The

Department of Biogeography of Trier University

invites for the

interdisciplinary conference

Macroecology meets Biogeography

A joint meeting of the

Arbeitskreis Biogeographie

(Verband der Geographen an Deutschen Hochschulen, VGDH)

and

Arbeitskreis Makroökologie

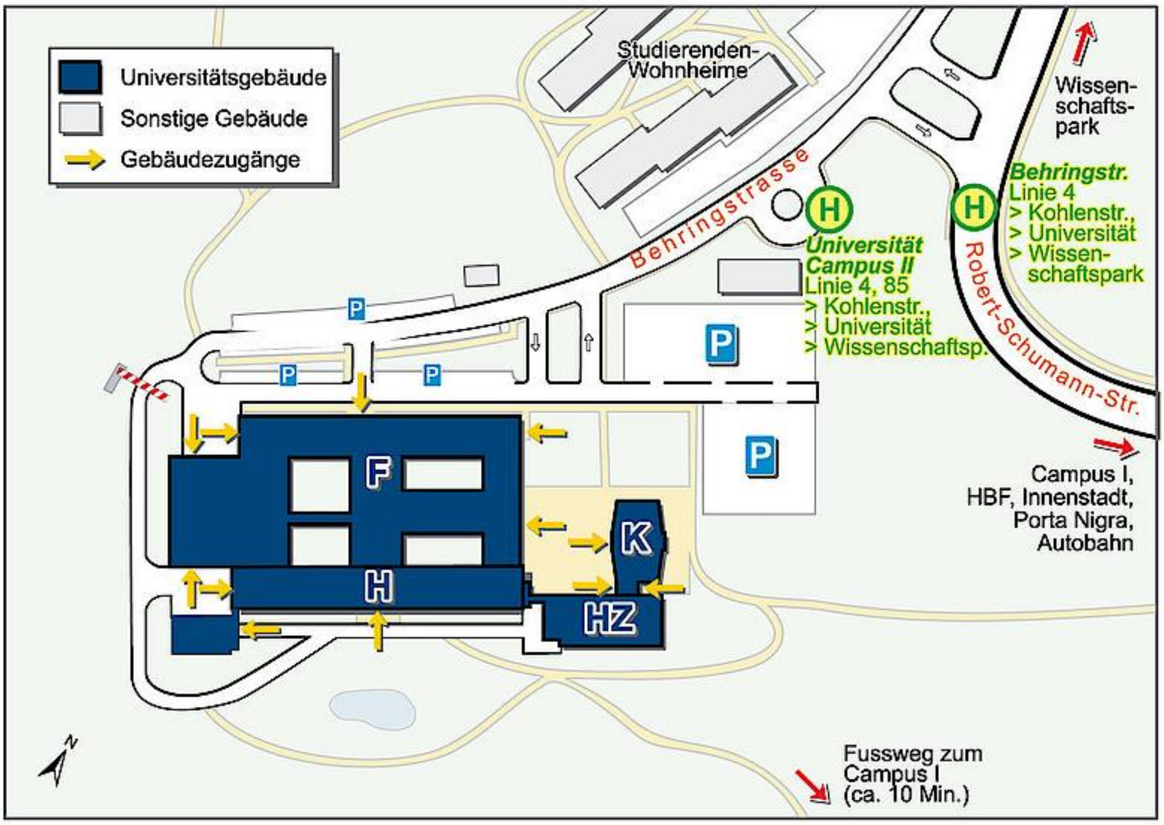
(Gesellschaft für Ökologie, GfÖ)

15 to 17 March 2016

Venue & how to get there by bus

Trier University, Campus II, Behringstraße, 54296 Trier
“Hörsaalzentrum“, rooms Hs 12 and HS 13

Below a map showing Campus II and the ”Hörsaalzentrum” indicated by HZ .
You can reach Campus II from the ”Hauptbahnhof” with **bus #4 to “Irsch”:** get of at “Universität Campus II”. After 6 PM also **bus # 85** stops here to take you back to town.



