activities. For this we estimated potential natural distributions for 726 species accepted by IUCN where we found evidence or at least strong indications for human-induced range changes, as well as for 259 species that went extinct before 1600AD, but later than 130,000 years BP. Going from current to potential natural distributions led to a substantial increase from 1,076,442 to 1,289,403 occurrences in 100 × 100 km cells, with especially large increases for terrestrial megafauna. We discuss how these drastic anthropogenic changes may influence conclusions from studies on the ecological and evolutionary drivers of diversity gradients, i.e., when current diversity patterns are assumed to represent the natural patterns. Notably, we show that they result in a consistent bias in estimates of the strength of several potential drivers of diversity.

8.7 Endemism-stability association on the Olympic Peninsula, Washington, assessed from palynological records

Daniel G. Gavin[1]
[1] Department of Geography, University of Oregon, USA
Contact: dgavin@uoregon.edu

Explanations for areas of endemism often invoke relative climatic stability over time scales ranging from the Pleistocene to the late Cenozoic. Given that many narrowly endemic taxa in forested landscapes display discrete habitat associations, habitat stability through climate change may be a critical feature that has led to the persistence of endemics. The Olympic Peninsula, Washington, supports a biota with several insular features including notable species absences and 29 endemic plants and animals. Here I examine the geographic distribution and habitat of the endemic taxa, and then examine the vegetation stability of the past 14,300 years from five pollen records associated with discrete vegetation zones on the peninsula. I show that 15 endemics have distributions centered on dry alpine meadows in the northeast, and nine occur in shaded riparian forests in the southwest. Vegetation turnover during the post-glacial period was smallest in these areas. Although this study supports an association of vegetation stability with endemism, records spanning the glacial maximum are needed to reveal vegetation stability through the most severe period of the late Pleistocene.

Keywords: areas of endemism; vegetation turnover; Quaternary paleoecology

8.8 ⚡ Niche dynamics of Early Modern Humans in the Palearctic reveal south Siberian dispersal route

Konstantinos Giampoudakis[1], Katharine Ann Marske[1], Andrew Ugan[2], Joy Singarayer[3], Michael Krabbe Borregaard[1], Paul Valdes[4], Carsten Rahbek[1], David Nogues-Bravo[1]
[1] Center for Macroecology, Evolution and Climate, Natural History Museum Of Denmark
[2] Department of Anthropology, University of Utah
[3] Department of Meteorology, University of Reading
[4] School of Geographical Sciences, University of Bristol
Contact: konstantinosg@snm.ku.dk

Whether the survival and dispersal of Anatomically Modern Humans (AMHs) during the Late Pleistocene was facilitated by expanding the environmental conditions they could inhabit, or by following suitable ones across Eurasia, remains hotly debated. Here, we reconstruct the changes in the climatic niche and geographic range of AMHs in Eurasia through time. We find that the climatic niche of Eurasian populations changed significantly during the last ~50,000 years. Specifically between 46kya-26kya we saw large changes in the orientation and breadth of the niche. In contrast from 26kya to 11kya we found that the climatic conditions that AMHs were able to inhabit were more static. These findings suggest two different phases of human dispersal: niche expansion allowed humans to colonize new climatic conditions in the period 46kya-26kya, and niche stasis during the period 26kya-11kya, when populations moved geographically to remain within their preferred niche. Models of the geographical range of AMHs suggest a potential dispersal route linking western Europe to Far East Asia through a mid-latitude belt in South Siberia, as well as a climatic refugium in Kamchatka and submerged areas of Beringia.

Keywords: Niche stability, Niche breadth, Homo sapiens sapiens, Climatic Envelope Models (CEMs), Late Pleistocene

8.9 ⚡ Geographic variation and environmental correlates of functional trait distributions in Neotropical palms (Arecaceae)

Bastian Göldel[1], W. Daniel Kissling[2], Jens-Christian Svenning[1]
[1] Deperatment for Bioscience, Aarhus University
[2] Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam
Contact: bastian.goeldel@biology.au.dk

Functional trait distribution and the impact of current and past environmental drivers are increasingly debated in recent years as functional traits play a key role in driving biodiversity effects on ecosystem functioning. Here, we examine the geographic distributions of three key functional traits in Neotropical palms (Arecaceae), one of the ecologically most important plant groups in the region, and their relationships with current climate, soil and Quaternary climate change. We combined palm range maps for all palm species (n=542) in the New World with data on key functional traits. We followed Westoby's LHS scheme (1998) and chose leaf size, stem height and fruit size for each species to compute mean trait values of each 110×110-km grid cell assemblage. Current temperature range and seasonality played an important role for explaining geographic variation in all three traits, while current precipitation was only related to leaf size, and soil (pH, sand %, CEC) did not strongly explain spatial variation in any of the studied traits. Quaternary glacial-interglacial temperature and precipitation change were related to geographic variation in mean fruit size, but less to mean leaf size and mean stem height.

Keywords: Biogeography, past climate change, functional diversity, macroecology, Neotropics, Palmae, Quaternary climate oscillations, species traits

8.10 Degradation of Pastoral Resources in the Kyrgyz Republic under Post -Soviet Transformation

Franziska Hoppe[1], U. Schickhoff[1]
[1] CEN Center for Earth System Research and Sustainability, Institute of Geography, University of Hamburg
Contact: Franziska.Hoppe@geowiss.uni-hamburg.de

Animal husbandry in mountainous regions has always played a major role in the life of Kyrgyz people and the livestock sector has been one of the strongest components of the regional economy during Soviet and post-Soviet times. Montane and alpine rangelands, which occupy 45% of the Kyrgyzstan's land area, represent the significant basis for this economic sector. During the Soviet regime the livestock industry had been massively expanded. The first years after independence saw, a drastic reduction in livestock numbers, and a temporarily decreasing grazing pressure. However, in the further course of post-Soviet transformation livestock numbers have been considerably increasing again. By current estimates, at least 25-35 % of pasture areas are subject of vegetation and soil degradation. Using an interdisciplinary approach, the project TRANSPAST aims at assessing the capability of rangeland ecosystems to cope with increased grazing pressure, and at predicting the future pastoral resource availability under different land use scenarios. First results indicate that degradation of winter pastures (kishtoos), which are closer to settlements, is more intense than degradation of summer pastures (jailoos) located at higher elevations.

8.11 ⚡ Paleobiogeography of the Pleistocene/Holocene transition in Central Europe: small mammals in a high-resolution fossil record

Ivan Horacek[1]
[1] Department of Zoology, Charles University Prague
Contact: horacek@natur.cuni.cz

Regarding appearance in fossil record the extant fauna of Central Europe splits in three chorologic units: (i) paleochoric elements of interglacial and (ii) glacial communities, and (iii) apochoric elements of the Holocene. Numerous faunal fossil sequences available in Central Europe suggest considerable geographic variation in post-glacial history of these units. Non-trivial aspects of the matter are demonstrated with two key sites: (A) The sedimentary sequence in Muran cave (high alpine zone of the High Tatra Mts., Slovakia) revealed that even in time of LGM a surface of the mountain glacier was inhabited by a rich community of small ground mammals incl. some (i) elements and local endemic spp. (B) A 10m thick sedimentary sequence in Byci skala cave (Moravian karst), covering the period 12 to 8.5 ky with 21 horizons and 4525 MNI of 52 mammalian spp., convincingly demonstrated that most of the apochoric elements appeared, against expectancy, already at time of the Pleistocene/Holocene transition. Their early expansion, probably forced by the Late Pleistocene temperature anomaly in the southern Europe, affected the Holocene faunal development in Central Europe in important ways.

Keywords: Pleistocene/Holocene transition, Central Europe, mammals

8.12 ⚡ Central European fen mollusc and plant assemblages in modern and quaternary perspective

Michal Horsák[1], Michal Hájek[1], Petra Hájková[1]
[1] Dept. of Botany and Zoology, Masaryk University
Contact: horsak@sci.muni.cz

Fens are nutrient-limited wetlands fed by mineral-rich ground waters, with a tight response of species richness and composition to the water chemistry. Fen habitats support species rich assemblages of both plants and molluscs, including many globally threatened habitat specialists and glacial relicts. Species richness generally increases towards alkaline fens and rather weak biogeographic signal can be found in species composition. While a clear species turnover is characteristic for plants, molluscs express the nested subsets along the calcium gradient. As fens accumulate organic sediments with a rich fossil material, an exact dating and the reconstruction of their development are easily possible. The Late Glacial origin of the oldest temperate fens maintains the existence of many glacial relicts, surviving there in isolated populations. The occurrence and number of these relicts was found to be associated with the age of fens and/or a continuous presence of suitable fens during the Holocene. The number of habitat specialists in these insular systems increases with habitat age and/or area, with habitat age becoming more important as species dispersal ability decreases.

8.13 ⚡ Endangered molluscs of European fens: current data and conservation of glacial relicts

Veronika Horsáková[1], Michal Horsák[1]
[1] Department of Botany and Zoology, Masaryk University
Contact: veronika.horsakova@seznam.cz

Mire habitats serve as an important carbon storage and refugia for rare and relict species, being at the same time seriously threatened by the ongoing environmental changes. In our research we focus on fens, i.e. groundwater-fed mires, and their mollusc fauna. In central Europe, fens are represented by small and isolated remnants of formerly larger fen areas and hence their mollusc diversity has long been overlooked. However, fens harbour exceptionally rich mollusc assemblages including many endangered fen specialists. All the four European Annex II *Vertigo* species are fen inhabitants with two of them, namely *V. genesii* and *V. geyeri*, being entirely restricted to fens. Recently, we found new isolated occurrences of these species as well as of the northern European *V. lilljeborgi*. According to the fossil record these species are regarded as glacial relicts and their occurrence gives evidence about the ancient origin and historical continuity of fens throughout the Holocene. Conservation of all preserved fens is thus of crucial importance, with respect to the genetic diversity and phylogenetic history of these species and maintenance of the habitats with species-rich mollusc fauna.

8.14 ⚡ The legacy and future of phylogenetic diversity in urbanizing areas

Sonja Knapp[1], Marten Winter[2], Stefan Klotz[1]
[1] Community Ecology, Helmholtz Centre for Environmental Research - UFZ
[2] German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Contact: sonja.knapp@ufz.de

Often concentrating in species rich regions, urban areas harbor many species but threaten natural species assemblages. Phylogenetic diversity measures the intrinsic evolutionary history of assemblages. Some hypothesize, that the closer related species within an assemblage the less stable it tends to be. Spatial studies show that today's urban areas have low vascular plant phylogenetic diversity. Still, snapshots in time do not show whether phylogenetic diversity is lost during urbanization and whether species extinction or immigration is driving loss. We answered these questions by analyzing a German urban flora using floristic inventories spanning 320 years. We split the flora into native species and archaeophytes (pre 1500-aliens) that went extinct vs. neophytes that immigrated in these 320 years. We calculated phylogenetic distinctness and phylogenetic signal per group compared to random values. Further, we identified today's red list species and neophytes potentially immigrating in the future, calculating how their loss/gain will affect future phylogenetic diversity. Both extinction and immigration decreased phylogenetic distinctness over time as would future loss and gain.

Keywords: biodiversity, evolutionary history, extinction, immigration, phyloecology, urbanization

8.15 ⚡ Flora and vegetation dynamics on the Zugspitzplatt (Bavarian Alps, Germany)

Oliver Korch[1], Arne Friedmann[1]
[1] Institute of Geography, University of Augsburg
Contact: eldonolli@gmx.de

Since 2009 the flora, spatial distribution of the vegetation and the vegetation dynamics of the upper subalpine, alpine and subnival belt of the Zugspitzplatt are being investigated. Based on over 200 phytosociological relevées a detailed vegetation map of the area has been constructed and a long-term vegetation monitoring program on permanent sample plots has been established. Evidence indicating past shifts of the krummholz limit was analyzed and dated. As a result, the heterogeneous boundary layer climate of the investigation site along with natural disturbances, the anthropogenic impact and the grazing of sheep during the summer period were identified as the main factors influencing the distribution of species and plant communities. The existence of some of these communities can even be linked directly to zoogenic site alteration such as eutrophication, trampling and selective grazing. As a consequence, vast areas above the timberline on the Zugspitzplatt must be regarded as a cultural landscape and natural wild vegetation can only be found on few remote sites.

8.16 ⚡ How dynamic are tropical forests? Long term human impact drives landscape " hyperdynamism" in an ancient tropical forest

Sandra Nogué[1], Carolina Tovar[1], Shonil Bhagwat[2], Walter Finsinger[3], Kathy Willis[1]
[1] University of Oxford
[2] Open University
[3] Institut de Botanique
Contact: sandranogue@gmail.com

Forests are often described as the lungs of the world. They provide multiple ecosystem services such as food provisioning, nesting grounds, and there is an increasing appreciation of the value of their associated plants and animals. Deep concern has been raised about the rates at which these forests are disappearing or being modified due to human activities. Land-use change is considered to be the largest driver of fragmentation in tropical forests. At present there is a great deal of interest in the temporal dynamics of tropical forests to help understanding forest resilience and/or the quality of the remnant forest patches. Human-dominated agricultural landscapes such as the ancient forest of Western Ghats in India represent key landscape to test how dynamic are tropical forests to land-use change over long-time scales and which are the main drivers of change. Here, we show enhanced temporal dynamics within and between forest

patches for the last 900 years due to combination of landscape burning, informal protection, and the opening of canopy. Our findings highlighted that agriculture has not precipitated the collapse of the Western Ghats forested-landscape.

Keywords: fossil pollen forest dynamics land-use change mosaic of successional stages tropical forest Western Ghats

8.17 A high-quality fossil database for addressing causes of Australian megafauna extinctions

Marta Rodríguez-Rey[1], Frédérik Saltré[1], Salvador Herrando-Pérez[2], Barry W. Brook[3], Corey J.A. Bradshaw[1]
[1] University of Adelaide, Australia
[2] National Museum of Natural Sciences, Spanish Research Council (CSIC)
[3] University of Tasmania, Australia
Contact: frederik.saltre@adelaide.edu.au

Causes and mechanisms of mass extinctions such as the abrupt disappearance of Australian megafauna in the late Pleistocene are still intensely debated. Statistical methods used to address these questions rely on many unreliable fossil records, and can therefore lead to incorrect conclusions regarding the timing and distribution of extinctions. We present the first high-quality Sahul (Australia and New Guinea) database for the Quaternary period compiling 9188 fossil records published since 1955. Our database provides a quality rating based on objective criteria and ecological characteristics for each species and each record. We show that 45% of the 280 deposits present fewer than six species, and that five major deposits throughout Sahul cover most species diversity in fossil records. Finally, we demonstrate that applying our quality rating to the database modified the assessment of species' ecological characteristics and reduced the number of records available to address hypotheses regarding extinction drivers. We discuss the potential applications of this dataset, with emphasis on the long-standing debate about the main causes of Late-Pleistocene megafauna extinction in Australia.

8.18 ⚡ Spatial pattern of Eurasian woolly mammoth extinctions during the Late Pleistoicene based on statistical inference from fossil records

Frédérik Saltré[1], Barry Brook[2], Joël Chadoeuf[3], Damien Fordham[1], Marta Rodriguez-Rey[1], Corey Bradshaw[1]
[1] University of Adelaide, Australia
[2] University of Tasmania, Australia
[3] INRA, France
Contact: frederik.saltre@adelaide.edu.au

Late Pleistocene extinctions affected most large and low-fecundity mammals such as the woolly mammoth (*Mammuthus primigenius*) in Eurasia. Despite recent advances in both genetic and modelling approaches and increasing fossil data, assessing the relative importance of climate variation and human hunting on the spatial pattern of mammoth extinction remains a challenge. This is because estimating incomplete fossil time series biases the true dates of extinction and appearance, potentially leading to incorrect conclusion of the relative importance of individual and synergistic drivers. We present a spatially explicit statistical inference of mammoth extinctions based on the recently developed Gaussian-resampled inverse-weighted McInerny (GRIWM) approach applied to 112 high-quality mammoth fossil records scattered across Eurasia. GRIWM generates a confidence interval of the true extinction time, which suggests a pattern of mammoths extinctions starting in central Europe and spreading toward both western Europe and north-eastern Siberia. We compared GRIWM results with those for humans and climate velocity to determine regional variations in their relative impacts on mammoth extinctions.

8.19 ⚡ Biome affinities of local floras: On the phytogeography of *Quercus pubescens* willd. in Italy

Francesco Spada[1], Vincenzo Zuccarello[2]
[1] Dip. Biologia Ambientale, University of Roma la Sapienza
[2] Università di Lecce
Contact: francesco.spada@uniroma1.it

Quercus pubescens is a widespread *taxon* in S E Europe and in the Mediterranean Near East Along the geographical gradient , the species gives origin to a whole array of communities from tall forest stands in C and S

Europe to savanoidopen woodlands and scrub in the East, where it reaches the outernmost fringe of the European forest biomes facing the steppes of W Asia . In Italian stands, the biome affinities of the associated floral stocks emerging from automatic classification procedures, apparently suggests the legacy of environmental changes of the last glacial cycle in the coexistence patterns along the geographical and topographical gradients.

8.20 ⚡ Reconstructing the paleoenvironment of the western German Alpine Foreland – a high resolution 14C-dated pollen diagram from the Mehlblockmoos (Allgäu, Bavaria)

Philipp Stojakowits[1], Arne Friedmann[1]
[1] Institute of Geography, University of Augsburg
Contact: stojakowits@geo.uni-augsburg.de

The pollen diagram consists of 435 samples on a core length of 8,21 m counted up to a minimum of 1000 arboreal pollen. The Late Glacial sequences were investigated by an interval of 1 cm and the Holocene of 2 cm. The chronology is based on 15 radiocarbon dates and the deposited Laacher See Tephra. The Late Glacial forest development begins during the Bølling with the immigration of Betula and Pinus sylvestris. The Younger Dryas leads to lighter and more sparse forests. In the early Holocene thermophilous trees and Picea abies arrive and replace the established forest formations. The 8200 cal. BP event is marked by a sharp depression of the Corylus avellana values and triggers the mass expansion of Picea abies. The hesitant spread of Abies alba and Fagus sylvatica is also related to climatic fluctuations. In the Late Subboreal (Bronze Age) the first significant influences of humans in the environment are detected. In the Subatlantic period further clearing phases (Iron Age, Roman Age, Middle Ages, Modern Era) are represented. The human impact in the Modern Era leads to the nearly complete decline of the mixed montane forest stocks.

Keywords: pollen analysis, vegetation history, Late Glacial, Holocene

8.21 ⚡ Marantaceae forest and mixed forest: Two alternative stable states in central Africa?

Carolina Tovar[1], Elinor Breman[2], Laurent Bremond[3], Jean-François Gillet[4], David Harris[5], Kathy Willis[1]
[1] University of Oxford
[2] Kew Royal Botanic Gardens
[3] Université Montpellier 2
[4] University of Liège
[5] Royal Botanic Garden Edinburgh
Contact: carolina.tovar@zoo.ox.ac.uk

The mechanisms by which fire acts in maintaining forest types have not been studied in detail for African tropical forest. We analyse the history of Marantaceae forests that are characterized by a sparse canopy and an understory of giant herbs as a case study. We hypothesized that forest-fire feedbacks maintain this forest type. Phytoliths (a vegetation proxy) and fossil charcoal (a fire proxy) were extracted from two sediment cores collected in current Marantaceae forests. The cores span the last 1200 years. Our results show a switch from broad-leaved dominated community (Mixed forest) to a more Marantaceae and palm dominated community (Marantaceae forest) around 450- 600 cal yr BP. This change has endured until present. We observe a significantly higher fire frequency in the period when Marantaceae forest dominated compared to mixed forest dominance. We postulate that Marantaceae forest is an alternative stable state to mixed forest that is maintained by high fire frequency. The mechanisms behind the maintenance of Marantaceae forest are more related to the opening of the canopy rather than to the establishment of the Marantaceae species themselves. The later seems to be affected by local factors in addition to fire.