Icebreaker, lunch time & conference Diner

The icebreaker will take place in the evening of on day 1 at the venue (included in the conference fee). On lunch time on day 2, there are various opportunities to get what you want in the vicinity of Campus II. Ask for a map and recommendations at our registration desk. On the same day, in the evening, the conference diner will take place at the nearby Monte Petris. Just follow the group to get over or ask for information at the registration desk. Conference diner starts at 7 PM and is not included in the conference fee. Additional costs are 35 Euros (excluding drinks).

Conference fee

Regular fee is 45 Euros and includes supporting materials, coffee breaks and the icebreaker. Students (BSc, MSc) get a reduction to 25 Euros. The conference diner is not included in the fee and costs 35 Euros. You will receive a receipt

Organization committee

Stefan Lötters, Joscha Beninde, Daniela Braun, Linda Bröder, Stefan Ehl, Stephan Feldmeier, Ute Herrmann, Sarah Kieren, Claude Kolwelter, Luis Fernando Marin, Michael Mayer, Valentin Mingo, Christina Müller, Katja Rohde, Daniela Rößler, Elena Rudolf, Norman Wagner, Sarah Wirtz & Michael Veith.
You can recognize us by our colored name tags.
In case of trouble, call Stefan Lötters (0151/28406943).

Concept

The conference foresees

- one **Plenary lecture** by Prof. Dr. Marcus Koch (Heidelberg). Other **Invited talks** are represented by six *Next Generation Scientists* in the interdisciplinary fields of macroecology and biogeography. We are pleased to have on board Dr. Juliano Cabral (Leipzig), Dr. Anna Cord (Leipzig), Dr. Susanne Fritz (Frankfurt), Dr. Christian Hof (Frankfurt), Dr. Manuel Steinbauer (Aarhus/DK) and Dr. Patrick Weigelt (Göttingen).

  Other presentations include:
- **10 Regular talks** (25 min plus 5 min discussion).
- **6 Short talks** (10 min plus 5 min discussion).
- **2 Ignites** – short presentations on ideas or unsolved problems (5 min plus 10 min discussion).
- **3 Posters**.

All speakers are requested to respect the time slots given to them. Chairs will show you yellow and red cards, as in football, to signal when you have to come to an end.
Please make sure to provide your talk latest in the break before the session into which your talk is incorporated. Please use *ppt, *.pptx or *.PDF. Likewise, you can bring your own laptop, if you are a Mac person.

Program

Tuesday	15-Mar	Trier University, Campus II, "Hörsaalzentrum": HS13
12:00	Registration opens	
13:00	Michael Veith & Stefan Lötters, Trier	Opening & remarks

Invited next generation scientists, chair is Stefan Lötters

13:15	Manuel Steinbauer, Bayreuth	Environmental signals in evolutionary patterns
ca 14:10	Anna Cord, Leipzig	Earth observation in biogeography and macroecology: mapping patterns and monitoring changes
ca. 15:00	Patrick Weigelt & Holger Kreft, Göttingen	Island biogeography meets macroecology
15:50-16:30	Coffee break (40 min)	

Regular talks (25 min + 5 min discussion) on modelling and large-scale patterns; chair is Stephan Feldmeier

16:30	Jan O. Engler, Bonn / Göttingen, et al.	Adding a genotypic perspective in niche modeling and theory
17:00	Aidin Niamir, Frankfurt, & Sam Khosravifard, Twente (NL)	Ensemble Forecasting of Raccoon Distribution in West Asia
17:30	Marlee A. Tucker, Frankfurt, et al.	Examining macroecological patterns of animal movement
18:00	Hanno Seebens, Frankfurt, & Bernd Blasius, Oldenburg	The macroecology of alien species – challenges, patterns and predictions
ca. 18:30	"Arbeitskreis" announcements & icebreaker at venue (open end)	

Wednesday	16-Mar	Trier University, Campus II, "Hörsaalzentrum": HS12

Plenary lecture; chair is Michael Veith

9:00	Marcus Koch, Heidelberg	The evolutionary history of *Cochlearia* (Brassicaceae) in Central Europe: Population genetics and phylogenomics of a cold relic in a warming world