Keywords: tropical forest, alternative stable states, forest-fire feedbacks, palaeoecology, phytoliths

8.22 ⚡ General introduction to paleobioDB, an rOpenSci R-package to get fossil data for research

Sara Varela[1]
[1] Charles University, Prague
Contact: svarela@paleobiogeography.org

The fossil records provide invaluable information on the morphology, ecology and biogeography of ancient species. However, paleontological data is not normally used in macroecology and biogeography, mainly because the fossil record is hard to access via the standard literature. Nowadays, there are open access paleontological databases, like the Paleobiology Database, which includes data from 50,700 references, consisting of 1,180,000 occurrences from 156,000 collections and 294,000 taxa, which could be used for research. For that reason we developed paleobioDB, an R-package designed to make easy and flexible queries of the Paleobiology Database, and to visualize, download and process the selected data. Here, I want to introduce this package, as well as the rOpenSci project. I hope that this new tool will facilitate the use of fossil data in both paleontological and neontological research, and enhance the ability to perform integrated analyses, where data from the deep past can be used to help inform our understanding of the living biota, and vice versa.

Keywords: fossil record, paleontology, open access, rOpenSci

8.23 ⚡ Biodiversity loss in the Maltese islands hits relictual species

Raluca Voda[1], Leonardo Dapporto[2], Vlad Dinca[3], Tim Shreeve[2], Mourad Khaldi[4], Ghania Barech[4], Khellaf Rebbas[4], Paul Sammut, Roger Vila[1]
[1] Institut de Biologia Evolutiva (CSIC-UPF), Spain
[2] Oxford Brookes University, UK
[3] University of Guelph, Canada
[4] University of M’Sila, Algeria
Contact: raluvoda@gmail.com

The Mediterranean basin is one of the world’s biodiversity hotspots. During the Pleistocene this region encompassed several mainland and insular glacial refugia, which generated a mosaic of genetic lineages and taxa that identify faunal subregions. We studied the butterfly fauna of the islands in the Sicilian strait and compared their genetics with those of populations from adjacent mainland. We observed a strong contrast between Italy and Sicily with Maghreb, while the patterns displayed by the islands in between highly mirror their Pleistocene paleogeography. In particular, the genetic structure of 5 species of Malta and Gozo show evidence of having colonized these islands from Sicily during the last glacial maximum, when a land bridge existed. Precisely these populations are currently experiencing strong decline or are already extinct from one or both main Maltese islands, a phenomenon that is apparently not affecting the rest of taxa. We conclude that current extinction processes are rapidly erasing Pleistocene biogeographic signatures that confer idiosyncrasy to islands, leaving only undifferentiated genetic diversity and faunas composed by highly dispersive generalist species.

8.24 ⚡ The effect of historic land use and climate change on taxa-climate relationships for major tree genera in northeastern US forests

John Williams[1], Simon Goring[1], Madeline Ruid[1], Charles Cogbill, Michael Dietze[2], Stephen Jackson[3], Jason McLachlan[4], David Mladenoff[1], Christopher Paciorek[5], Sydne Record[6]
[1] University of Wisconsin-Madison
[2] Boston University
[3] University of Arizona
[4] Notre Dame University
[5] University of California, Berkeley
[6] Bryn Mawr
Contact: jww@geography.wisc.edu

The species composition and structure of forests are heavily affected by legacies of past land use, yet these effects are rarely accommodated by species distribution models relating contemporary species distributions to climatic

predictors. As part of the PalEON project, we present new reconstructions of relative forest composition during early Euro-American settlement, for a domain stretching from Minnesota to Maine, and apply them to assess the stability of taxa-climate relationships for major tree genera over the past several centuries. These reconstructions, based upon data from Public Land Survey and Township Proprietor Surveys, are compared to 20th-century tree distributions from Forest Inventory and Analysis data. Historic land use substantially affected taxa-climate relationships, due to selective distribution of past land use causing large reductions of some tree taxa from former portions of their geographic and climatic range. Effects of 20th century climate change on taxa-climate relationships are secondary but detectable. Combining historic and modern datasets thus creates a fuller, but still incomplete, description of the realized climatic niches for these tree taxa.

Keywords: Realized Niche Historic Vegetation Land Use Paleoecology Species Distribution Models Vegetation

8.25 From past to future: Ecological, spatial divergence and range dynamics of *Halenia* in China

Xuefei Yang[1], Linlin Wang[1], Eike Luedeling[2], Yongping Yang[1], Yuanwen Duan[1]
[1] Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany, Chinese Academy of Sciences
[2] World Agroforestry Centre, Nairobi
Contact: xuefei@mail.kib.ac.cn

We focused on three taxon groups of genus *Halenia* that are distributed in China. To explore the ecological niche and spatial divergence of these three groups and their distribution pattern in history and in the future, niche analysis and assembled species spatial distribution modeling approach were employed. Six time periods were studied, extending from last interglacial (LIG), last maximum glacial (LMG), to current, 2040s, 2060s and 2080s. Results show that three taxon groups occupy different niche positions and in different geographic space. *H. elliptica* and *H. elliptica* var. *grandiflora* prefer warmer and wetter environment in southwest China than that of *H. corniculata* distributed in North China. Temperature related factors, especially in winter terms, are most probably the driver that causes the divergence of *Halenia*. *H. corniculata* experienced a dramatic range shift from LIG to LGM, showed a long distance and down elevation migration from Qinghai-Tibet Plateau to Northern part of China. We speculate that *Halenia* originated from Southwest China; glacial events drive its migration to Northeastern China, from where it spread to Berlin strait and North America. Under the future scenarios of global warming, *H. corniculata* will suffer from habitat loss while the range of H. elliptica and its relative variety will expand.

10.1 ⚡ Seedling emergence of invasive plants is limited by low temperature and humidity in experimental target-climate and can be predicted by climate of native and non-native origin

Mohammed Abu Sayed Arfin Khan[1], Anke Jentsch[1]
[1] Disturbance Ecology, BayCEER, University of Bayreuth
Contact: nobelarfin@yahoo.com

Where are the limits of global plant invasion? The role of climate in target-area versus area-of-origin is important and may improve our understanding in predicting cross continental range expansion of invasive plants and shaping performances of their native and non-native populations. We experimentally determined the seedling emergence success of three global invaders - *Lupinus polyphyllus*, *Senecio inaequidens*, and *Verbascum thapsus* (6 native and 6 non-native populations) - under seven experimental target-climates. All species germinated and emerged in 3 warm and in 2 moderate cold climates. However, no germination and seedling emergences observed in 1 cold (temperature ≤ 5 °C) and in 1 dry (humidity ≤ 50%) climates. Non-native *V. thapsus* populations performed better, similar or worse than native populations. Responses of populations were significantly correlated with climate of origin. We concluded that seedling establishment success of invasive plants is only limited by low temperature and low humidity. Climate of origin is a good predictor for cross continental range expansion of invasive plants and shaping responses of their native and non-native populations.

Keywords: Abiotic factors, Biological invasion, Cross-continental range expansion, Ecosystem vulnerability, Ecotype, Provenance

10.2 ⚡ Macroscale invasion patterns and processes

Songlin Fei[1], Basil Iannone[1], Chris Oswalt[2], Qinfeng Guo[2], Bryan Pijanowski[1], Kevin Potter[3], Teresa Clark[1], Gabriela Nunez-Mir[1]
[1] Purdue University
[2] US Forest Service
[3] North Carolina State University
Contact: sfei@purdue.edu

Invasion of exotic species poses a major threat to many ecosystems, resulting significant ecosystem degradation and economic loss. Research on the invasion of exotic species has been a major topic in the last two decades and much knowledge has been accumulated on invasion ecology from small plot research. However, our understanding of the long-term invasion process at regional to continental scale is limited, partially due to the lack of long-term, large-scale empirical data. In this presentation, we use invasive plant data from ca. 120,000 plots across the continental United States to explore the following two research questions: (1) Are some regions more vulnerable to invasion than others, and what cross- and within-taxonomic generalizations can be made about these patterns? (2) What are the underlying processes that lead to the emergence of the spatiotemporal invasion patterns and how can the key within- and cross-scale interactions and thresholds/tipping points in invasion processes be identified?

Keywords: Invasive species, scale dependency, tipping point, macrosystems, spatial autocorrelation

10.3 ⚡ The legacy of biogeography and evolutionary history explains pine invasiveness

Laure Gallien[1], Bianca Saladin[1], Florian Boucher[2], Niklaus Zimmermann[1]
[1] Swiss Federal Research Institute WSL
[2] Zürich Institute of Systematic Botany (Switzerland)
Contact: laure.gallien@gmail.com

Worldwide biological invasions are now a major threat for biodiversity. Generally, species functional characteristics and climatic preferences are used as indicators of species invasiveness, but they are of limited power. Here, by studying the most threatening invasive tree genus: *Pinus*, we show that accounting for species past colonisation events (historical biogeography), speed of trait and niche evolution, and lineage rates of extinction, significantly improves the detection of invasive species. By doing so we notably demonstrate for the first time that currently

invasive Pine species belong to lineages that have migrated a lot across continents (i.e. they have a long invasion history). Interestingly, we also show that these lineages that migrated most had slower rates of functional trait evolution, and thus our results support the famous “evolve or migrate” hypothesis. Finally, once the Pines species most at risk of becoming invasive are identified, it becomes possible to locate the regions where they are more likely to succeed. Thus such an approach offers great opportunities for early detection and management of invasive species.

Keywords: Biogeography, Invasiveness, Pinus genus, Trait and niche evolution

10.4 ⚡ Invasion biogeography: comprehensive information from native ranges is needed

Qinfeng Guo[1]
[1] FS, USDA
Contact: qguo@fs.fed.us

Biotic invasions alter the world biogeography in multiple ways, e.g., (1) increasing distribution of certain species while reducing that of others, (2) forming neo-disjuncts and disrupting native distributions, (3) rapid evolution/hybridization, and (4) biotic homogenization. Early studies have mainly focused on the climate and distribution (e.g., species with larger native distributions are more successful invaders), but other factors in the native regions have not been jointly considered. Yet, such comprehensive data are critical for explaining species’ invasiveness and predicting future spread. Here, in an initial analysis, we show that exotics spread faster in species-poor than in species-rich regions. Many species are limited by dispersal, natural enemies, and human use, not climate, thus could establish new habitats within and beyond their native ranges. We compare the composition of phylogenetic assemblages and related habitat features between native and exotic regions to examine the factors limiting exotics in native vs. exotic region? To inform management, we classify exotics based on limiting factors, i.e., climate, dispersal, natural enemy, human use, and genetics.

Keywords: biotic homogenization, comparison, disjunct, model, niche, prediction, species diversity

10.5 ⚡ Conservatism of realized climatic niches among herpetofaunal invaders

Xuan Liu[1], Xianping Li[1], Blaise Petitpierre[2], Olivier Broennimann[2], Antoine Guisan[2], Yiming Li[1]
[1] Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences
[2] Department of Ecology and Evolution, University of Lausanne
Contact: liuxuan@ioz.ac.cn

Understanding of climatic niche dynamics is key to improve forecasts of invasive species distributions and anticipate future spreads. We apply a robust niche dynamics framework and analyze conservatism of realized climatic niches using a global sample of alien herpetofaunal invasions. When we conducted the analyses based on multiple thermal and hydrological variables simultaneously, we found a high proportion of the shift in realized climatic niche. Niche shifts were more likely for species with smaller native range sizes, increasing residence time or invaded lower latitudes than the native range. Furthermore, when we conducted univariate analyses to evaluate whether realized niche shift of alien species occur in all or only a few climatic dimensions, our results show strong conservatism of the upper thermal limits compared with other thermal and hydrological variables. Our study suggests that the ‘climate-matching hypothesis’ should be used with caution for species undergoing niche shifts, and highlights the importance of preferentially choosing conserved climatic niches to develop robust predictions of biological invasions or responses to climate change.

10.6 *Rosa Rugosa*: Differences between native and invasive ranges

Julie Sheard[1]
[1] Center for Macroecology, Evolution and Climate, Copenhagen University
Contact: lfj315@alumni.ku.dk

Invasive species provide unique natural experiments of what limits geographical ranges and much work has been done on when and why some species become invasive. Using species distribution models (SDMs) to predict biological invasions is a rapidly developing area, but mostly focuses on regions where native distributions correctly

predict invaded ranges. Recently, there has been some investigation into the use of reciprocal comparisons between predicted native and invaded ranges, which might facilitate a better understanding of the biogeography of invasive and native species and of the role of SDMs in predicting future distributions. The aim of this project is to use reciprocal SDM to investigate the realized niche of *Rosa rugosa* by comparing its native range (Asia) with its two invasive ranges (Europe and North America) separately in an attempt to determine what factors, mainly climatic, that might limit the geographic range of the species and the reasons behind. Analyses are carried out by ensemble modelling using the R-package Biomod2.

Keywords: Invasive. Ranges. Species distribution models. Niche shifts. Japanese rose. Geographical distribution.

10.7 ⚡ The invasive vector mosquito *Aedes japonicus* in Europe: Still no end in sight!

Stephanie Thomas[1], Nils Benjamin Tjaden[1], Anja Jaeschke[2], Helge Kampen[3], Doreen Werner[4], Jürgen Kreyling[1], Carl Beierkuhnlein[1]
[1] Biogeography, BayCEER, University of Bayreuth, Germany
[2] Biogeographical Modelling, BayCEER, University of Bayreuth, Germany
[3] Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Greifswald – Insel Riems, Germany
[4] Leibniz Centre for Agricultural Landscape Research, Muencheberg, Germany
Contact: stephanie.thomas@uni-bayreuth.de

The interplay between global warming and invasive arthropods in temperate zones is of utmost interest in terms of the potential expansions of vector-borne diseases. During the last years, *Aedes japonicus,* an aedine vector mosquito native in Korea, Japan, Taiwan, southern China and Russia, was found in Switzerland, Germany and the Netherlands.

Here, we modelled climatically suitable areas for the establishment of *Aedes japonicus* in Europe during the upcoming century using an ensemble of different modelling algorithms and a set of five different global climate models (biomod2; cesm1_bgc, fio_esm, giss_e2_r, inm_cm4, mpi_esm_lr; IPCC 5 scenarios rcp 4.5 and rcp 8.5).

In parallel, we detected low temperature thresholds for *Aedes japonicus* egg survival under in a climate chamber experiment. We observe that the minimum temperature act as a stronger ecological constraint than the duration or diurnal temperature range of the treatment.

Finally, we combined the outcome of the experimental procedures and species distribution models to substantially improve the compilation of risk maps by considering areas where an establishment of *Aedes japonicus* is unlikely due to winter conditions.

10.8 Influences of land management and exotic weed invasion on grassland seedbank diversity

Huong Thu Thi Nguyen[1], Jennifer Firn[1], Emma Ladouceur[2]
[1] Queensland University of Technology, Australia
[2] Museo delle Scienze, University of Pavia, Italy
Contact: jennifer.firn@qut.edu.au

Eragrostis curvula (African lovegrass) is a major problem weed in the agricultural landscapes of Australia where it is both non-desirable for grazing and is replacing local biodiversity, putting species rich native grasslands at risk. The seedbanks of these fragmented landscapes are an indicative relic of historical species composition, land history and management. There is no accepted strategy by which this weed can be managed or eradicated, a variety of methods are being applied by land managers. Native seeds can persist and remain viable in the soil of agricultural landscapes over time, and these seed banks can be a rich source of native diversity despite the above ground dominance of weeds. At 58 sites within 15 farms invaded by African lovegrass we compare above ground vegetation and seedbank diversity with land history and current management practices. We expect to find that the native seedbank composition is diverse despite widespread exotic dominance, and intensive land management. Overall evidence suggests that if effective weed control strategies can reduce exotic competition, then the seedbank holds potential for the natural regeneration of grassland biodiversity.

Keywords: invasion; grasslands; biodiversity; conservation; restoration; seed bank; biogeography

10.9 ⚡ Taxonomic and functional diversity of freshwater fish accross the world

Aurèle Toussaint[1], Nicolas Charpin[1], Sébastien Villéger[2], Sébastien Brosse[1]
[1] Laboratory Ecology and Biological Diversity, University of Toulouse 3
[2] Laboratory Écologie des Systèmes Marins Côtiers, Montpellier
Contact: toussaint.aurele@gmail.com

In the current context of biodiversity loss over the world, colossal efforts have been devoted to assess the consequences of human's activities and to understand how biodiversity supports ecosystem services. Although most of the studies focused on the taxonomic facet of biodiversity (i.e. species richness), biodiversity encompasses others facets such as functional diversity. Determining the congruence between taxonomic and functional facets of biodiversity is an urgent issue for biodiversity assessments and conservation planning. We here developed a functional database through the measure of eco-morphological characteristics on more than 9,600 freshwater fish species. This database was used to assess the functional structure of fish assemblages in more than 800 river basins over the world and then to quantify functional changes induced by fish introductions and extirpations. We reported a mismatch between taxonomic and functional diversity. The consequences of introductions and/or extirpations also differed according to the considered facet of biodiversity (functional or taxonomic). Our findings suggest that functional richness is a major target for conservation planning.

Keywords: freshwater fish; functional traits; taxonomic diversity; functional diversity

11.1 A phylogenetic approach to detecting competition in a global dataset

Hercules Araclides[1], Jonathan Davies[1], Pedro Peres-Neto[2]
[1] Biology, McGill University
[2] Université du Québec à Montréal (UQAM)
Contact: eraclis.araclides@mail.mcgill.ca

I examine global patterns of competition strength across a global dataset of 723 Carnivora communities. Using a new phylogenetic approach, I use simple models of character evolution (i.e. Brownian and Ornstein-Uhlenbeck) to generate an expected distribution of trait values in the absence of competition. I then compare the dispersion of observed trait values relative to this null distribution. If competition has structured the distribution of trait values among co-occurring species, we would predict these traits to be more evenly distributed than expected. Conversely, habitat filtering would be indicated by clustering of the trait distribution. I contrast this new approach to more traditional ecological analyses that generate a null expectation by sampling from regional species pools. Extending these ideas, I examine the role that environment plays, and test the hypothesis that competition is stronger in the tropics than at higher latitudes. I model the strength of competition against climatic variables, taking into account spatial autocorrelation, to examine potential environmental drivers, and compare the differences in global patterns using phylogenetic and non-phylogenetic approaches.

11.2 ⚡ Francisco José de Caldas: a missing link in the origins of phytogeography

Malte Ebach[1], Carlos E. González-Orozco[2], Regina Varona[3]
[1] University of New South Wales
[2] , Institute for Applied Ecology and Collaborative Research Network for Murray-Darling Basin Futures, University of Canberra
[3] Fundacion Caldas
Contact: carlos.gonzalez-orozco@canberra.edu.au

In 1803 Colombian cartographer and astronomer Francisco José de Caldas (1768-1816) produced the first method for creating accurate phytogeographical regions, however until recently; his phytogeographical maps remained unpublished and largely unknown to the public and scientific community. Between 1796 and 1802 Caldas conducted a systematic study to develop a series of phytogeographical profiles, which provided the first known three-dimensional view of a landscape in the form of a map. Moreover, these maps proposed the first phytogeographical regions (bioregionalisation), mostly based on taxic distributions of commercial crops, across present day Ecuador in South America. Caldas's phytogeographical method consisted of four steps: (a) topographic characterisations, (b) measurement of elevation and temperature, (c) calculation of latitude and longitude and, (d) the distribution of known taxic distributions obtained from botanical collections. Despite the age of Caldas's method, his discovery is of great significance to contemporary science and should be given due credit as shares key principles in present-day bioregionalisation and phytogeography.

11.3 ⚡ Global patterns of diversity and diversification in ants

Evan Economo[1], Benoit Guénard[1], Michael Weiser[2], Nitish Narula[1]
[1] Okinawa Institute of Science and Technology Graduate University
[2] University of Okahoma
Contact: evaneconomo@gmail.com

Resolving global biodiversity patterns and understanding their evolutionary and ecological drivers remain key challenges for basic and applied biology. Recently, large-scale data syntheses and analyses have opened a broad spatial and temporal view of biodiversity patterns and dynamics, but this progress has been mostly limited to vertebrates and plants. Here, we compile and analyze a global distribution dataset for all 15,000+ described ant species, consisting of over 1.3 million literature and specimen records. Using these data, we identify the main gradients and hotspots of species richness around the globe. To investigate the evolutionary history underlying spatial richness patterns, we reconstruct time-calibrated phylogenies covering all ant diversity and perform Bayesian analysis of diversification rate variation across the tree. We find complex patterns of diversification rate variation but little effect of latitude despite a steep latitudinal gradient in species richness. We also found that overall temperate taxa are highly phylogenetically clustered and nested within tropical clades, but that transitions out of the tropical habitats only partially coincide with climatic cooling periods.

Keywords: diversification rate, latitudinal gradient, macroecology, macroevolution

11.4 ⚡ Origin of the latitudinal species richness gradient in the New World

Kristine Engemann[1], Brody Sandel[1], Brian Enquist[2], Jens-Christian Svenning[1]
[1] Ecoinformatics & Biodiversity Group, Institute for Bioscience, Aarhus University, Denmark
[2] Department of Ecology and Evolution, University of Arizona, USA
Contact: engemann@bios.au.dk

Spatial variation in richness patterns must be due to variation in rates of speciation, extinction, immigration and emigration. Hotspots of diversity can occur either because they are hotspots of speciation (cradles) or cold spots of extinction (museums) – two major hypotheses that make contrasting predictions for the phylogenetic structure of communities. We test these hypotheses by comparing centers of species richness and phylogenetic clustering for vascular plants in the New World. Range maps for 88,417 plant species were extracted from the Botanical Information and Ecology Network (BIEN) database and combined with the BIEN mega phylogeny of >80,000 species. We calculated the Phylogenetic Diversity Index (PDI) and Net Relatedness Index (NRI) for each cell in a 100×100 km grid using a new computationally efficient algorithm. Species richness patterns were compared to patterns of PDI and NRI. We found that, for all vascular plants, high species richness is associated with high phylogenetic clustering, supporting a “cradle” model of biodiversity hotspots. However, there is marked variation across plant families, which may be explained by variation in lifespans and growth forms.

Keywords: species richness, biogeography, phylogenetic diversity, latitudinal richness pattern, environmental niche

11.5 The contribution of migrants to diversity and energy use in North American bird communities across the seasons

Trevor Fristoe[1]
[1] University of New Mexico
Contact: tfristoe@unm.edu

On the order of 5 billion birds comprising more than 700,000 tonnes of biomass migrate into North American breeding bird communities each year. While many migrants depart to the tropics after breeding, others overwinter throughout the temperate zone. Despite the impressive scale, little is known about the metabolic role of these migrants within their breeding or winter communities across temperate ecosystems. I use data on community composition from citizen science projects and scaling relationships for field metabolic rate as a function of body size to calculate the contribution migrants to community diversity and energy use in over 2000 breeding and winter bird communities. In breeding communities, the relative contribution of migrants to community diversity and energy use increase with latitude. Across winter bird communities the pattern is more complex. In forested habitats, the contribution of migrants decreases with latitude. In grasslands, where migrants reach their highest diversity and energy use, their relative contribution to communities increases with latitude. During both seasons, the northern Great Plains seem to provide the greatest opportunities for migrants.

Keywords: Migration Metabolic ecology Community ecology Diversity gradient Macroecology

11.6 ⚡ Why endotherms dominate cold, productive oceans

John Grady[1], James Brown[2]
[1] Biology, University of New Mexico, USA
[2] Biology, University of New Mexico
Contact: jgrady@unm.edu

Endothermic mammals and birds tend to be most diverse and abundant in cold, rather than warm coastal waters. Pinnipeds and penguins, for instance, are almost completely absent from the productive Indo-Pacific - the center of marine biodiversity. In contrast, ectothermic competitors - such as sharks and marlin - are well represented in the tropics. Why? I present an energetic model of foraging to account for these patterns, focusing on the role of temperature in shaping the velocity, vulnerability and abundances of prey.

Keywords: Endotherm, ectotherm, energetics, metabolism, competition, locomotion, foraging

11.7 Migration mode influences geographical patterns in clutch size of European Passerines

Lenka Kopsová[1], David Hořák[1]
[1] Department of Ecology, Faculty of Science, Charles University, Czech Republic
Contact: l.kopsova@gmail.com

Geographical variation in avian clutch size has attracted much attention over past decades. Recent availability of high-quality broad-scale data allows us to test for factors affecting clutch size variation in detail. We focused on spatial variation in assemblage mean clutch size of European Passerines and investigated the influence of migration behavior on spatial patterns of the trait on background of environmental conditions. We calculated mean values of clutch size in grids 50x50 km separately for residents, all migrants, short and long distance migrants. We related them to environmental characteristics such as length of breeding season, productivity and seasonality of productivity using GLS and OLS. Clutch size in all Passerines increases with estimates of productivity but this is true only for residents. Clutch size in migrants (especially long distance ones) is negatively influenced mainly by length of breeding season which might reflect intense time limitations to which migrants are exposed during breeding.

Keywords: productivity, length of breeding season, latitudinal gradients, spatial statistics

11.8 ⚡ Global dynamics of mammalian diversity

Antonin Machac[1], Catherine Graham[1]
[1] Dept of Ecology and Evolution, Stony Brook University, New York
Contact: A.Machac@email.cz

Global diversity patterns are shaped by the processes of speciation, extinction, and dispersal. These processes, however, vary geographically for reasons that remain poorly understood. Our study evaluates the historical, environmental, and biotic factors potentially responsible for the variation using the newest data for mammals (>5,000 species). We explore the global dynamics of mammalian diversity and find that some biomes generate excessive diversity which then spreads worldwide (source biomes) while other biomes act as recipients (sink biomes). Interestingly, the source-sink dynamics cannot be explained by any of the traditionally suspected variables, including the historical, environmental, or biotic factors. Instead, high mammalian diversity within the source biomes, especially in the tropics, seems to facilitate evolutionary diversification. The expanding tropical diversity then spills over to other biomes, following a climatically regulated cascade. Our findings illustrate how the diversity itself may perpetuate global diversity dynamics, with the tropics acting as an effective engine of mammalian richness.

Keywords: biomes, diversification, niche conservatism, dispersal

11.9 ⚡ Exploring mechanisms underlying global mammal beta-diversity patterns

Caterina Penone[1], Ben J. Weinstein[2], Catherine H. Graham[2], Gabriel C. Costa[1]
[1] Departamento de Ecologia, Universidade Federal do Rio Grande do Norte, Natal, Brasil
[2] Department of Ecology and Evolution, Stony Brook University, NY
Contact: caterina.penone@gmail.com

Change in community composition between places, or betadiversity, provides the opportunity to explore mechanisms influencing spatial patterns of diversity. We analyze the three dimensions of betadiversity (taxonomic, phylogenetic and trait) at a global scale to explore the mechanisms underlying mammal diversity patterns. We calculated all pairwise comparisons of assemblages at 1-degree scale for 5,000 mammal species across the globe. We obtained ~70 million comparisons for each of the three dimensions and tested their relation with geographic and

environmental distances. In most cases the three dimensions were positively correlated between them and betadiversity increased with geographic or environmental distance. However, assemblages that were in similar environments but separated by large spatial distances showed low trait dissimilarity while taxonomic and phylogenetic betadiversities were significantly higher than expected. This suggested that isolated and distantly related assemblages converged to similar characteristics, driven by environmental conditions. Our results bring new evidence for convergent evolution of mammal traits in similar environments at global scale.

Keywords: betadiversity, trait, phylogeny, mammal, biome, realm, pairwise comparisons, betadiversity mapping, parallelization, predictive framework, deserts

11.10 Differential effects of environmental heterogeneity on global mammal species richness

Anke Stein[1], Jan Beck[2], Carsten Meyer[1], Elisabeth Waldmann[3], Patrick Weigelt[4], Holger Kreft[1]
[1] Biodiversity, Macroecology and Conservation Biogeography Group, University of Göttingen, Germany
[2] Department of Environmental Science (Biogeography), University of Basel, Switzerland
[3] Department of Epidemiology, University of Liverpool, UK
[4] Systemic Conservation Biology and Biodiversity, Macroecology and Conservation Biogeography Group, University of Göttingen, Germany
Contact: astein@uni-goettingen.de

Spatial environmental heterogeneity (EH) is an important driver of species richness and has been quantified in many different ways. However, the literature is dominated by only a few common EH measures like elevation range. Here, we calculate and compare 51 EH measures across three spatial grains and at global extent. These measures represent five subject areas (land cover, vegetation, climate, soil, and topography) and nine calculation methods. We explore the similarity among EH measures and find that despite some redundancy, correlations and different spatial patterns indicate clear differences between measures. Moreover, we analyse the relationship between species richness of terrestrial mammals and each EH measure alone and while accounting for effects of current climate, biogeographic region and human influence. We find a clearly differential importance of EH subject areas and calculation methods: measures of climatic and topographic EH and measures calculated as counts and ranges receive particularly high model support across spatial grains. Our results highlight that methodological decisions greatly determine the outcome of EH–richness studies.

Keywords: habitat diversity, heterogeneity measures, macroecology, mammal species richness, spatial scale

P12 Biodiversity hotspots

12.1 At a crossroads of two global biodiversity hotspots: Amphibian assemblage wide evaluation of the biogeographic patterns of the Shimba Hills of Kenya.

Beryl Akoth[1], Peter Nagel[1], Simon Loader[1]
[1] Biogeography, University of Basel
Contact: beryl.bwong@unibas.ch

The Shimba Hills (SH) is one of the largest patches of Coastal forests of East Africa (CFEA). They are categorized as part of CFEA, however biogeographically there are suggestions of a more complex history. From old and current collection of its herpetofauna it harbours species also associated to the Eastern Afromontane (EAM) forests. Both EAM and CFEA are global biodiversity hot spots. Despite this "crossroad" position no study has been conducted to verify its actual biogeographical affiliation and the historical patterns of species that occupy these regions. We aim to determine the biogeographic patterns in fine detail by conducting a phylogenetic analysis and testing two alternative hypotheses across the whole amphibian assemblage. We will outline preliminary data outlining whether SH species either group with CFEA or EAM populations/species. Preliminary calculations of absolute and relative times of divergence events will be presented, allowing us to understand the timing of separation across multiple lineages and whether single or multiple events can explain current biogeographic patterns. We will begin to establish if divergences are recent or old events, and whether they correlate with any geographic events.

12.2 Speciation patterns in the lowland forests of East Africa

Chris Barratt[1], Michele Menegon[2], Nike Doggart[3], Peter Nagel[1], Simon Loader[1]
[1] Biogeography Research Group, Department of Environmental Sciences, University of Basel, Switzerland
[2] Tropical Biodiversity Section, Science Museum of Trento, Italy
[3] Tanzania Forest Conservation Group, Dar es Salaam, Tanzania
Contact: christopher.barratt@unibas.ch

The Coastal Forests of Eastern Africa (CFEA) are a global biodiversity hotspot. It is uncertain how biodiversity accumulated in this region, and there have been no studies to date on this (Burgess & Clarke, 2000). It is unclear whether the present distribution of CFEA diversity is mainly: A) The result of recent colonisation from adjoining refugial areas due to habitat instability and inundation (e.g. Dimitrov et al. 2012), or B) the result of radiations from relicts within which were present in suitable climatically stable environments (e.g. Hochkirch, 2010). We are using amphibians to test these predictions (A or B) using next generation sequencing methods (RAD-seq) and species distribution models. A comparative demographic approach and tree-based methods will provide a first evaluation of speciation patterns in the CFEA. By investigating three widespread amphibian species we seek to explain general biogeographic patterns and what makes this area an important biodiversity hotspot.
Keywords: Biogeography, speciation, amphibians, Kenya, Tanzania, Mozambique, coastal forest

12.3 ⚡ Biogeography and biodiversity of cacti – a first complete biogeographical analysis of a large plant family

Wilhelm Barthlott[1], Kirsten Burstedde[1], Laurens Geffert[1], Pierre Ibisch[2], Nadja Korotkova[3], Daud Rafiqpoor[1], Anke Stein[4], Jens Mutke[1]
[1] Nees Institute for Biodiversity of Plants, Rheinische Friedrich-Wilhelms-Universität Bonn
[2] Centre for Econics and Ecosystem Management, Eberswalde University for Sustainable Development
[3] Botanischer Garten und Botanisches Museum Berlin-Dahlem
[4] Free Floater Group Biodiversity, Macroecology and Conservation Biogeography, Georg-August University of Göttingen
Contact: mutke@uni-bonn.de

The Cactaceae with c. 1,435 species are the most important plant family of the arid regions of the Americas. Recent revisions and molecular studies resulted in an improved knowledge of the phylogeny and taxonomy of this group. Due to their high value as ornamental plants, countless publications with data on ecological preferences and geographic occurrence of the species are available. Based on these data, we mapped the distribution areas of all

cactus species and identified seven geographical centers of cactus diversity. The dataset together with additional analyses is just published as Volume 7 of 'Schumania'. It is the most comprehensive biogeographical analysis of one of the larger plant families, illustrated by 333 colored maps and 60 color figures on c. 200 pages. We analyzed overall diversity patterns of the family, as well as, diversity patterns of all taxonomic subgroups, growth forms, and pollination syndromes. The results are discussed in the context of the phylogeny and the conservation of Cactus diversity. More than 50% of the species have extremely small distribution ranges, resulting in potential threat and insufficient coverage by existing protected areas.

Keywords: Cactaceae, Neotropics, Distribution Atlas, Diversity mapping

12.4 ⚡ Identifying critical habitats for conservation focus in eastern Africa and Madagascar with the aid of MODIS-based cloud climatologies

Rahama Beida[1], Michael Douglas[1], Marcia Fuentes[2]
[1] Cooperative Institute for Mesoscale Meteorological Studies, University of Oklahoma, USA
[2] Instituto Federal de Santa Catarina, Florianopolis, Brazil
Contact: douglasnoaa@gmail.com

Cloud climatologies produced from visible MODIS imagery reveal mean cloudiness patterns that strongly reflect the underlying topography in tropical and subtropical regions. We have compared our MODIS climatologies for parts of eastern Africa and Madagascar with conventional precipitation climatologies and with WORLDCLIM products. This poster focuses on the narrow band of inland slope forest that extends North-South for over 1000 km in eastern Madagascar. We also examined the varied terrain in eastern Kenya and Tanzania, focusing on the Ngorongoro to Kilimanjaro region. The MODIS-based climatologies (with a resolution of 250m) are much more closely associated with forest patches, and with the underlying relief, than WORLDCLIM precipitation products. Conservation applications of the MODIS products include 1) mapping climatological corridors and isolated cloudiness maxima that are not suggested by either existing climatological products or from the current partially deforested landscape, and 2) identifying isolated mountain cloudiness maxima that are missed by conventional climatic data or WORLDCLIM analyses. This should facilitate rapid ecological assessment efforts.

Keywords: Africa, MODIS, climatology, cloudiness, REA, conservation, Madagascar, Kilimanjaro, WORLDCLIM

12.5 ⚡ Arbopro - A project to protect Afromontane tree species diversity of Ethiopia

Peter Borchardt[1], Habtamu Assaye[2], Ben Jones[3], Kirsty Shaw[4]
[1] University of Hamburg, CEN Center for Earth System Research and Sustainability, Inst. of Geography, Germany
[2] Hawassa University, Wondo Genet College, Ethiopia
[3] University of Oxford, Botanic Garden - Harcourt Arboretum, United Kingdom
[4] Botanic Gardens Conservation International, United Kingdom
Contact: pbo1@gmx.de

Tree species are of particular importance at the Horn of Africa. In this region of low forest cover, but high diversity of shrub and tree species, the remnant forest stands are adversely affected by anthropogenic disturbance and climate change. Under these circumstances, the re-establishment of the Wondo Genet College (WGC) Arboretum is of outstanding importance for biodiversity conservation in this region. The Arboretum was established in 1978, but since more than ten years out of use. The purpose of the Wondo Genet Arboretum Project (ARBOPRO) is to foster the exchange between international experts on biodiversity and conservation in order to support the WGC, and to establish native tree species and therewith to enhance the collection. Therefore, we will establish exchange between botanical gardens, both within Ethiopia and internationally to support the development of a national botanic garden network and ensure WGC Arboretum is part of relevant existing international networks. Our goal is to enable the WGC to act as a platform for future ex situ and in situ conservation, for joint research on biodiversity and nature conservation in the challenging environment of East Africa.

Keywords: capacity building, ex situ conservation, indigenous tree species, sustainable resource management

12.6 ⚡ Amphibian evolutionary hotspots in the Iberian Peninsula

Silvia Carvalho[1], Ricardo Cardoso[2], Pedro Tarroso[2], Mafalda Barata[2], Craig Moritz[3], Salvador Carranza[4], Guillermo Velo-Antón[2]
[1] CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto
[2] CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto
[3] Research School of Biology and Centre for Biodiversity Analysis, The Australian National University
[4] Institute of Evolutionary Biology, CSIC-Universitat Pompeu Fabra
Contact: silviacarvalho@cibio.up.pt

Genetic diversity underpins biodiversity generation and persistence. Thus, spatial patterns of genetic variation should be identified and accounted for in the design of conservation areas. The Iberian Peninsula is important for amphibian's conservation, as it comprises several endemic and threatened species, many exhibiting high intra-specific genetic variation, which is often spatially structured. We aimed at identifying evolutionary hotspots of Iberian amphibians, *i.e.* areas of occurrence of multiple intra-specific lineages and areas of occurrence of multiple contact zones. We used published and new mtDNA sequences to estimate the phylogenetic relationships within each species, and grouped distinct haplotypes into main lineages. We then used a modified version of kriging interpolation to predict areas of occurrence of each lineage and areas of potential contact zones between distinct lineages. We identified evolutionary hotspots by summing the number of distinct lineages (lineage richness) and of potential contact zones (contact zones richness) across the 14 species. Our results highlight Northern Iberia as a major evolutionary hotspot.

Keywords: Phylogeography, Lineage distribution, Contact zones, Kriging, Conservation.

12.7 ⚡ Geographical variation and context-dependency in an ant-plant interaction in the Western Ghats biodiversity hotspot, India

Joyshree Chanam[1], Srinivasan Kasinathan[1], Gautamkumar Pramanik[1], Amaraja Jagdeesh[1], Kanchan Joshi[1], Renee Borges[1]
[1] Indian Institute of Science
Contact: vijay_rhaco@yahoo.com

Variation in strength of species interactions has been proposed to influence evolutionary trajectories of co-evolving species at different geographical locations, ultimately affecting the organisation of earth's biodiversity. We investigated geographic variation in strength of protection-mutualism between an endemic ant-plant *Humboldtia* brunonis and its non-obligate associated ants, across five sites spanning its distributional range in the Western Ghats of India. We observed that protection by ants is highest at the site where herbivory is highest and "rewards", viz., nesting sites and extrafloral nectar, are also highest, indicating a context-dependency in the interaction. Overall, there was an increase in strength of different interaction parameters from northern to southern sites. This is note-worthy, especially since a congeneric ant-plant species in Sri Lanka, which is further south, is known to be in an obligate mutualism with the same ant species which we found to give significant protection in our system. Taken together, these findings suggest a north-south gradient in the strength of this mutualism in the Western Ghats – Sri Lanka biodiversity hotspots.