Ignites: ideas, unsolved problems (5 min + 10 min discussion); chair is Christian Hof

10:00-10:15	Luis D. Verde Arregoitia, Bern (CH)	Testing for body size divergence in Neotropical bats
10:15-10:30	Diana Bowler & Katrin Böhning-Gaese, Frankfurt	A model-based approach to calculating the community temperature index
10:30-11:15	Coffee break (45 min)	

Regular talks (25 min + 5 min discussion) on mountain ecology; chair is Daniela Braun

11:15	Jens Mutke, Bonn, et al.	Latitudinal and altitudinal plant diversity patterns in the tropical Andes
11:45	Kim André Vanselow, Erlangen	Degradation and Greening in an arid mountain ecosystem – the case of the Western Pamirs of Tajikistan
12:15	Roland Pape & Jörg Löffler, Bonn	Seasonality of habitat selection shown to buffer alpine reindeer pastoralism against climate variability
12:45-13:45	Lunch break (1 hour)	

Regular talks (25 min + 5 min discussion) on miscellaneous topics; chair is Katharina J. Filz

13:45	Shan Huang, Frankfurt, et al.	Body-mass evolution in Neogene large mammals and the status of Cope's rule
14:15	Bernd Lenzer, Vienna and Bayreuth, et al.	Ecological implications of flower color change in fertilized and unfertilized grassland over the past 150 years
14:45	Hannes Feilhauer, Erlangen, et al.	Spatial patterns of Leaf Mass per Area in a wetland under water stress
15:15-16:30	Coffee break (45 min), includes	Beckers et al.: Patterns of Carabid beetle diversity in the Central-Norwegian Scandes
	Poster presentation (representatives are with their posters)	Filz & Lötters: Worldclim versus glUV: which variables tip the scales in predicting alien reptile distributions?
		Hein et al.: Ecology, biogeography and DNA barcoding in spiders of alpine tundra ecosystems

Continue on next page

Short talks (10 min + 5 min discussion) on miscellaneous topics; chair is Jan O. Engler

16:30	Axelle Zacaï, Dijon (F), et al.	Scales have a major impact on the cross-relationships among phylogeny, spatial distribution and species duration in fossil cephalopods
16:45	Andreas H. Schweiger & Carl Beierkuhlein, Bayreuth	Cross-scale similarity of species temperature niches
17:00	Roxanne Leberger, Ispra (I) and Leipzig, et al.	Where are the most unique forested area to preserve? – A cross-scale study
17:15	Maria Eugenia Correa-Cano, Cornwall (UK), et al.	Erosion of natural darkness in the geographic ranges of cacti
17:30	Katharina Filz, Dortmund, et al.	Abandoned foreigners: is the stage set for pet reptiles to invade Central Europe?
17:45	Corentin Gibert & Gilles Escarguel, Villeurbanne (F)	Estimation of taxonomic richness variation through geological times: a simulation approach
18:00 (end 18:15)	David Kienle, Bayreuth, et al.	Do biogeographic drivers modify global treeline elevations?
19:00	Conference dinner at the nearby "Monte Petris" (open end)	

Thursday	**17-Mar**	**Trier University, Campus II, "Hörsaalzentrum": HS12**

Invited next generation scientists; chairs are Michael Mayer & Valentin Mingo

9:00	Susanne Fritz, Frankfurt	Macroecology in space and time: how recent advances allow adding the temporal dimension
ca. 9:55	Juliano Cabral, Leipzig	Eco-evolutionary simulation models for macroecology and biogeography
10:45-11:15	Coffee break (30 min)	
11:15	Christian Hof, Frankfurt	Understanding responses of biodiversity to global change: integration at the macro-scale
ca. 12:10	Representatives of each "Arbeitskreis"	Remarks & closure

Abstracts

Posters (in alphabetical order by first author)