Keywords: geographical variation, species interactions, plant-animal interactions, mutualism, ants, Western Ghats, chemical ecology

Continued next page

12.8 ⚡ Global patterns of vascular plant species richness, endemic richness and endemicity: a new approach to identify hotspots and cold spots

Jürgen Dengler[1], Carl Beierkuhnlein[2], Franz Essl[3], Jose Maria Fernández-Palacios[4], Carsten Hobohm[5], Anke Jentsch[1], Holger Kreft[6], Pavel Krestov[7], Swantje Löbel[8], Reinhold Stahlmann[9], Manuel J. Steinbauer[2], David Storch[10], Kostas Triantis[11], Patrick Weigelt[6], Alessandro Chiarucci[12]
[1] Disturbance Ecology, BayCEER, University of Bayreuth
[2] Biogeography, BayCEER, University of Bayreuth
[3] Department of Botany and Biodiversity Research, University of Vienna
[4] Island Ecology and Biogeography, University of La Laguna
[5] Interdisciplinary Institute of Environmental, Social and Human Sciences, University of Flensburg
[6] Biodiversity, Macroecology & Conservation Biogeography Group, Faculty of Forest Sciences and Forest Ecology, University of Göttingen
[7] Botanic Garden Institute of the Far-Eastern Branch of the Russian Academy of Sciences
[8] Department of Ecology and Genetics, Uppsala University
[9] Biogeography, University of Bayreuth
[10] Center for Theoretical Study, Charles University in Prague and Academy of Sciences of the Czech Republic
[11] Department of Biology, National and Kapodistrian University of Athens
[12] Department of Life Sciences, University of Siena
Contact: juergen.dengler@uni-bayreuth.de

Endemism fascinated botanists since centuries. We refer to endemism as the general phenomenon, endemic richness as the number of endemic species in an area and endemicity as its fraction. Like species richness, also endemic richness and endemicity increase with area. Our aims thus were to describe these scale-dependencies mathematically and to identify areas that show positive or negative deviations. We compiled data triplets of vascular plant species richness, endemic richness and area for more than 800 geographic entities worldwide. We modelled the scale-dependency of the three parameters biome-wise, as they varied greatly between the biomes. With non-linear regression and AIC, we compared a set of different function types. Power functions generally provided reasonable models, but the model fit was much better with a breakpoint. Consistently, the species-area relationships had higher z-values above c. 100,000 km². Then, the various diversity-area relationships were combined into global mean functions, weighted by fractional area of the biomes. We propose a normal endemicity index to quantify how much a geographic entity of any size is below or above the expected value.

Keywords: Species-area relationship; endemism; species richness; scale dependency; diversity map; non-linear regression

12.9 ⚡ Direct and indirect effects of the uplift of the Qinghai-Tibetan Plateau on the evolution of Tibetan biotas

Adrien Favre[1], Martin Päckert[2], Steffen Pauls[3], Sonja Jähnig[4], Dieter Uhl[5], Ingo Michalak[1], Alexandra Muellner-Riehl[6]
[1] University of Leipzig
[2] BiK-F, Senckenberg Natural History Collections Dresden
[3] BiK-F
[4] BiK-F, Leibniz-Institute of Freshwater Ecology and Inland Fisheries
[5] Senckenberg Research Institute and Natural History Museum Frankfurt
[6] BiK-F, iDiv, University of Leipzig
Contact: adrien.favre@uni-leipzig.de

Hotspots of biodiversity are often associated with areas that have undergone recent orogenic activity. Yet, the origin and evolution of diversity hotspots associated with the Qinghai-Tibetan Plateau (QTP), the largest geological feature on Earth, remains poorly understood. We reviewed literature related to the diversification of organisms linked to the uplift of the QTP. We also found that the contribution of biological interchange between the QTP and other hotspots of biodiversity has not been sufficiently studied. To promote hypothesis-based research, we here provide a geological and climatic scenario for the QTP. We argue that further studies should provide a complete set of complementary analyses (including biogeographic analyses) to test for correlations between organismic diversification and past environmental changes. The biological consequences of the uplift of the QTP would be best understood using a meta-analysis approach, encompassing studies on a variety of organisms from diverse habitats and thermal belts. Finally, since species diversity in the QTP region is better documented for some taxa than for others, we suggest that exploratory taxonomic work should be promoted.

Keywords: biodiversity biogeography birds diversification rates flowering plants freshwater diversity mountain formation molecular clocks organismic evolution Qinghai-Tibetan Plateau

12.10 Patterns and drivers of vertebrate species richness in West Africa

Amir Lewin[1], Shai Meiri, Anat Feldman, Yuval Itescu
[1] Zoology, Tel Aviv University
Contact: amirlewin@hotmail.com

We mapped West African amphisbaenian, crocodile, lizard, snake, and turtle distributions to explore the congruency of these groups with amphibians, birds, and mammals. We found that vertebrate distributions in West Africa are largely congruent because they respond similarly to environmental conditions. These taxa show a classic latitudinal gradient, from low richness in the southern Sahara increasing towards the most equatorial latitudes in the region. However, patterns of lizard species richness stand distinct from all remaining taxa: their distributions are patchy with hotspots in both rainforest and arid regions, and it is less well explained by environmental correlates. Furthermore, lizard richness is weakly correlated with all of the vertebrate groups. Endemic amphisbaenians, lizards, snakes, and turtles are widely dispersed and do not necessarily overlap with each other and with total species richness. Many lizard species, including many endemics are found in the southern parts of Cameroon and eastern Nigeria, a regular hotspot of species richness for all of the vertebrate classes examined.

Keywords: Reptiles; snakes; lizards; amphibians; birds; mammals; species richness; West Africa; cross-taxon congruence; hotspots; environmental variables; temperature; net primary productivity; habitat heterogeneity; range size; endemics.

12.11 ⚡ Mapping the distribution of ancient plant and animal lineages in southern Africa

Ashlyn Levadia Padayachee[1]
[1] School of Environmental Sciences, University of KwaZulu-Natal
Contact: ashlyn.levadia@gmail.com

The focus of this project was to identify ancient endemic biological lineages (faunal and floral) and map the distributions of these lineages across Southern Africa. The mechanisms of survival of these lineages were investigated and their importance for conservation in Southern Africa emphasized. Seventy-four operational geographic units (OGUs) were created. Twenty-seven ancient lineages were selected, from which individual distribution maps were created. A total endemism and weighted endemism map was created collectively for all lineages. Furthermore, four stages of Cluster Analysis were conducted to find clusters of OGUs with similar lineage composition, and three dendograms were produced. Characteristic lineages were determined for each of the cluster units at the different stages of clustering. Five characteristic lineages were found in stage one clustering, 3, 9 and 2 characteristic lineages were found for stages two, three and four respectively. These were used to further emphasize areas of conservational importance.

Keywords: endemism, biogeography, ancient endemic lineages

12.12 ⚡ Phylogenetic diversity in conservation planning: large PD gains with slight expansion of protected areas

Laura Pollock[1], Andrew Thornhill[2], Heini Kujala[1]
[1] The University of Melbourne
[2] James Cook University
Contact: lajosy@gmail.com

Evolutionary history is rarely considered in conservation planning despite its popularity in the scientific literature. One reason for this is that we are missing a framework and method for including evolutionary diversity measures such as Phylogenetic Diversity (PD) in widely-used conservation planning software. Many studies map diversity hotspots across the landscape, but these tend to be poor conservation priorities as they do not account for aspects of complementarity and irreplaceability which are the key principles of cost-effective conservation planning. Here, we demonstrate a recently developed method combining spatial conservation prioritization with PD and species distribution models for 680 eucalypt species that dominate forest canopies across Australia. Currently, 25% of the total remaining eucalypt PD is protected in reserves, which cover 15% of the land area. Importantly, with just a 2% expansion of the current protected areas, we could include 70% more PD. The largest intact 'candidate' area for protected area expansion coincides with both a world biodiversity hotspot and an area of active mining exploration.

Keywords: Phylogenetic diversity, systematic conservation planning, species distribution models

12.13 ⚡ Avian phylogenetic diversity: global patterns and their drivers

Alke Voskamp[1], David J. Baker[1], Philip A. Stephens[1], Stephen G. Willis[1]
[1] School of Biological and Biomedical Sciences, Durham University
Contact: alke.voskamp@durham.ac.uk

The aim of species conservation should be not only to maximise contemporary preserved biodiversity but also to maximise its evolutionary potential, increasing the likelihood biodiversity of future persistence. Metrics of phylogenetic diversity (PD) that are not purely based on species richness (SR) can identify areas of broader conservation value. Here, we contrast global avian SR with Faith's PD to determine to what extent the two differ. We show that, whilst SR and PD are strongly correlated, there are key regions where they differ. Studies of global mammal and amphibian PD have also highlighted areas of differences with SR. However, the key regions of differences for birds differ from those found for mammals and amphibians. We explored the relationship between avian PD and potential explanatory variables, including SR, temporal climate stability, habitat diversity, altitudinal range and distance to the margin of biological realms. We found strong support that the most important drivers for avian phylogenetic diversity differ between biological realms. Our study suggests that different drivers underlie processes of speciation and extinction in different parts of the world.

Keywords: avian phylogenetic diversity, global species richness, conservation

P13 Marine biogeography

13.1 Modelling the ecological niche of highly mobile species in a dynamic environment

Marc S. Fernandez[1], Chris Yesson[2], Alexandre Gannier[3], Peter Miller[4], James Bowcot[4], Jose Manuel Neto Azevedo[1]
[1] CIIMAR/CIMAR, Interdisciplinary Centre of Marine and Environmental Research, University of Porto & CIRN, Department of Biology, University of the Azores, Portugal
[2] Institute of Zoology, Zoological Society of London
[3] Groupe de Recherché sur les Cétacés
[4] Remote Sensing Group, Plymouth Marine Laboratory, UK
Contact: marc.fern@gmail.com

Ecological niche models are usually based on relatively stable environmental variables. However some environments can be very dynamic (i.e. marine habitats). We tested different temporal approaches for modelling the ecological niche of mobile species in an oceanic environment. Two virtual species were created: one more influenced by dynamic variables (sea surface related), the other by static variables (bottom related). Areas of daily potential occurrence were selected using a threshold approach. Different sets of presences for each species were randomly selected 1,000 times. Three temporal classes were considered: daily, weekly and total. A binomial GLM with a stepwise AIC procedure was applied to select the best fitting models. The daily classes performed better in detecting the effects of the dynamics variables, however it introduces some noise. The weekly approach detected the effects of almost all the dynamic variables and also reduced the noise. The total approach succeeded in detecting the static variables, but failed for sea surface variables. Using a weekly timeframe seems a good compromise for modelling the niche of highly mobile species in a dynamic environment.

Keywords: Ecological niche, dynamic variables, mobile species, marine environment

13.2 Analysis of historical and evolutionnary constraints on reef fishes distribution at the Indo-pacific scale

Théo Gaboriau[1], Nicolas Hubert[2], David Mouillot[1]
[1] Université Montpellier 2 UMR Ecosym
[2] IRD Institut des sciences de l'évolution de Montpellier
Contact: theogaboriau@gmail.com

The coral triangle, located between the Indonesian archipelago, the Philippines islands and the north of Australia, is recognized as the global centre of marine biodiversity. Several hypotheses related to historical and evolutionary events have been put forward to explain the origin and maintenance of this biodiversity peak with an active debate. Owing to the recent advances in the fields of phylogenetics and historical biogeography combined to the collection of extensive datasets, we can test predictions made by these hypotheses. We reconstructed the phylogenetic relationships among species from three tropical reef fish families (Chaetodontidae, Labridae, Pomacentridae) at the scale of the Indo-Pacific region. Divergence times between sister species (estimated using fossil data) were then compared to their level of distribution overlap (estimated separately at local and regional scale) to determine whether closely related species tend to spatially converge after speciation and which process are driving those dynamics. Our results suggest that allopatric speciation is a predominant mode of speciation for those families and tend to support the 'centre of overlap' hypothesis

Keywords: Centre of overlap, speciation, phylogenetics, Coral Triangle

13.3 Biodiversity of coral reefs and geographical pattern of marine protected area

Yasuhiro Kubota[1], Youta Miyagi[1], Buntarou Kusumoto[2]
[1] Faculty of science, University of the Ryukyus
[2] The Institute of Statistical Mathematics
Contact: kubota.yasuhiro@gmail.com

Mapping species distribution and specifying geographical areas harboring high species richness are essential first step to derive conservation strategy for protecting biodiversity. In the marine biome, multiple mechanisms have been proposed to explain global biodiversity patterns, specifically focusing on the roles of environmental filter, habitat area and dispersal. In this study, we created global-scale maps of 128 scleractinian coral species and marine protected area. Using the dataset of species geography, we calculated the metrics of species diversity, phylogenetic community structure and evolutionary distinctiveness at the global scale, and explored correlations between these metrics and environmental variables. We also examined relationships between marine protected area and the biodiversity patterns of coral reefs. Finally, we identified priority area for maintaining evolutionary potentials of coral diversity hotspots.

13.4 Global-scale patterns of phylogenetic structure in tropical reef fish assemblages

Fabien Leprieur[1], Simona Colosio[2], Patrice Descombes[2], Valeriano Parravicini[3], Michel Kulbicki[4], Peter Cowman[5], David Bellwood[6], David Mouillot[1], Loic Pellissier[2]
[1] UMR ECOSYM 5119, Université Montpellier 2, France
[2] University of Fribourg, Unit of Ecology & Evolution, Switzerland
[3] CNRS-EPHE, CRIOBE – CBETM, Université de Perpignan, France
[4] Institut de Recherche pour le Développement, UR 227 CoReUs, France
[5] University of Yale, Department of Ecology & Evolutionary Biology, USA
[6] ARC Centre of Excellence for Coral Reef Studies, James Cook University, Australia
Contact: fabien.leprieur@univ-montp2.fr

The distribution of tropical reef fishes is characterized by a hotspot in the Indo-Australian Archipelago (IAA), which contrasts with the much lower diversity in the Atlantic Ocean. Investigating the phylogenetic structure of reef fish assemblages may help unravel the processes at the origin of spatially contrasted biodiversity patterns across tropical seas. Here, we mapped the phylogenetic structure of tropical reef fish assemblages worldwide and related it to contemporary and past environmental conditions. We found that the phylogenetic structure of species assemblages of the Pomacentridae family and to a lower extent of the Chaeotodontidae and Labridae families were associated with the historical distribution of coral reefs during the Quaternary. The marked phylogenetic clustering in the IAA suggests that the fragmentation of reef fish habitat into smaller refugia during the glacial periods promoted allopatric speciation and the formation of closely related lineage within this geographical region. Distinct responses among fish families suggest that dispersal abilities interacted with past climatic fluctuations in shaping the phylogenetic structure of tropical reef fish assemblages.

Keywords: allopatric speciation, Chaetodontidae, Labridae, phylogenetic community structure, Pomacentridae, quaternary climate change, refugia.

13.5 Modelling the past, present and future distribution of macrofauna species in the Jade Bay (North Sea, Germany)

Anja Singer[1], Ulrike Schückel[2], Heiko Westphal[3], Karsten Lettmann[4], Gerald Millat[5], Melanie Beck[6], Ingrid Kröncke[2]
[1] University of Bremen, INTERCOAST Research Training Group, Germany
[2] Senckenberg am Meer, Marine Research Department, Wilhelmshaven, Germany
[3] Coastal Research Station - Lower Saxony Water Management, Coastal Defence and Nature Conservation Agency, Norderney, Germany
[4] Institute for Chemistry and Biology of the Marine Environment (ICBM), Department of Physical Oceanography, Carl von Ossietzky University, Oldenburg, Germany
[5] Common Wadden Sea Secretariat, Wilhelmshaven, Germany
[6] Institute for Chemistry and Biology of the Marine Environment (ICBM), Department of Microbiogeochemistry, Carl von Ossietzky University, Oldenburg, Germany
Contact: anja.singer@senckenberg.de

Species Distribution Models were applied to hindcast and forecast the distribution pattern of characteristic macrofauna species in the Jade Bay in response to expected climatic- and environmental changes. Additionally, potential harbour effects (JadeWeserPort) were considered. Due to the sessile habit, benthic species are ideal organisms for small-scale distribution modelling and important indicators for disturbances. The species-specific present distribution was predicted based on high resolution environmental grids (MAXENT algorithm). Results for past distribution scenarios were compared with historical macrofauna data (1930s and 1970s). For the future distribution scenarios, regional climate scenarios (2050 and 2085) will be used to predict the effects of: Ongoing sea-level rise, increasing water temperatures, increasing mudflats, increasing sediment volume and extending seagrass beds. The past distribution scenarios show a good match with historical macrofauna data and are therefore a reliable validation of the MAXENT algorithm. The modelled future distribution scenarios indicate range gains for those species tolerating high mud content, high topography and high shear stress.

Keywords: Predictive modelling, marine ecosystem, MAXENT, environmental change, UNESCO Wadden Sea World Heritage

13.6 Planktic foraminifera: modelling the climatic constraints on modern and palaeo-biogeography

Amy Waterson[1], Kirsty Edgar[1], Daniela Schmidt[1], Paul Valdes[1]
[1] Geographical Sciences & Earth Sciences, University of Bristol
Contact: aw13663@bristol.ac.uk

Planktic foraminifera are globally distributed marine protozoa that precipitate a carbonate shell. Their exceptional fossil record plays a fundamental role in the reconstruction of palaeoclimates using assemblage composition and chemical properties of their calcite shells. Our ability to reconstruct climate is based on relationships derived in the modern ocean assuming stability of the ecological niche. A greater understanding of the environmental controls on foraminiferal biogeography is thus central to accurate interpretation of such proxies. We apply ecological niche models (ensemble modelling platform biomod2) to identify the constraints on species distributions for both the modern and the Last Glacial Maximum (21 ky BP), using a comprehensive global compilation of planktic foraminiferal census counts, with consistent age controls and constraints on preservational biases. Outputs produced from the Hadley Centre general circulation model (HadCM3) are used to assess the importance of a range of environmental factors on the potential distributions of foraminifers. This allows us to determine the stability of species climatic niches during a fundamentally different climate.

Keywords: climatic niche, planktic foraminifera, ecological niche models, Last Glacial Maximum, palaeoclimate, preservational bias

14.1 Feed values variation in arid mountain pastureland under grazing impact in Qilian Shan, NW China

Alina Baranova[1], Udo Prof. Dr. Schickhoff[1], Shunli Wang[2]
[1] Institut für Physische Geographie, Hamburg Universität, Hamburg; Germany
[2] Academy of Water Resource Conservation Forest of Qilian Mountains (AWRCFQM), Gansu Province, China
Contact: earth0909@gmail.com

Uncontrolled sheep and yak grazing on the mountain areas in Qilian Shan (Gansu province, NW China) has considerably increased over the recent past inflicting adverse ecological effects on vegetation. Most of the grasslands have become secondary vegetation, with a considerable percentage of unpalatable, toxic and thorny shrub and herb species that have a lower grazing value. In order to understand, how does differential grazing pressure changes biomass and productivity and what is the effect of grazing on vegetation types, vegetation surveys have been performed during the growing period over different slope aspects and in areas with differing grazing intensities. Vegetation inventories aim at determining biomass production as well as assessing grazing index as being attributed to the composition of plant functional types and species. To determine feed values of vegetation types, dry matter of biomass samples have been analysed with regard to neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), ash as well as inorganic content (nitrogen, phosphorus).
Keywords: mountain pastures, degradation, feed values

14.2 Mosquito (Diptera: *Culicidae*) biodiversity in south-central Florida and the dilution effect for exposure to zoonotic disease

Caitlyn Debevec[1]
[1] Biology, University of Central Florida
Contact: caitrosed@gmail.com

The likelihood of a mosquito-borne zoonosis event to occur depends on mosquito abundance and diversity and other host/disease species in the area. The hypothesized effect of diversity on zoonosis is the “dilution effect.” Areas with greater mosquito diversity may have limited zoonosis risks because vectoring mosquitoes may be “diluted” in prevalence. This study aims to identify the effects of region, vegetative structure, and land use on mosquito diversity to gain insight into the vector dilution effect. Across ~1/2 the Florida peninsula (USA), 18 sites were sampled June-November, 2012. All combinations of vegetation structure (3 types) and land use (2 types) were sampled in each of 3 regions. Multivariate analyses of mosquito community composition indicate overlap among sites, but with some separation for individual environmental factors. Model selection among 44 alternative models of environmental factors as predictors of mosquito composition indicate seasonality best predicts mosquito composition in the study area. Species-specific habitat preference appears to be a more parsimonious explanation for zoonosis risk than a general dilution effect across the sampling area.
Keywords: Mosquito, dilution effect, mosquito ecology

14.3 Causes and consequences of riparian tree recruitment in a steep Mediterranean river

Lisa Guan[1], Chris DiVittorio[2], Justin Chin[2], Julianne Hay[1], Natalie Holt[3], Tyner Pesch[4], Amelia Weiss[4], William Dietrich[4], Mary Power[2]
[1] Environmental Science, Policy and Management, University of California, Berkeley
[2] Integrative Biology, University of California, Berkeley
[3] Forestry, University of California, Berkeley
[4] Earth and Planetary Science, University of California, Berkeley
Contact: lisaguan2@gmail.com

White alder (*Alnus rhomibifolia*) recruitment plays an important role in altering the geomorphology of riparian zones. Here we report the causes and consequences of alder recruitment in a Mediterranean-type stream in Northern California. We found that recruitment was promoted by a series of two or more low-peak-flow winters that allow saplings to grow to a less vulnerable size, creating even aged stands synchronously. Despite this, not all predicted

recruitment windows were accompanied by recruitment events. Cohort demography showed that germination fluctuates with life history stage and survival was positively density-dependent, likely due to the effect of neighboring trees reducing flood scour and shear stress. Channel cross sectional surveys suggest that modification of the channel by alders themselves may explain the relationship between survival and density. The surveys show that alders promote deposition around mid-channel islands and decrease sediment size within and downstream of dense stands. Together, the contingency of seed dispersal, the dependence on rainfall patterns and the nonlinear population dynamics can explain the episodic patterns of tree recruitment along this river.

Keywords: alder recruitment, riparian, geomorphology, dendrochronology

14.4 ⚡ Towards generality in studies of disturbance and ecosystem dynamics

Anke Jentsch[1]
[1] Disturbance Ecology, BayCEER, University of Bayreuth
Contact: anke.jentsch@uni-bayreuth.de

The last decades have seen a tremendous growth in our understanding of the role of disturbance in ecosystems. We have established the importance of disturbance in many habitats, documented disturbance regimes, experimented with restoration of natural disturbance regimes, determined the array of functional adaptations to disturbance, and discovered the key role of disturbance in maintaining biological diversity. Among the most important recent challenges are interactions among disturbances and effects of climate extremes on ecosystem functioning. Here, I present an overview of disturbance theory and discuss approaches to generality at patch and multi-patch scales, and through the classification of species role.

Keywords: disturbance ecology, stability, resilience, resistance, theory, fire, drought, flooding, system dynamics, human impact, climate extremes, ecosystem functions

14.5 Variation of plant drought tolerance in temperate grasslands: Effects on community assembly and ecosystem resilience

Eunyoung Jung[1], Bettina Engelbrecht[1]
[1] BayCEER, University of Bayreuth
Contact: eun-young.jung@uni-bayreuth.de

Drought is expected to increase in its frequency and severity, which can have an impact on plant community composition and diversity. Species' drought tolerance can be examined by evaluating relevant traits in driving the variation in species' responses to drought. Our main objective is to identify the key traits for differential drought responses of grassland species through linking traits to a quantitative assessment of drought responses. With that information, the role of drought for community assembly will be evaluated across land-use gradient. To address these objectives, we will perform an *ex situ* field experiment for 40 common species in the Biodiversity Exploratory grasslands. Plants will be planted into 72 plots in a meadow site in the Ecological Botanical Garden at the University of Bayreuth and exposed to two treatments, i.e. wet and dry treatment. Drought tolerance of each species will be assessed as response ratios and their physiological, anatomical and morphological traits will be measured. Our study will contribute to understand a role of drought on functional traits composition and diversity, which can be translated into function and resilience of grasslands.

Keywords: Plant functional traits, temperate grassland, drought

Continued next page

14.6 Geographical fundamenthals of the plant diversity at the south of the Göksu Valley (TAŞELI Plateau) Turkey

İpek Özalp[1], Meral Avci[1]
[1] İstanbul University, Physical Geography Department
Contact: ipek.ozalp@istanbul.edu.tr

Taşeli Plateau, being considered as one of the most important karst plateau areas in Mediterranean Region, having peaks which are of 2000 m high in places, is deeply split by Göksu River and its tributaries (Ermenek River). The field, being situated in the Mediterranean floristic area. Deeply split valleys and karstic lithology being formed on the surface of high plateaus are obviously among the most prominent morphological elements, causing the diversification of plants. This area is classified as *Important Plant Areas (IPA)* due to the substantial diversity of flora and endemic species. Ermenek valley, forming the northern boundary of the study area, is also rich in floristic aspects.

14.7 Disturbances in an alpine valley, Reintal, Wetterstein

Birgit Schwabe[1]
[1] Institut für Geographie, Friedrich Alexander Universität ERlangen-Nürnberg
Contact: birgit.schwabe@fau.de

The poster presents the results of a study on typical gemorphologically induced disturbances in a mountain valley of the Bavarian Alps (Reintal, Wettestein Mountains). Several disturbance were investigated by 93 samples for species composition, life strategies and environmental and ecological factors. Analyzing aerial photos of the years 2003, 2006 and 2009 for changes and the evaluation of literature on the geomorphological dynamics (debris flows, rockfall, debris slopes, avalanche tracks) supports the characterization of the disturbances in terms of duration, abruptness and magnitude.

Keywords: disturbances, high mountains, ecology

List of participants

List of participants

A

Aas, Gregor, gregor.aas@uni-bayreuth.de, BayCEER, University of Bayreuth, Ecological-Botanical-Garden, Germany
Abellán, Pedro, pabellan@um.es, Queens College, CUNY, Dept Biology, United States
Abraham, Vojtěch, vojtech.abraham@gmail.com, Faculty of Science, Departmet of Botany, Charles University in Prague, Czech Republic
Aduse-Poku, Kwaku, ka374@cam.ac.uk, University of Cambridge, Zoology, United Kingdom
Agarwal, Ishan, ishan.agarwal@gmail.com, National Centre for Biological Sciences, India
Akkurt, Seda, seda.akkurt@bilecik.edu.tr, Bilecik Seyh Edebali University, Department of Geography, Turkey
Akoth, Beryl, beryl.bwong@unibas.ch, University of Basel, Biogeography, Switzerland
Alahuhta, Janne, janne.alahuhta@oulu.fi, University of Oulu, Department of Geography, Finland
Alba-Sanchez, Francisca, falba@ugr.es, University of Granada, Botany, Spain
Albouy, Camille, albouycamille@gmail.com, Université du Québec à Rimouski, Canada
Aletrari, Elina, elina.aletrari@kcl.ac.uk, King's College London / Natural History Museum London, United Kingdom
Alexander, Lois, lois.alexander1@gmail.com, College of Southern Nevada, Biological Sciences, United States
Algar, Adam, adam.algar@nottingham.ac.uk, University of Nottingham, School of Geography, United Kingdom
Allen, Harriet, hda1@cam.ac.uk, University of Cambridge, Department of Geography, United Kingdom
Allen, Jenica, jenicaa@eco.umass.edu, University of Massachusetts, Dept. Environmental Conservation, United States
Alnafie, Abdulatif, aalnafie@gmail.com, Al-Imam Muhammad Ibn Saud Islamic University, College of Social Sciences, Department of Geography, Saudi Arabia
Alvarez-Cansino, Leonor, leonor.alvarez-cansino@uni-bayreuth.de, BayCEER, University of Bayreuth, Plant Ecology, Germany
Anadón, José, jose.anadon@qc.cuny.edu, Queen's College CUNY, Biology, United States
Appelhans, Marc, marc.appelhans@biologie.uni-goettingen.de, University of Goettingen, Department of Systematic Botany, Germany
Araclides, Hercules, eraclis.araclides@mail.mcgill.ca, McGill University, Biology, Canada
Archner, Oliver, oliver.archner@uni-bayreuth.de, BayCEER, University of Bayreuth, Germany
Arfin Khan, Mohammed Abu Sayed, nobelarfin@yahoo.com, BayCEER, University of Bayreuth, Disturbance Ecology, Germany
Arlé Ribeiro de Souza, Carlos Eduardo, kaduarle@gmail.com, Universidade Federal do Estado do Rio de Janeiro, Brazil
Armstrong, Ellie, ellieearmstrong@gmail.com, University of Hawaii, United States
Axmacher, Jan, j.axmacher@ucl.ac.uk, University College London, Geography, United Kingdom

B

Bader, Maaike, maaike.bader@geo.uni-marburg.de, University of Marburg, Faculty of Geography, Germany
Badgley, Catherine, cbadgley@umich.edu, University of Michigan, Dept of Ecology & Evolutionary Biology, United States
Bailey, Joseph, joseph.bailey@outlook.com, University of Nottingham, Geography, United Kingdom
Balk, Meghan, mabalk04@unm.edu, University of New Mexico, Biology, United States
Banag, Cecilia, ceciliabanag@gmail.com, University of Santo Tomas, Department of Biological Sciences College of Science, Philippines
Baranova, Alina, earth0909@gmail.com, University of Hamburg, Institut für Physische Geographie, Germany
Barbe, Lou, lou.barbe@free.fr, Université de Rennes 1, France
Barbet-Massin, Morgane, barbet@mnhn.fr, National Museum of Natural History, France
Barbosa, A. Márcia, barbosa@uevora.pt, University of Evora, CIBIO/InBIO, Portugal
Barnes, Andrew, abarnes@gwdg.de, University of Goettingen, Systemic Conservation Biology, Germany
Barratt, Chris, christopher.barratt@unibas.ch, University of Basel, Biogeography, Switzerland
Baselga, Andres, andres.baselga@usc.es, University of Santiago de Compostela, Dept. of Zoology, Spain
Bauer, Dennise Stefan, dennise.bauer@rub.de, Ruhr-Universität Bochum, Evolution and Biodiversity of Plants, Germany
Baumann, Esther, esther_baumann@gmx.de, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Beck, Jan, jan.beck@unibas.ch, University of Basel, Environmental Science (Biogeography), Switzerland
Beierkuhnlein, Carl, carl.beierkuhnlein@uni-bayreuth.de, BayCEER, University of Bayreuth, Chair of Biogeography, Germany
Bellard, Céline, celine.bellard@u-psud.fr, CBER, University College of London, United Kingdom
Benito, Blas M., blas.benito@biology.au.dk, Aarhus University, Centre for Biocultural History / Ecoinformatics and Biodiversity, Denmark

Bennett, Joanne, joanne.bennett@idiv.de, German Centre for Innovative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Synthesis Centre for Biodiversity Sciences - sDiv, Germany
Bernardino de Souza Pereira, Jovani, jovanibio@gmail.com, Ruhr-Universität Bochum, Department of Evolution and Biodiversity of Plants, Germany
Bertola, Laura, laura.bertola@gmail.com, Leiden University, Institute of Environmental Sciences, Netherlands
Bethke, Laura, laura.bethke@stmail.uni-bayreuth.de, University of Bayreuth, Germany
Betz, Patrice, pmbetz@mail.fhsu.edu, Fort Hays State University, Department of Biology, United States
Biber, Matthias, mbiber@mail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Bieber, Maike, maike.bieber@gmx.de, Leibniz Universität Hannover, Landscape Science, Germany
Biereznoj-Bazille, Urszula, donaroza@gmail.com, Uniwersytet w Białymstoku, Biology Department, Poland
Bilous, Liudmila, bilouslf@univ.kiev.ua, Taras Shevchenko National University of Kyiv, Faculty of Geography, Ukraine
Bittencourt, Gabriela, gabrielabitt.ufrrj@gmail.com, University of Basel, Department of Biogeography, Switzerland
Bjorkman, Anne, annebj@gmail.com, German Centre for Integrative Biodiversity Research, Germany
Bleyhl, Benjamin, benjamin.bleyhl@geo.hu-berlin.de, Humboldt-Universität zu Berlin, Geography, Germany
Blois, Jessica, jblois@ucmerced.edu, School of Natural Sciences, Life and Environmental Sciences, United States
Blonda, Palma, blonda@ba.issia.cnr.it, CNR, Institute of Intelligent Systems for Automation (ISSIA), Italy
Bobrowski, Maria, maria.bobrowski@uni-hamburg.de, University of Hamburg, Institute of Geography, Germany
Boehmer, Juergen, boehmer_h@usp.ac.fj, University of the South Pacific, School of Geography, Earth Science and Environment, Fiji
Böhning-Gaese, Katrin, katrin.boehning-gaese@senckenberg.de, Biodiversity and Climate Research Centre, Germany
Borchardt, Peter, pbo1@gmx.de, University of Hamburg, Biogeography, Germany
Borgeest, Bernhard, b.borgeest@focus-magazin.de, Focus Magazine Germany, Germany
Borges, Paulo, pborges@uac.pt, University of Azores, Department of Agriculture, Portugal
Borregaard, Michael, mkborregaard@snm.ku.dk, University of Copenhagen, Center for Macroecology, Evolution and Climate, Denmark
Botta, Filippo, botta@nbi.ku.dk, University of Copenhagen, Denmark
Boucher-Lalonde, Véronique, veronique.boucher.lalonde@gmail.com, University of Ottawa, Biology, Canada
Bradley, Bethany, bbradley@eco.umass.edu, University of Massachusetts, Amherst, Environmental Conservation, United States
Braun, Daniela, aleinad.nuarb@gmail.com, Trier University, Faculty of Regional and Environmental Sciences; Dept. of Biogeography, Germany
Brehm, Gunnar, gunnar.brehm@uni-jena.de, University of Jena, Phyletisches Museum, Germany
Brown, Rafe, rafe@ku.edu, University of Kansas, Biodiversity Institute, United States
Brummer, Mathias, mathias.christian.brummer@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Bugoni, Jeferson, jbugoni@yahoo.com.br, Universidade Estadual de Campinas, Plant Biology, Brazil
Bung, Sven Günther, vitaforst@gmx.de, IG BAU, Landesvertretung, Germany
Bürzle, Birgit, birgit.buerzle@posteo.de, University of Hamburg, CEN, Institute of Geography, Germany

C

Cailliau, Cathrin, cathrin.cai@hotmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Calixto-Perez, Edith, edith.calixto@st.ib.unam.mx, UNAM, Instituto de Biología, Mexico
Capinha, César, capinha@uevora.pt, University of Lisbon, Centre for Environmental Biology, Portugal
Carli, Emanuela, emanuela.carli@gmail.com, University of Cagliari, Dipartimento di Scienze della Vita e dell'Ambiente, Italy
Carlson, Ben, ben.s.carlson@gmail.com, Yale, Ecology and Evolutionary Biology, United States
Carvalho, Plauto, plauto.decarvalho@gmail.com, Universidade Estadual de Goiás, Botânica, Brazil
Carvalho, Silvia, silviacarvalho@cibio.up.pt, ICETA, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto, Portugal
Cerrato, Cristiana, cri.entessa@virgilio.it, Institute of Atmospheric Sciences and Climate, National Research Council, Italy
Chaddock, Janice, janice.chaddock@gmail.com, University of Bayreuth, Germany
Chambers, Rachael, rachaelchambers@hotmail.co.uk, University of Amsterdam, Netherlands
Chanam, Joyshree, joyshreechanam@gmail.com, Centre for Ecological Sciences, Indian Institute of Science, India
Chase, Jonathan M., jonathan.chase@idiv.de, German Centre for Integrative Biodiversity Research (iDiv), Biodiversity Synthesis Research Group, Germany
Chen, Jing, chenjing@ioz.ac.cn, Institute of Zoology, Chinese Academy of Sciences, China
Chen, Shengbin, chainpin@126.com, Nanjing Institute of Environmental Sciences, Ecology Center, China

Chiarucci, Alessandro, alessandro.chiarucci@unibo.it, University of Bologna, Department of Biological, Geological and Environmental Sciences, Italy
Chipperfield, Joseph, joechip90@googlemail.com, University of Bergen, Biology, Norway
Chisholm, Chelsea, chelsea.chisholm@gmail.com, University of Copenhagen, Center for Macroecology, Evolution and Climate, Denmark
Chomicki, Guillaume, guillaume.chomicki@gmail.com, University of Munich (LMU), Biology, Germany
Chytrý, Milan, chytry@sci.muni.cz, Masaryk University, Department of Botany and Zoology, Czech Republic
Claßen, Alice, alice.classen@uni-wuerzburg.de, University of Würzburg, Department of Animal Ecology and Tropical Biology, Germany
Clavel, Julien, julien.clavel@hotmail.fr, Ecole Normal Supérieure, IBENS, France
Collaro, Carolina, carolina.collaro@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Cord, Anna, anna.cord@ufz.de, Helmholtz Centre for Environmental Research - UFZ, Department of Computational Landscape Ecology, Germany
Cornell, Howard, hvcornell@ucdavis.edu, University of California, Davis, Environmental Science and Policy, United States
Cornu, Jean-Francois, Jean-Francois.Cornu@univ-montp2.fr, CNRS, France
Cowley, David, dcowley@nmsu.edu, New Mexico State University, Fish, Wildlife & Conservation Ecology, United States
Coyle, Jes, jrcoyle@live.unc.edu, University of North Carolina, Dept. of Biology, United States
Curcic, Nina, nina.b.curcic@gmail.com, Geographical Institute "Jovan Cvijic" of the Serbian Academy of Sciences and Arts, Serbia
Currie, David, dcurrie@uottawa.ca, University of Ottawa, Biology Department, Canada
Curtis, Caroline, cacurtis@cns.umass.edu, University of Massachusetts, United States

D

D'Amen, Manuela, manuela.damen@unil.ch, University of Lausanne, DEE, Ecospat Group, Switzerland
Dapporto, Leonardo, leondap@gmail.com, Oxford Brookes University, United Kingdom
Dauber, Jens, jens.dauber@ti.bund.de, Thünen Institute of Biodiversity, Germany
Davalos, Liliana, lmdavalos@gmail.com, SUNY Stony Brook, Ecology and Evolution, United States
Davis, Edward, edavis@uoregon.edu, University of Oregon, Department of Geological Sciences, United States
Dawson, Michael, mdawson@ucmerced.edu, University of California, Merced, School of Natural Sciences, United States
Debevec, Caitlyn, caitrosed@gmail.com, University of Central Florida, Biology, United States
de Boer, Erik, deboer.erikjan@gmail.com, University of Amsterdam, Netherlands
De Camargo, Rafael, rafael.x.camargo@gmail.com, University of Ottawa, Department of Biology, Canada
Dehling, Matthias, matthias.dehling@senckenberg.de, Biodiversity and Climate Research Centre (BiK-F), Germany
del Viento, Yrneh, yrneh.ulloa@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Dengler, Jürgen, juergen.dengler@uni-bayreuth.de, BayCEER, University of Bayreuth, Disturbance Ecology, Germany
Denk, Thomas, thomas.denk@nrm.se, Swedish Museum of Natural History, Palaeobiology, Sweden
Denninger Snyder, Kristen, kldenninger@ucdavis.edu, University of California - Davis, United States
Di Cola, Valeria, valeriadicola@gmail.com, University of Lausanne, DEE, Switzerland
Digel, Christoph, cdigel@gwdg.de, University of Göttingen, Systemic Conservation Biology, Germany
Divíšek, Jan, divisekjan@mail.muni.cz, Institute of Geonics AS CR, Department of Environmental Geography, Czech Republic
Dobrovolski, Ricardo, rdobrovolski@gmail.com, Universidade Federal da Bahia, Departamento de Zoologia, Brazil
Dobson, LuAnna, LDobson@uci.edu, University of California, Irvine, Ecology and Evolutionary Biology, United States
Dolos, Klara, dolos@kit.edu, Karlsruhe Institute of Technology, Institute for Geography and Geoecology, Germany
Domínguez Lozano, Felipe, felipe.dominguez@bio.ucm.es, University Complutense of Madrid, Biología Vegetal I, Spain
Dörnchen-Neumann, Jana, j.doernchen@hszg.de, Hochschule Zittau/Görlitz, Naturwissenschaften, Germany
Dörner, Sebastian, sebastiandoerner@geoecology.org, University of Bayreuth, Germany
Dostal, Petr, dostal@ibot.cas.cz, University of Bern, Institute of Plant Sciences, Switzerland
Douglas, Michael, douglasnoaa@gmail.com, University of Oklahoma, Cooperative Institute for Mesoscale Meteorological Studies, United States
Duarte, Milen, mylenduarte@gmail.com, University of Chile / IEB-Chile, Chile
Duque Lazo, Joaquin, joaquin.duque_lazo@uni-leipzig.de, University of Leipzig, Institute of Biology, Systematic Botany and Functional Biodiversity, Germany
Dynesius, Mats, mats.dynesius@emg.umu.se, Umeå University, Ecology and Environmental Science, Sweden

E

Ebersbach, Jana, jana.ebersbach@uni-leipzig.de, Leipzig University, Molecular Evolution and Plant Systematics, Germany
Economo, Evan, evaneconomo@gmail.com, Okinawa Institute of Science and Technology Graduate University, Japan
Ellis Soto, Diego, Diego.Ellis-Soto@uni-konstanz.de, Universität Trier, Biological Sciences, Germany
Engelbrecht, Bettina, bettina.engelbrecht@gmail.com, BayCEER, University of Bayreuth, Plant Ecology, Germany
Engemann Jensen, Kristine, engemann@bios.au.dk, Aarhus University, Institute for Bioscience, Denmark
Engler, Jan, JEngler@gmx.de, Zoological Research Museum Alexander Koenig, Vertebrate Department, Germany
Esselstyn, Jacob, esselstyn@lsu.edu, Louisiana State University, Museum of Natural Science, United States
Essl, Franz, franz.essl@univie.ac.at, University of Vienna, Austria
Estrada, Alba, albaestradaa@gmail.com, University of Evora, CIBIO/InBIO, Portugal

F

Faller, Karen, biogeography.ibs@gmail.com, International Biogeography Society, Membership Services, United States
Fassnacht, Fabian, fabian.fassnacht@kit.edu, Karlsruhe Institute of Technology (KIT), Institute for Geography and Geoecology, Germany
Faßold, Verena, sekwis@bayceer.uni-bayreuth.de, University of Bayreuth, BayCEER, Germany
Faurby, Søren, soren.faurby@biology.au.dk, Aarhus University, Denmark
Favre, Adrien, adrien.favre@uni-leipzig.de, University Leipzig, Department of Molecular Evolution and Plant Systematics, Germany
Fei, Songlin, sfei@purdue.edu, Purdue University, United States
Feilhauer, Hannes, hannes.feilhauer@fau.de, Friedrich Alexander Universität Erlangen-Nuremberg, Geography, Germany
Feng, Gang, gang.feng@biology.au.dk, Aarhus University, Denmark
Ferenc, Michal, ferenc.michal85@gmail.com, Charles University in Prague, Department of Ecology, Czech Republic
Ferger, Stefan, stefan.ferger@yahoo.de, Biodiversity and Climate Research Centre (BiK-F), Germany
Fernandes, Rui, ruifilipe.freitasfernandes@unil.ch, University of Lausanne, Department of Ecology and Evolution (DEE), Switzerland
Fernandez, Jorge, jorgefernandez783@gmail.com, University of Bayreuth, Germany
Fernandez, Marc, marc.fern@gmail.com, Universidade dos Açores, Departamento de Biologia/CIRN, Portugal
Fernandez-Palacios, Jose Maria, jmferpal@gmail.com, La Laguna University, Spain
Fichtner, André, andre.fichtner@fau.de, University of Erlangen-Nuremberg, Germany
Field, Richard, richard.field@nottingham.ac.uk, University of Nottingham, School of Geography, United Kingdom
Firn, Jennifer, jennifer.firn@qut.edu.au, Queensland University of Technology, Australia
Fischer, Georg, georgf81@gmail.com, OIST, Economo Unit, Japan
Fitzpatrick, Matthew, mfitzpatrick@umces.edu, University of Maryland Center for Environmental Science, Appalachian Lab, United States
Florez-Rodriguez, Alexander, alexflorezr@gmail.com, Natural History Museum of Denmark, Center for Macroecology, Evolution and Climate, Denmark
Fois, Mauro, mau.fois1@studenti.unica.it, University of Cagliari, Centro Conservazione Biodiversità, Italy
Fordham, Damien, damien.fordham@adelaide.edu.au, The University of Adelaide, The Environment Institute, Australia
Friedmann, Arne, friedmann@geo.uni-augsburg.de, University of Augsburg, Institute of Geography, Germany
Fristoe, Trevor, tfristoe@unm.edu, University of New Mexico, Department of Biology, United States
Fritz, Susanne, sfritz@senckenberg.de, Biodiversity & Climate Research Centre (BiK-F) & Senckenberg, Germany

G

Gaboriau, Théo, theogaboriau@gmail.com, Université Montpellier 2, France
Gabriel, Rosalina, rgabriel@uac.pt, University of the Azores, DCA, Portugal
Gallien, Laure, laure.gallien@gmail.com, Swiss Federal Research Institute WSL, Switzerland
Garcia Vazquez, David, deivizzz@hotmail.com, Institute of Evolutionary Biology, Spain
Gauffre Autelin, Pauline, pauline.gauffre@hotmail.fr, Justus Liebig University Giessen, Animal Ecology and Systematics, Germany
Gavin, Daniel, dgavin@uoregon.edu, University of Oregon, Geography, United States
Gaviria, Julian, julian_gaviria@hotmail.com, University of Bayreuth, Germany
Gazdar, Shazneen, shazneen.c.gazdar@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Gebauer, Margit, margit.gebauer@uni-bayreuth.de, University of Bayreuth, Germany

Georgopoulou, Elisavet, elisavet.georgopoulou@nhm-wien.ac.at, Natural History Museum of Vienna, Geological-Paleontological, Austria
Giampoudakis, Konstantinos, konstantinosg@snm.ku.dk, Natural History Museum of Denmark, Center for Macroecology, Evolution and Climate, Denmark
Giladi, Itamar, itushgi@bgu.ac.il, Ben Gurion University, Mitrani Department of Desert Ecology, Israel
Gil-Delgado, Jose Antonio, gild@uv.es, University of Valencia, Microbiology and Ecology, Spain
Gill, Jacquelyn, jacquelyn.gill@maine.edu, University of Maine, Climate Change Institute, School of Biology and Ecology, United States
Gillespie, Rosemary, gillespie@berkeley.edu, University of California Berkeley, United States
Girardello, Marco, marco.girardello@bios.au.dk, University of Aarhus, Section for Ecoinformatics and Biodiversity, Denmark
Glor, Richard, glor@ku.edu, University of Kansas, Herpetology/Ecology and Evolutionary Biology, United States
Goldblum, David, dgoldblum@niu.edu, Northern Illinois University, Department of Geography, United States
Göldel, Bastian, bastian.goeldel@biology.au.dk, Aarhus University, Department for Bioscience, Denmark
Gonzalez-Hernandez, Antonio, aglezhdez@gmail.com, University of Granada, Botany, Spain
González-Orozco, Carlos E., carlos.gonzalez-orozco@canberra.edu.au, Institute for Applied Ecology and Collaborative Research Network for Murray-Darling Basin Futures, University of Canberra, Australia
Gossel, Ellen, ellen.gossel@uni-bayreuth.de, University of Bayreuth, Chair of Biogeography, Germany
Gouveia, Sidney, sgouveia@ufs.br, Federal University of Sergipe, Department of Ecology, Brazil
Grady, John, jgrady@unm.edu, University of New Mexico, Biology, United States
Graham, Catherine, catherine.graham@stonybrook.edu, Stony Brook University, United States
Graham, Laura, lgxlg3@nottingham.ac.uk, University of Nottingham, Geography, United Kingdom
Gratton, Paolo, paolo_gratton@eva.mpg.de, Max Planck Institute for Evolutionary Anthropology, Primatology, Germany
Grenyer, Rich, Richard.Grenyer@ouce.ox.ac.uk, University of Oxford, United Kingdom
Greve, Michelle, michelle_greve@yahoo.com, University of Pretoria, Department of Plant Science, South Africa
Groudeva, Veneta, vgr@biofac.uni-sofia.bg, Sofia University, General and Industrial Microbiology, Bulgaria
Grytnes, John-Arvid, grytnes@bio.uib.no, University of Bergen, Department of Biology, Norway
Guan, Lisa, lisaguan2@gmail.com, University of California, Berkeley, Environmental Science Policy and Management, Germany
Guilhaumon, François, francoisguilhaumon@gmail.com, IRD, ECOSYM, France
Guisan, Antoine, antoine.guisan@unil.ch, University of Lausanne, DEE, Switzerland
Guo, Qinfeng, qguo@fs.fed.us, USDA, FS, United States

H

Habel, Jan Christian, Janchristianhabel@gmx.de, Technical University München, Terrestrial Ecology, Germany
Hahn, Ingo, ingo.hahn@hm.edu, Munich University of Applied Sciences (MUAS), Faculty for Geo-Information, Germany
Hällfors, Maria, maria.hallfors@helsinki.fi, Finnish Museum of Natural History, Botany Unit, Finland
Halmy, Marwa, marwawaseem@yahoo.com, Alexandria University, Egypt
Hamlin, Jennafer, jhamlin@uga.edu, University of Georgia, Genetics, United States
Hane, Susanne, susanne_hane@gmx.de, University of Hannover, Germany
Harmáčková, Lenka, harmlen@seznam.cz, Palacky University, Department of Zoology, Czech Republic
Harris, Rebecca, rbharris@uw.edu, University of Washington, Biology, United States
Harter, David, david.harter@uni-bayreuth.de, University of Bayreuth, Department of Biogeography, Germany
Hawkins, Bradford, bhawkins@uci.edu, University of California, United States
He, Jiekun, jiekunhe@m.scnu.edu.cn, South China Normal University, School of Life Science, China
He, Kate, xhe@murraystate.edu, Murray State University, Department of Biological Sciences, United States
Heaney, Lawrence, lheaney@fieldmuseum.org, Field Museum of Natural History, Research Center, United States
Heino, Jani, jani.heino@environment.fi, Finnish Environment Institute, Natural Environment Centre, Finland
Helm, Aveliina, aveliina.helm@ut.ee, University of Tartu, Estonia
Hemrova, Lucie, lucie.hemrova@ibot.cas.cz, Academy of Sciences of the Czech Republic, Institute of Botany, Czech Republic
Hepp, Johanna, hepp.johanna@web.de, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Hernández, Laura, hernandez.laura@inia.es, INIA-CIFOR, Silviculture and Forest Management Department, Spain
Hickler, Thomas, Thomas.Hickler@senckenberg.de, Senckenberg Research Institutes and Natural History Museum, Biodiversity and Climate Research Centre, Germany
Hochheimer, Janin, janin_hochheimer@posteo.de, Martin-Luther-University Halle-Wittenberg, Department of Geobotany and Botanical Garden, Germany

Hof, Christian, christian.hof@senckenberg.de, Biodiversity & Climate Research Centre (BiK-F) & Senckenberg Gesellschaft für Naturforschung, Germany
Hoffmann, Samuel, sam.hoffmann@gmx.de, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Holden, Sarah, sarah.holden@gmx.de, University of Bayreuth, Germany
Hollenbeck, Emily, Emily_Hollenbeck@brown.edu, Brown University, Ecology and Evolutionary Biology, United States
Honzáková, Kateřina, khonzakova@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Hooghiemstra, Henry, H.Hooghiemstra@uva.nl, University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, Netherlands
Hoppe, Franziska, Franziska.Hoppe@geowiss.uni-hamburg.de, University of Hamburg, Institute of Geography, Germany
Horacek, Ivan, horacek@natur.cuni.cz, Charles University in Prague, Department of Zoology, Czech Republic
Horak, David, david.horak@natur.cuni.cz, Charles University in Prague, Department of Ecology, Czech Republic
Hornstein, Daniel, daniel.hornstein@hswt.de, Hochschule Weihenstephan-Triesdorf, Vegetation Science & Botany, Germany
Horsák, Michal, horsak@sci.muni.cz, Masaryk University, Dept. of Botany and Zoology, Czech Republic
Horsakova, Veronika, veronika.horsakova@seznam.cz, Masaryk University, Department of Botany and Zoology, Czech Republic
Hortal, Joaquin, jhortal@mncn.csic.es, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Dept. Biogeography & Global Change, Spain
Hoshino, Buho, aosier@rakuno.ac.jp, Rakuno Gakuen University, Department of Environmental Symbiotic College of Agriculture, Food and Environment Sciences, Japan
Hossain, Md. Lokman, lokmanbbd@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Houdayer, Marion, ma.houdayer@gmail.com, University of Bayreuth, Germany
Huaizhou, Zheng, zhz@fjnu.edu.cn, Fujian Normal University, Institute of Geography, China
Hula, Marcellinus, akamas3@yahoo.com, Benue State University, Geography, Nigeria
Hundsdoerfer, Anna, anna.hundsdoerfer@senckenberg.de, Senckenberg Dresden, Museum of Zooloy, DNA Laboratory, Germany

I

Irl, Severin, severin.irl@uni-bayreuth.de, University of Bayreuth, Biogeography, Germany
Itescu, Yuval, yuvitescu@gmail.com, Tel Aviv University, Zoology, Israel

J

Jackson, Steve, stjackson@usgs.gov, US Geological Survey, USA, Southwest Climate Science Center, United States
Jaeschke, Anja, anja.jaeschke@uni-bayreuth.de, University of Bayreuth, Biogeography, Germany
Jansson, Roland, roland.jansson@emg.umu.se, Umeå University, Dept. of Ecology and Environmental Science, Sweden
Jarzyna, Marta, marta.jarzyna@yale.edu, Yale University, Ecology and Evolutionary Biology, United States
Jenkins, Dave, David.Jenkins@ucf.edu, University of Central Florida, Dept. of Biology, United States
Jentsch, Anke, anke.jentsch@uni-bayreuth.de, BayCEER, University of Bayreuth, Disturbance Ecology, Germany
Jetz, Walter, walter.jetz@yale.edu, Yale University, United States
Jia, Zhiyun, jiazy@ioz.ac.cn, Chinese Academy of Sciences, Editorial Office, Current Zoology, Institute of Zoology, China
Joshi, Jahnavi, jj.jahnavi@gmail.com, National Centre for Biological Sciences, Ecology and Evolution Group, India
Jung, Eunyoung, eun-young.jung@uni-bayreuth.de, BayCEER, University of Bayreuth, Germany

K

Karg, Susanne, susanne.karg@hotmail.de, Georg-August-Universität Göttingen, Germany
Karger, Dirk Nikolaus, dirk.karger@utu.fi, University of Turku, Department of Biology, Finland
Kattge, Jens, jkattge@bgc-jena.mpg.de, Max Planck Institute for Biogeochemistry, Research Group Functional Biogeography, Germany
Kawan, Rasmila, Rasmila.kawan@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Kehoe, Laura, laura.kehoe@geo.hu-berlin.de, Humboldt University Berlin, Germany
Keil, Petr, pkeil@seznam.cz, Charles University in Prague, Center for Theoretical Study, Czech Republic
Keith, Sally, sally.a.keith@gmail.com, University of Copenhagen, Center for Macroecology, Evolution and Climate, Denmark
Kennedy, Jonathan, jonathan.kennedy@bio.ku.dk, University of Copenhagen, Denmark

Kessler, Michael, michael.kessler@systbot.uzh.ch, University of Zurich, Switzerland
Khaliq, Imran, imran.khaliq@senckenberg.de, Biodiversity and Climate Research Centre (BiK-F), Project Area B: Biodiversity Dynamics and Climate, Germany
Kienle, David, david.kienle@web.de, University of Bayreuth, Biogeography, Germany
Kiessling, Wolfgang, wolfgang.kiessling@fau.de, Friedrich-Alexander Universität Erlangen-Nürnberg, GeoZentrum Nordbayern, Germany
Kindler, Carolin, carolin.kindler@senckenberg.de, Museum of Zoology, Senckenberg Dresden, Phylogeography, Germany
Klaus, Kristina Vanessa, kristina.klaus@rub.de, Ruhr-Universität Bochum, Institute of Evolution and Biodiversity of Plants, Germany
Kluge, Jürgen, klugej@geo.uni-marburg.de, University of Marburg, Germany
Knapp, Sonja, sonja.knapp@ufz.de, Helmholtz Centre for Environmental Research - UFZ, Community Ecology, Germany
Knight, Tiffany, tiffany.knight@idiv.de, The German Centre for Integrative Biodiversity Research (iDiv), Germany
Koch, Robert, robert.koch@tu-berlin.de, Technical University of Berlin, Germany
Kondraskov, Paulina, paulina.kondraskov@smns-bw.de, Stuttgart State Museum of Natural History/University of Heidelberg, Botany, Germany
König, Christian, chr.koenig@hotmail.de, University of Goettingen, Biodiversity, Macroecology & Conservation Biogeography Group, Germany
Kopecký, Martin, ma.kopecky@gmail.com, Czech Academy of Sciences, Institute of Botany, Czech Republic
Kopsová, Lenka, l.kopsova@gmail.com, Charles University in Prague, Department of Ecology, Czech Republic
Korch, Oliver, eldonolli@gmx.de, University of Augsburg, Institute of Geography, Germany
Kou, Xiaojun, xj_kou@bnu.edu.cn, Beijing Normal University, College of Life Sciences, China
Kramer-Schadt, Stephanie, kramer@izw-berlin.de, IZW, Evolutionary Ecology, Germany
Kraus, Petra, petra.kraus@uni-bayreuth.de, University of Bayreuth, Germany
Kreft, Holger, hkreft@uni-goettingen.de, University of Göttingen, Biodiversity, Macroecology & Conservation Biogeography, Germany
Krehenwinkel, Henrik, krehenwinkel@evolbio.mpg.de, Max Planck Institute for Evolutionary Biology, Evolutionary Genetics, Germany
Krestov, Pavel, pavel.krestov@icloud.com, Botanical Garden-Institute FEB RAS, Russian Federation
Kreyling, Juergen, juergen.kreyling@uni-bayreuth.de, University of Greifswald, Germany
Kropf, Matthias, matthias.kropf@boku.ac.at, Universität für Bodenkultur Wien, Institut für Integrative Naturschutzforschung, Austria
Kubota, Yasuhiro, kubota.yasuhiro@gmail.com, University of the Ryukyus, Faculty of Science, Japan
Kueffer, Christoph, kueffer@env.ethz.ch, ETH Zurich, Switzerland
Kuemmerle, Tobias, tobias.kuemmerle@geo.hu-berlin.de, Humboldt-University Berlin, Department of Geography, Germany
Kühl, Norbert, kuehl@uni-bonn.de, University of Bonn, Germany
Kühn, Ingolf, ingolf.kuehn@ufz.de, Helmholtz Centre for Environmental Research - UFZ, Community Ecology, Germany
Kusumoto, Buntarou, kusumoto.buntarou@gmail.com, The Institute of Statistical Mathematics, Risk Analysis Research Center, Japan

L

Laag, Christian, christian@laagonline.eu, University of Bayreuth, Germany
Ladouceur, Emma, emmala@gmail.com, Museo delle Scienze, Botany, Italy
Landucci, Flavia, flavia.landucci@gmail.com, Masaryk University, Department of Botany and Zoology, Czech Republic
La Sorte, Frank, fal42@cornell.edu, Cornell University, Lab of Ornithology, United States
Lauerer, Marianne, marianne.lauerer@uni-bayreuth.de, BayCEER, University of Bayreuth, Ökologisch-Botanischer Garten, Germany
Lawing, Michelle, alawing@tamu.edu, Texas A&M University, Ecosystem Science and Management, United States
Lei, Fumin, leifm@ioz.ac.cn, Institute of Zoology, Chinese Academy of Sciences, Key Lab of Animal Evolution and Systematics, China
Leinonen, Kirsti, kirsti.leinonen@ymparisto.fi, Finnish Environment Institute, Finland
Lenzner, Bernd, bernd_lenzner@gmx.de, University of Bayreuth, Department of Biogeography, Germany
Leprieur, Fabien, fabien.leprieur@univ-montp2.fr, University Montpellier 2, France
Leroy, Boris, leroy.boris@gmail.com, Muséum National d'Histoire Naturelle, UMR Biologie des Organismes et Ecosystèmes Aquatiques, France

Lewin, Amir, amirlewin@hotmail.com, Tel Aviv University, Zoology, Israel
Li, Ching-Feng, chingfeng.li@gmail.com, Masaryk University, Department of Botany and Zoology, Czech Republic
Li, Qin, qin.li@biodiversity.ubc.ca, University of British Columbia, Department of Botany, Biodiversity Research Centre, Canada
Li, Sen, sen.li@snm.ku.dk, University of Copenhagen, Natural History Museum of Denmark, Denmark
Li, Xueyan, x.li14@imperial.ac.uk, Imperial College London, United Kingdom
Li, Yiming, liym@ioz.ac.cn, Chinese Academy of Sciences, Key Laboratory of Animal Ecology and Conservation Biology, China
Liede-Schumann, Sigrid, sigrid.liede@uni-bayreuth.de, University of Bayreuth, Dept. of Plant Systematics, Germany
Lim, Jun Ying, junyinglim@berkeley.edu, University of California, Berkeley, Integrative Biology, United States
Linder, Hans Peter, peter.linder@systbot.uzh.ch, University of Zurich, Systematic Botany, Switzerland
Lines, Emily, e.lines@qmul.ac.uk, Queen Mary University of London, School of Geography, United Kingdom
Lise Arlette, Zemagho Mbouzang, lisemez@yahoo.fr, University of Bayreuth, Department of Plant Systematics, Germany
Liu, Hongyan, lhy@urban.pku.edu.cn, Peking University, College of Urban and Environmental Sciences, China
Liu, Xuan, liuxuan@ioz.ac.cn, Institute of Zoology, Chinese Academy of Sciences, Key Laboratory of Animal Ecology and Conservation Biology, China
Liu, Ye, lye@pku.edu.cn, Peking University, China
Loader, Simon, simon.loader@unibas.ch, University of Basel, Biogeography Research Group, Switzerland
Lois, Sabela, sabela.lois@gmail.com, University of Santiago de Compostela, Zoology, Spain
Lomolino, Mark, island@esf.edu, College of Environmental Science, United States
Lötters, Stefan, loetters@uni-trier.de, Trier University, Biogeography, Germany

M

Ma, Ziyu, ziyu.ma@biology.au.dk, Aarhus University, Department of Bioscience, Denmark
Machac, Antonin, A.Machac@email.cz, Stony Brook University, New York, Dept of Ecology and Evolution, United States
Maguire, Kaitlin Clare, kmaguire@ucmerced.edu, University of California, Merced, United States
Mahecha, Miguel, mmahecha@bgc-jena.mpg.de, Max Planck Inst. for Biogeochemistry, Germany
Malyshev, Andrey, amalyshe@alumni.uwo.ca, Universität Bayreuth, Biogeography, Germany
Marcantonio, Matteo, matteo.marcantonio@fmach.it, Fondazione Edmund Mach, Department of Biology and Molecular Ecology, Italy
Margus, Aigi, aigi.margus@jyu.fi, University of Jyväskylä, Department of biological and environmental science, Finland
Marignani, Michela, marignani@unica.it, University of Cagliari, Dept. Life and Environmental Sciences, Italy
Márquez, Ana Luz, almarquez@uma.es, Universidad de Málaga, Biología Animal, Spain
Marske, Katharine, kamarske@snm.ku.dk, Natural History Museum of Denmark, Center for Macroecology, Evolution and Climate, Denmark
Martínez, Brezo, brezo.martinez@urjc.es, Rey Juan Carlos University, Biodiversity and Conservation Unit, Spain
Martini, Markus, s1mamart@stmail.uni-bayreuth.de, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Marx, Hannah, h.marx.h@gmail.com, University of Idaho, United States
Masters, Judith, jdthmasters@gmail.com, University of Fort Hare, African Primate Initiative for Ecology & Speciation, South Africa
Matos-Maravi, Pavel, pavelm14@gmail.com, Institute of Entomology, Biology Center AS CR, Czech Republic
Matthews, Tom, txm676@gmail.com, University of Oxford, United Kingdom
Matzke, Nicholas, matzke@nimbios.org, Univ. of Tennessee, NIMBioS, United States
Maul, Karola, karola.maul@uni-bonn.de, University of Bonn, Germany
May, Felix, felix.may@ufz.de, Helmholtz Centre for Environmental Research - UFZ, Department of Ecological Modelling, Germany
McCain, Christy, christy.mccain@colorado.edu, University of Colorado, Dept. of Ecology & Evolutionary Biology, United States
McCarragher, Shannon, smccarragher@gmail.com, Northern Illinois University, Geography Department, United States
McGuire, Jenny, jmcguire@gatech.edu, Georgia Institute of Technology, School of Biology, United States
Meade, Conor, conor.v.meade@nuim.ie, Maynooth University, Ireland, Biology, Ireland
Meiri, Shai, uncshai@post.tau.ac.il, Tel Aviv University, Zoology, Israel
Menzel, Andreas, andreas.menzel@ufz.de, Helmholtz Centre for Environmental Research GmbH - UFZ, Community Ecology, Germany

Merkler, Douglas, doug@griswolds.net, NRCS - USDA, United States
Mertes, Katherine, katherine.mertes@yale.edu, Yale University, United States
Mesquita-Joanes, Francesc, mezquita@uv.es, University of Valencia, Cavanilles Institute of Biodiversity and Evolutionary Biology, Spain
Meve, Ulrich, ulrich.meve@uni-bayreuth.de, University of Bayreuth, Dept. of Plant Systematics, Germany
Meyer, Carsten, cmeyer2@uni-goettingen.de, University of Göttingen, Germany
Meyer, Jürgen, meyer@kocks-ing.de, Kocks Consulting Engineers, Germany
Michalak, Ingo, ingo.michalak@uni-leipzig.de, Leipzig University, Department of Molecular Evolution and Plant Systematics, Germany
Michel, Elena, elenamichel@gmx.net, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Mielich, Nicolas, niko_mielich@hotmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Mooers, Arne, amooers@sfu.ca, Simon Fraser University, BioSciences, Canada
Morales-Castilla, Ignacio, ignacio.morales-castilla@mcgill.ca, McGill University, Department of Biology, Canada
Moreno Saiz, Juan Carlos, jcarlos.moreno@uam.es, Autonomous University of Madrid, Department of Biology, Spain
Morlon, Hélène, morlon@biologie.ens.fr, Ecole Normale Supérieure, Biology, France
Morueta-Holme, Naia, morueta-holme@berkeley.edu, University of California - Berkeley, Integrative Biology, United States
Muellner-Riehl, Alexandra, muellner-riehl@uni-leipzig.de, University of Leipzig, Molecular Evolution and Plant Systematics, Germany
Muffler, Lena, lena.muffler@googlemail.com, Universität Bayreuth, Geoökologie, Germany
Müller, Anna Lena, anna-lena.mueller@ti.bund.de, Thünen Institute of Biodiversity, Germany
Müller, Gerhard, gerhard.mueller@bayceer.uni-bayreuth.de, Universität Bayreuth, Germany
Müller, Katharina, katharina.luise.mueller@gmail.com, Georg-August University Göttingen, Biodiversity, Ecology and Evolution, Germany
Müller-Hohenstein, Klaus, University of Bayreuth, Biogeography, Germany
Muñoz, Antonio Roman, roman@uma.es, Universidad de Malaga, Spain
Münzbergová, Zuzana, zuzmun@natur.cuni.cz, Institute of Botany, Czech Republic
Musavi, Talie, tmusavi@bgc-jena.mpg.de, MPI of Biogeochemistry, Germany
Muscarella, Robert, bob.muscarella@gmail.com, Columbia University, Ecology, Evolution, Environmental Biology, United States
Mutke, Jens, mutke@uni-bonn.de, Rheinische Friedrich-Wilhelms-Universität Bonn, Nees Institute for Biodiversity of Plants, Germany
Mutton, Thomas, thomas.mutton@connect.qut.edu.au, Queensland University of Technology, Ecology and Evolutionary Biology, Australia
Myers, Corinne, cmyers@fas.harvard.edu, Harvard University, Dept. of Organismic & Evolutionary Biology, United States

N

Nagel, Peter, peter.nagel@unibas.ch, University of Basel, Environmental Sciences / Biogeography, Switzerland
Naimi, Babak, b.naimi@utwente.nl, University of Twente, Natural Resources, Netherlands
Negoita, Luka, lnegoita@syr.edu, Syracuse University, United States
Neubauer, Thomas A., thomas.neubauer@nhm-wien.ac.at, Natural History Museum Vienna, Geological-Paleontological Department, Austria
Niamir, Aidin, niamir@gmail.com, Senckenberg, BIK-F, Germany
Nieto-Lugilde, Diego, dnieto@al.umces.edu, University of Maryland Center for Environmental Science, Appalachian Laboratory, United States
Nila, Mst Umme Salma, mst.umme.salma.nila@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Nipperess, David, david.nipperess@mq.edu.au, Macquarie University, Department of Biological Sciences, Australia
Noben, Sarah, sarah.noben@uzh.ch, Universität Zürich, Systematische Botanik, Switzerland
Nogué, Sandra, sandranogue@gmail.com, University of Oxford, Zoology, United Kingdom
Nogués-Bravo, David, dnogues@snm.ku.dk, University of Copenhagen, Center for Macroecology, Evolution and Climate, Denmark
Norder, Sietze, S.J.Norder@uva.nl, University of Amsterdam, Institute for Interdisciplinary Studies (IIS), Netherlands
Noriega, Jorge Ari, jnorieg@hotmail.com, Museo Nacional de Ciencias Naturales, Dpto. Cambio global y Biogeografia, Spain
Novosolov, Maria, marianovosolov@gmail.com, Tel Aviv University, Department of Zoology, Israel
Nüchel, Jonas, j.nuchel@bios.au.dk, Aarhus University, Department of Bioscience, Denmark

Nunes, Laura, laura.nunes.13@ucl.ac.uk, University College London, Department of Genetics, Evolution and Environment, United Kingdom
Nunes, Rui, rui.mr.nunes@gmail.com, University of the Azores, Azorean Biodiversity Group, Portugal
Nuppenau, Jan-Niklas, Jan-Niklas_Nuppenau@web.de, University Bayreuth, M.Sc. Global Change Ecology, Germany

O

Oikonomou, Anthi, anthi.oikon@gmail.com, University of Ioannina, Department of Biological Applications and Technology, Greece
Oldeland, Jens, jens.oldeland@uni-hamburg.de, University of Hamburg, Biodiversity, Ecology and Evolution of Plants, Germany
Olubisi, Oluwasegun, ebomawaves@yahoo.com, Obafemi Awolowo University, Faculty of Agriculture, Department of Soil Science and Land Resource Management, Nigeria
Ordonez, Alejandro, alejandro.ordonez@biology.au.dk, Aarhus University, Biosciences, section of Ecoinformatics, Denmark
Orsini, Luisa, l.orsini@bham.ac.uk, University of Birmingham, Biosciences, Environmental Genomics Group, United Kingdom
Østergaard Pedersen, Rasmus, rasmus.pedersen@bios.au.dk, Aarhus University, Ecoinformatics & Biodiversity Group, Denmark
Ott, David, dott@gwdg.de, University of Göttingen, Department of Biology, Germany
Özalp, İpek, ipek.ozalp@istanbul.edu.tr, Istanbul University, Turkey

P

Padayachee, Ashlyn Levadia, ashlyn.levadia@gmail.com, University of KwaZulu-Natal, School of Environmental Sciences, South Africa
Padullés, Josep, josep.padulles@udg.edu, University of Girona, Spain
Paeckert, Martin, martin.paeckert@senckenberg.de, Senckenberg Natural History Collections Dresden, Museum of Zoology, Germany
Palpurina, Salza, salza.palpurina@gmail.com, Masaryk University, Department of Botany and Zoology, Czech Republic
Panitsa, Maria, mpanitsa@upatras.gr, University of Patras, Greece
Papadopoulou, Anna, apapadop@umich.edu, University of Michigan, EEB Department, United States
Pataro, Luciano, luciano.pataro@gmail.com, Universidad Autónoma de Madrid, Spain
Patiño, Jairo, jpatino.llorente@gmail.com, University of Liege, Department of Biology, Ecology and Evolution, Belgium
Penone, Caterina, caterina.penone@gmail.com, Universidade Federal do Rio Grande do Norte, Ecologia, Brazil
Peres-Neto, Pedro, peres-neto.pedro@uqam.ca, University of Quebec in Montreal, Canada
Perkins, Hannah, hperkins@knights.ucf.edu, University of Central Florida, Biology, United States
Persson, Maria, ecography@oikosoffice.lu.se, Oikos Editorial Office, Ecography, Sweden
Peters, Marcell, marcell.peters@uni-wuerzburg.de, University of Würzburg, Department of Animal Ecology and Tropical Biology, Germany
Peyre, Gwendolyn, g.peyre@ub.edu, Aarhus University / University of Barcelona, France
Pigot, Alex, a.l.pigot@rug.nl, University of Groningen, Department of Biology, Netherlands
Pilsl, Christine, christine.pilsl@uni-bayreuth.de, University of Bayreuth, Department of Biogeografy, Germany
Piquer-Rodriguez, Maria, maria.piquer-rodriguez@geo.hu-berlin.de, Humboldt University of Berlin, Biogeography Lab in the Geography Department, Germany
Pironon, Samuel, samuel.pironon@free.fr, Instituto Pirenaico de Ecologia (IPE-CSIC), Spain
Pither, Jason, jason.pither@ubc.ca, University of British Columbia, Biology, Canada
Plenk, Kristina, kristina.plenk@boku.ac.at, University of Natural Resources and Life Sciences, Vienna, Institute for Integrative Nature Conservation Research, Austria
Pollock, Laura, lajosy@gmail.com, The University of Melbourne, Australia
Pott, Richard, pott@geobotanik.uni-hannover.de, Leibniz Universität Hannover, Institut für Geobotanik, Germany
Price, Jonathan, jpprice@hawaii.edu, University of Hawaii at Hilo, Geography and Environmental Studies, United States
Provenzale, Antonello, antonello.provenzale@cnr.it, National Research Council of Italy, Institute of Atmospheric Sciences and Climate, Italy
Psonis, Nikolaos, nikos.psonis@gmail.com, University of Crete, Department of Biology, Greece
Purschke, Oliver, oliver.purschke@idiv.de, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany

Q

Qiao, Ge-Xia, qiaogx@ioz.ac.cn, Institute of Zoology, Chinese Academy of Sciences, China
Qiu, Chunjing, qiuchunjing2011@163.com, Peking University, China

R

Rabosky, Daniel, drabosky@umich.edu, University of Michigan, United States
Radchuk, Viktoriia, radchuk@izw-berlin.de, Leibniz Institute for Zoo and Wildlife Research (IZW), Evolutionary ecology, Germany
Rahbek, Carsten, crahbek@snm.ku.dk, University of Copenhagen, Center for Macroecology, Evolution and Climate, Denmark
Ramakrishnan, Uma, uramakri@ncbs.res.in, National Centre for Biological Sciences, India
Ransijn, Johannes, johannes.ransijn@uni-bayreuth.de, University of Bayreuth, Disturbance Ecology, Germany
Rattis, Ludmila, ludmilarattis@gmail.com, Campinas State University, Ecology, Brazil
Razgour, Orly, Orly.Razgour@gmail.com, University of Stirling, Biological & Environmental Sciences, United Kingdom
Real, Raimundo, rrgimenez@uma.es, Universidad de Málaga, Departamento de Biología Animal, Spain
Reddy, Sushma, sreddy6@luc.edu, Loyola University Chicago, Biology, United States
Reinermann, Sophie, sophie.reinermann@web.de, University of Bayreuth, Austria
Reithmaier, Gloria, gloria.r@gmx.de, University of Bayreuth, M.Sc. Global Change Ecology
Remes, Vladimir, vladimir.remes@upol.cz, Palacky University, Department of Zoology, Czech Republic
Renner, Susanne, renner@lmu.de, University of Munich, Systematic Botany and Mycology, Germany
Reu, Björn, bjoern.reu@uni-leipzig.de, University of Leipzig, Institute of Biology, Germany
Revermann, Rasmus, rasmus.revermann@uni-hamburg.de, University of Hamburg, Germany, Biodiversity, Ecology and Evolution of Plants, Germany
Ricklefs, Robert, ricklefs@umsl.edu, University of Missouri-St. Louis, Department of Biology, United States
Riddle, Brett, brett.riddle@unlv.edu, University of Nevada Las Vegas, School of Life Sciences, United States
Rigal, François, rigal@uac.pt, University of Azores, Portugal
Rigg, Lesley, lrigg@niu.edu, Northern Illinois University, Research & Innovation Partnerships, United States
Rijsdijk, Kenneth, k.f.rijsdijk@uva.nl, University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, Netherlands
Ristić, Anđela, djinabu@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Rius, Marc, M.Rius@soton.ac.uk, University of Southampton, Ocean and Earth Science, United Kingdom
Robin, V.V., robinvijayan@gmail.com, National Centre for Biological Science, Ecology and Evolution, India
Rocchia, Emanuel, ema.rocchia@gmail.com, University of Milano Bicocca, Department of Environmental Sciences and Territory, Italy
Rocchini, Duccio, ducciorocchini@gmail.com, Fondazione Edmund Mach, Dpt. Biodiversity and Molecular Ecology, GIS and Remote Sensing Unit, Italy
Rocha, Yuri, yuritr@usp.br, University of São Paulo, Department of Geography, Brazil
Rockinger, Alexander, a.rockinger@gmail.com, University of Munich (LMU), Systematic Botany and Mycology, Germany
Roderick, George, roderick@berkeley.edu, University of California, Berkeley, Environmental Sciences (ESPM), United States
Rodriguez, Miguel A., miguela.rodriguez@uah.es, Universidad de Alcala, Departamento de Ciencias de la Vida, Spain
Rodriguez, Pilar, pilar_rodriguez_5@hotmail.com, Nacional Financiera Fideicomiso Fondo para Biodiversidad (CONABIO), CGIA, Mexico
Rodriguez-Sanchez, Francisco, frodriguez.work@gmail.com, Estacion Biologica de Donana - CSIC, Integrative Ecology Group, Spain
Rominger, Andy, ajrominger@gmail.com, University of California Berkeley, United States
Rosati, Leonardo, leonardo.rosati@unibas.it, University of Basilicata, School of Agriculture, Forestry, Food and Environment, Italy
Ruiz-Benito, Paloma, palomaruizbenito@gmail.com, University of Stirling, United Kingdom
Runck, Amy, arunck@winona.edu, Winona State University, Biology, United States
Ruokolainen, Kalle, kalle.ruokolainen@utu.fi, University of Turku, Dept. of Biology, Finland

S

Saar, Liina, liina.saar@ut.ee, University of Tartu, Department of Botany, Estonia
Saladin, Bianca, bianca.saladin@wsl.ch, Swiss Research Institute WSL, Switzerland
Saltre, Frederik, frederik.saltre@adelaide.edu.au, University of Adelaide, Australia
Sánchez de Dios, Rut, rut.sanchez@bio.ucm.es, University Complutense of Madrid, Biología Vegetal I, Spain

Sánchez-Fernández, David, davidsan@um.es, Institute of Evolutionary Biology (CSIC-UPF), Spain
Sánchez Meseguer, Andrea, asanchezmeseguer@gmail.com, Institut National de la Recherche Agronomique (INRA), The Center for Biology and Management of Populations, France
Sandel, Brody, brody.sandel@biology.au.dk, Aarhus University, Department of Bioscience, Denmark
Sanders, Nate, nathan.sanders@snm.ku.dk, University of Copenhagen, Center for Macroecology, Evolution, and Climate, Denmark
Sarmento Cabral, Juliano, jsarmen@uni-goettingen.de, University of Göttingen, Biodiversity, Macroecology and Conservation Biogeography, Germany
Sawaya, Ricardo, sawayarj@gmail.com, Federal University of São Paulo (UNIFESP), Ecology and Evolutionary Biology, Brazil
Sax, Dov, dov.sax@gmail.com, Brown University, United States
Sbordoni, Valerio, valerio.sbordoni@uniroma2.it, Tor Vergata University, Rome, Italy, Department Biology, Italy
Schaller, Carsten, carsten.schaller@stmail.uni-bayreuth.de, University of Bayreuth, Germany
Scharf, Ulrike, kontakt@ulrike-scharf.de, Bavarian State Ministry of the Environment and Consumer Protection, Germany
Scheiter, Simon, simon.scheiter@senckenberg.de, Senckenberg Gesellschaft für Naturforschung, Biodiversität und Klima Forschungszentrum (BiK-F), Germany
Schickhoff, Udo, schickhoff@geowiss.uni-hamburg.de, University of Hamburg, Geography, Germany
Schidelko, Kathrin, k.schidelko@zfmk.de, Zoological Research Museum Alexander Koenig, Section of Ornithology, Germany
Schiebelhut, Lauren, lschiebelhut@ucmerced.edu, University of California, Merced, United States
Schillinger, Corinna, schillingerco@aol.com, University of Bayreuth, Biogeography, Germany
Schmidtlein, Sebastian, schmidtlein@kit.edu, Karlsruhe Institute of Technology (KIT), Inst. of Geography and Geoecology, Germany
Schmitt, Thomas, thomas.schmitt@senckenberg.de, Senckenberg German Entomological Institute, Germany
Schneeweiss, Gerald M., gerald.schneeweiss@univie.ac.at, University of Vienna, Botany and Biodiversity Research, Austria
Scholz, Barbara, babsi.scholz@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Schönswetter, Peter, peter.schoenswetter@uibk.ac.at, University of Innsbruck, Institute of Botany, Austria
Schrodt, Franziska, f.i.schrodt@gmail.com, Max Planck Institute for Biogeochemistry, Germany
Schuh, Leila, leilaschuh@yahoo.com, University of Bayreuth, Germany
Schulte to Buehne, Henrike, henrike.stb@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Schulz, Christian, Christian.Schulz-3@rub.de, Ruhr-Universität Bochum, Germany
Schumacher, Andreas, schumach55@yahoo.com, University of Heidelberg, Germany
Schüßler, Christina, christina.schuessler@smns-bw.de, Stuttgart State Museum of Natural History, Germany
Schwab, Niels, niels.schwab@uni-hamburg.de, University of Hamburg, Physical Geography, Center for Earth System Research and Sustainability (CEN), Germany
Schwabe, Birgit, birgit.schwabe@fau.de, Friedrich Alexander Universität Erlangen-Nürnberg, Institut für Geographie, Germany
Schwarz, Helmut, Alexander von Humboldt Foundation, President, Germany
Schweiger, Andreas, andreas.schweiger@uni-bayreuth.de, BayCEER, University of Bayreuth, Biogeography, Germany
Serra Varela, María Jesús, majes85@hotmail.com, INIA, Sustainable Forest Management Research Institute, Spain
Servais, Thomas, Thomas.servais@univ-lille1.fr, French National Centre for Scientific Research, France
Sheard, Julie, lfj315@alumni.ku.dk, Copenhagen University, Center for Macroecology, Evolution and Climate, Denmark
Shen, Zehao, shzh@pku.edu.cn, Peking University, Ecology, China
Shooner, Stephanie, svshooner@gmail.com, Concordia University, Biology, Canada
Si, Xingfeng, xingfengsi@gmail.com, Zhejiang University, College of Life Sciences, China
Sieber, Anika, anika.sieber@geo.hu-berlin.de, Humboldt-Universität zu Berlin, Geography Department, Biogeography and Conservation Biology, Germany
Silva, Ana, ana.silva@anu.edu.au, University of Lisbon and Australia National University, Australia
Silva, Andre, andre.silva@ebc.uu.se, Uppsala University, Department Animal Ecology, Sweden
Silva, Bruno, brunovilelasilva@hotmail.com, Universidade Federal de Goiás, Departamento de Ecologia, Spain
Simberloff, Daniel, dsimberloff@utk.edu, University of Tennessee, Department of Ecology and Evolutionary Biology, United States
Šímová, Irena, office@cts.cuni.cz, Charles University in Prague, Center for Theoretical Study, Czech Republic
Singer, Anja, anja.singer@senckenberg.de, MARUM, University of Bremen, Biology/Chemistry, Germany
Singh, Randeep, randeep04@rediffmail.com, Wildlife Institute of India, Animal Ecology and Conservation Biology, India

Sizling, Arnost, Leos, sizling@cts.cuni.cz, Charles University, Center for Theoretical Studies, Czech Republic
Slavenko, Alex, gluttony14@gmail.com, Tel Aviv University, Department of Zoology, Israel
Smid, Jiri, jirismd@gmail.com, National Museum in Prague, Department of Zoology, Czech Republic
Smith, Felisa, fasmith@unm.edu, University of New Mexico, Biology Department, United States
Sonne, Jesper, jesper2904@hotmail.com, University of Copenhagen, Denmark
Spada, Francesco, francesco.spada@uniroma1.it, University of Roma la Sapienza, Dip. Biologia Ambientale, Italy
Speciale, Claudia, claudiaspeciale@gmail.com, University of Salento, Laboratory of Archaeobotany and Paleoecology, Italy
Stahlmann, Reinhold, reinhold.stahlmann@uni-bayreuth.de, University of Bayreuth, Biogeography, Germany
Steen, Valerie, valerie.steen@gmail.com, Colorado State University, United States
Steffan-Dewenter, Ingolf, ingolf.steffan@uni-wuerzburg.de, University of Würzburg, Animal Ecology and Tropical Biology, Germany
Stein, Anke, astein@uni-goettingen.de, University of Göttingen, Biodiversity, Macroecology and Conservation Biogeography, Germany
Steinbauer, Manuel, manuel.steinbauer@uni-bayreuth.de, BayCEER, University of Bayreuth, Germany
Stelbrink, Björn, bjoern.stelbrink@allzool.bio.uni-giessen.de, Justus Liebig University Giessen, Germany
Stevens, George, georgecstevens@gmail.com, Coastal Community Foundation, United States
Stiels, Darius, d.stiels@zfmk.de, Zoological Research Museum Alexander Koenig, Section of Ornithology, Germany
Stigall, Alycia, stigall@ohio.edu, Ohio University, Geological Sciences, United States
Stojakowits, Philipp, stojakowits@geo.uni-augsburg.de, University of Augsburg, Institute of Geography, Germany
Storch, David, storch@cts.cuni.cz, Charles University, Center for Theoretical Study, Czech Republic
Strijk, Joeri Sergej, jsstrijk@hotmail.com, Guangxi University, College of Forestry, Plant Ecophysiology and Evolution Group, China
Strozier, Lynika, lstrozier@luc.edu, Loyola University Chicago, Biology Department, United States
Strutzenberger, Patrick, patrick.strutzenberger@senckenberg.de, Senckenberg Natural History Collections Dresden, Museum of Zoology, Germany
Sugden, Andrew, asugden@science-int.co.uk, Science Magazine, AAAS Science International, United Kingdom
Svenning, Jens-Christian, svenning@biology.au.dk, Aarhus University, Section for Ecoinformatics & Biodiversity, Department of Bioscience, Denmark
Szewczyk, Tim, tim.szewczyk@gmail.com, University of Colorado at Boulder, Ecology and Evolutionary Biology, United States

T

Taheri, Shirin, taheri.shi@gmail.com, Imperial College London, Department of Life Science, United Kingdom
Tamar, Karin, karintmr@gmail.com, Tel Aviv University, Department of Zoology, Israel
Tamma, Krishnapriya, priya.tamma@gmail.com, National Centre for Biological Sciences, India
Täuber, Angelika, angelika.taeuber@uni-bayreuth.de, University of Bayreuth, Germany
Teitelbaum, Claire, claire.teitelbaum@gmail.com, Biodiversity and Climate Research Centre, Germany
Teng, Shuqing, shuqing.teng@bios.au.dk, Aarhus University, Denmark
Thies, Birgit, birgit.thies@uni-bayreuth.de, University of Bayreuth, BayCEER, Germany
Thiv, Mike, mike.thiv@smns-bw.de, Staatliches Museum für Naturkunde Stuttgart, Botany, Germany
Thomas, Stephanie, stephanie.thomas@uni-bayreuth.de, University of Bayreuth, Biogeography/Global Change Ecology, Germany
Thrippleton, Timothy, timothy.thrippleton@usys.ethz.ch, ETH Zurich, Forest Ecology, Switzerland
Tietze, Dieter Thomas, mail@dieterthomastietze.de, Heidelberg University, Institute of Pharmacy and Molecular Biotechnology, Germany
Tjaden, Nils, nils.tjaden@uni-bayreuth.de, University of Bayreuth, Department of biogeography, Germany
Tjørve, Even, even.tjorve@hil.no, Lillehammer University College, ØKORG, Norway
Toivonen, Johanna, jomito@utu.fi, University of Turku, Department of Biology, Finland
Tolonen, Katri, katri.e.tolonen@ymparisto.fi, Finnish Environment Institute (Syke), University of Oulu,, Natural Environment Centre/Biodiversity, Department of Biology, Finland
Toussaint, Aurèle, toussaint.aurele@gmail.com, University of Toulouse 3, Laboratory Ecology and Biological Diversity, France
Tovar, Carolina, carolina.tovar@zoo.ox.ac.uk, University of Oxford, Department of Zoology, United Kingdom
Traini, Camille, camille.traini@yahoo.com, University of Bayreuth, Biogeography, Germany
Triantis, Kostas, island.biogeography@gmail.com, University of Athens, Biology Department, Greece
Tsianou, Mariana, mtsianou@upatras.gr, University of Patras, Department of Environmental and Natural Resources, Greece

Tuanmu, Mao-Ning, mao-ning.tuanmu@yale.edu, Yale University, Department of Ecology and Evolutionary Biology, United States
Tucker, Caroline, carolinemtucker@gmail.com, University of Colorado, Boulder, EBIO, United States
Tucker, Marlee, tucker.marlee@gmail.com, Biodiversity and Climate Research Centre (BiK-F), Germany
Tuomisto, Hanna, hanna.tuomisto@utu.fi, University of Turku, Department of Biology, Finland
Turner, Woody, woody.turner@nasa.gov, NASA, Earth Science Division, United States

U

Ulrich, Werner, ulrichw@umk.pl, Nicolaus Copernicus University Torun, Chair of Ecology and Biogeography, Poland

V

Valente, Luis, valente@uni-potsdam.de, University of Potsdam, Germany
Vamberger, Melita, melita.vamberger@senckenberg.de, Senckenberg Dresden, Pyhlogeography, Germany
Van Dam, Matthew, matthewhvandam@gmail.com, Zoologische Staatssammlung München, Entomology, Germany
Vanselow, Kim André, kim.vanselow@fau.de, FAU Erlangen-Nürnberg, Institute of Geography, Germany
Varela, Sara, svarela@paleobiogeography.org, Charles University, Czech Republic
Vasconcelos, Tiago, zoologia@ig.com.br, Sao Paulo State University, Brazil
Vázquez-Domínguez, Ella, evazquez@ecologia.unam.mx, Instituto de Ecología, UNAM, Ecología de la Biodiversidad, Mexico
Večeřa, Martin, martinvec@seznam.cz, Masaryk University, Department of Botany and Zoology, Czech Republic
Veith, Michael, veith@uni-trier.de, Trier University, Department of Biogeography, Germany
Velasquez, Eleanor, em.velasquez@student.qut.edu.au, Queensland University of Technology, Australia
Vetaas, Ole R., ole.vetaas@global.uib.no, University of Bergen, Department of Geography, Norway
Vieira, Christophe, cvcarp@gmail.com, Institut de Recherche pour le Developpement, Biocomplexité des Ecosystèmes Coralliens de l'Indo-Pacifique, New Caledonia
Vigalondo, Beatriz, beatriz.vigalondo@uam.es, Universidad Autonoma de Madrid, Departamento de Biología, Unidad de Botánica, Spain
Vijayakumar, S P, vijay_rhaco@yahoo.com, National Centre for Biological Sciences, India
Villalobos, Fabricio, fabricio.villalobos@gmail.com, Universidade Federal de Goiás, Ecologia, Brazil
Villeger, Sebastien, sebastien.villeger@univ-montp2.fr, Centre National de la Recherche Scientifique (CNRS), ECOSYM, France
Voda, Raluca, raluvoda@gmail.com, Institut de Biologia Evolutiva (CSIC-UPF), Butterfly Diversity and Evolution Lab, Spain
von Gillhaußen, Philipp, philipp.gillhaussen@uni-bayreuth.de, University of Bayreuth, Disturbance Ecology, Germany
Voskamp, Alke, alke.voskamp@durham.ac.uk, Durham University, School of Biological and Biomedical Sciences, United Kingdom

W

Wallis, Christine, christine.wallis@biologie.uni-marburg.de, University of Marburg, Conservation Ecology, Germany
Walton, Craig, notsowognow@hotmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Waterson, Amy, aw13663@bristol.ac.uk, University of Bristol, Geographical Sciences/Earth Sciences, United Kingdom
Weaver, Jennifer, jennweaver@berkeley.edu, UC Berkeley, United States
Weber, Simon, webersimon89@gmail.com, University of Bayreuth, Germany
Weigel, Robert, s2roweig@stmail.uni-bayreuth.de, Universität Bayreuth, Geoökologie, Germany
Weigelt, Patrick, weigelt.patrick@gmail.com, University of Göttingen, Biodiversity, Macroecology & Conservation Biogeography Group, Germany
Weiser, Frank, frank_weiser@gmx.de, University of Bayreuth, M.Sc. Global Change Ecology
Wells, Carrie, cwells19@uncc.edu, University of North Carolina at Charlotte, Biological Sciences, United States
Wepfer, Patricia, patricia.wepfer@oist.jp, Okinawa Institute of Science and Technology, Japan
Westover, Marie, mariewestover@gmail.com, University of New Mexico, Biology, United States
Weyer, Jessica, jessica.weyer@senckenberg.de, Senckenberg German Entomological Institute, Ecology, Germany
Weyrich, Philippe, philippeweyrich@hotmail.fr, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Whittaker, Robert, robert.whittaker@ouce.ox.ac.uk, University of Oxford, School of Geography and the Environment, United Kingdom
Wiggering, Benedikt, B.Wiggering@gmx.net, Humboldt Universität zu Berlin, Germany
Williams, John, jwilliams45@ucmerced.edu, University of California, Merced, United States

Williams, John, jww@geography.wisc.edu, University of Wisconsin-Madison, Department of Geography, United States
Willis, Kathy, K.Willis@kew.org, Royal Botanic Gardens, Kew, Director of Science, United Kingdom
Willner, Wolfgang, wolfgang.willner@vinca.at, VINCA, Austria
Wilson, Adam, adam.wilson@yale.edu, Yale University, Ecology & Evolutionary Biology, United States
Winter, Marten, marten.winter@idiv.de, German Centre for Integrative Biodiversity Research (iDiv), sDiv - Synthesis Centre, Germany
Wirth, Christian, cwirth@uni-leipzig.de, University of Leipzig, Systematic Botany and Functional Biodiversity, Germany
Wohlwend, Michael, m.wohlwend@gmx.de, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Wolf, Kathrin, kati.wolf@mailbox-tu-berlin.de, University of Bayreuth, M.Sc. Global Change Ecology
Wollschläger, Laura, laucore@aol.com, University of Bayreuth, Germany

X

Xu, Yue, xuyue10@pku.edu.cn, Peking University, China

Y

Yadav, Romesh Kumar, romeshyadav99@gmail.com, University of Bayreuth, M.Sc. Global Change Ecology, Germany
Yang, Xuefei, xuefei@mail.kib.ac.cn, Kunming Institute of Botany, Chinese Academy of Sciences, Key Laboratory of Economic Plants, China
Young, John, jyoung@usgs.gov, US Geological Survey, Leetown Science Center, United States

Z

Zelený, David, zeleny@sci.muni.cz, Masaryk University, Department of Botany and Zoology, Czech Republic
Zenner, Juliane, JulianeZenner@web.de, Biodiversity and Climate Research Centre (BiK-F) & Goethe University Frankfurt, Germany
Zeuss, Dirk, dirk.zeuss@biologie.uni-marburg.de, University of Marburg, Department of Ecology, Germany
Zimmermann, Maja, maja.zimmermann@geoecology.org, University of Bayreuth, Germany
Zimmermann, Niklaus, niklaus.zimmermann@wsl.ch, Swiss Federal Research Institute WSL, Landscape Dynamics, Switzerland
Ziv, Yaron, yziv@bgu.ac.il, Ben Gurion University of the Negev, Israel
Zohner, Constantin, constantin.zohner@t-online.de, University of Munich (LMU), Systematic Botany and Mycology, Germany
Zonninger, Irene, irene.z007@yahoo.de, Chalet India, Switzerland
Zurell, Damaris, damaris.zurell@wsl.ch, Swiss Federal Research Institute WSL, Landscape Dynamics, Switzerland

List of authors

List of authors

A

Abdelaziz, Karamalla: PPS2.8
Abraham, Vojtěch: P8.1
Achmadi, Anang: CT1.5
Adamo, Maria: PPS2.2
Adrian, Pachzelt: CT6.1
Aduse-Poku, Kwaku: P7.1
Agarwal, Ishan: CT2.3
Ahmed, Manal: P5.21
Ah-Peng, Claudine: CT11.2, P2.18
A. Jonathan, Shaw: P1.26
Akkurt, Seda: P5.1
Akoth, Beryl: P12.1
Alahuhta, Janne: P5.2, P5.7, P5.22
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