Patterns of Carabid beetle diversity in the Central-Norwegian Scandes

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In recent years, increased focus has been put on the study of alpine ecosystems in high latitudes. Still there is an immense lack of knowledge regarding their faunistic characteristics. The present study analyzes diversity patterns of ground beetles (Carabidae) in the Central-Norwegian Scandes and aims to describe these patterns across a mesoscale alpine elevational gradient and a microscale topographical gradient. Non-linear decrease in species density along the elevational gradient supports current theories on species–elevation relationships in emphasizing the importance of overlapping species-habitats in ecotone borders, i.e. the constitution of a "mid-domain" effect. Our study shows Carabidae to be strongly selective regarding habitat choices along the topographical gradient. Regarding future work it is imperative to understand the biotic and abiotic factors that limit each species distribution individually to allow for precise and coherent approaches with regard to ongoing climatic and environmental change.

Worldclim versus glUV: which variables tip the scales in predicting alien reptile distributions?

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Correlative Species Distribution Models (SDMs) are common tools applied to predict invasions of alien species. We use information from the recently published global UV-B radiation dataset glUV to study SDM performance in UV-B sensitive animals – i.e. alien reptile species – that are considered candidates for biological invasions. We processed different variable combinations (i.e. out of bioclim 1-19, partly combined with glUV's UV-B variables) to generate global SDMs, employing three different modelling algorithms. The predictive power of SDMs built on native records only and different variable combinations was compared with focus on regions of known species introductions. Bioclim-only models and those incorporating UV-B variables revealed largely similar results with high spatial congruence independent from the algorithm used. In some species model results differed considerably showing regions only predicted suitable by either one of the two modelling approaches. Also, in some species all modelling

approaches failed to deliver accurate reflections of known alien occurrences, partly due to scaling issues. Our results acknowledge UV-B variables to be valuable in reptile SDM building. However, when predicting alien species' invasive potential in geographic space, model quality does not necessarily increase when incorporating UV-B compared to bioclim-only models, but highly depends on variable choice, resolution and algorithm.

Ecology, biogeography and DNA barcoding in spiders of alpine tundra ecosystems

N. Hein[1*], J. Astrin[2], V.G. Fonseca[2], B. Misof[2], J. Löffler[1]
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This study addresses the spatial distribution of spiders (Araneae) along multiple ecological and biogeographical gradients. Two study regions were sampled for ground-dwelling spiders using pitfall traps. The study regions were situated in the oceanic and the continental part of Central Norway. We sampled a total of 6,628 adult specimens in 109 species, at 73 sampling sites. Thereof, we identified various indicator species for typical alpine tundra habitats that could be described as either 'chionophobous' or 'chionophilous', depending on the topography-related snow cover at the sampling sites. Local climatic conditions had a stronger influence on the spatial distribution of the spiders than did broad-scale climatic conditions. Species identification proved to be the major workflow bottleneck. We therefore tested the COI barcoding technique on 77 spider species selected from the routine material. A Neighbour Joining tree shows the individual representatives from 77 Araneae species present in the eastern, continental research region. Here, even applying genetic distance thresholds as the simplest species delimitation criterion, it differentiates well among species using a standard genetic distance cut-off value of 3%. The majority of morphological species identification was corroborated. Nonetheless, some morphology-based identifications could only be taxonomically scrutinized by molecular methods and subsequent morphological re-identification.

Invited plenary lecture

The evolutionary history of *Cochlearia* (Brassicaceae) in Central Europe: Population- and phylogenomics of a cold relic in a warming world

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The genus Cochlearia represents an isolated evolutionary lineage that diverged from its Mediterranean sister clade during the Miocene and since that did not underwent any significant speciation until Pleistocene glaciation and deglaciation cycles. During the Pleistocene approximately 20 taxa evolved, with most of the species closely associated with cold-characterized habitats. Similar eco- and phenotypes of varying ploidy levels emerged and are scarcely distributed all over Europe and the Circumarctic. One sub-group of species is occurring mostly along coastal lines and a second sub-group is highly restricted to mountain and high elevation/altitude regions. The proposed project aims to unravel the evolutionary history of the various species, subspecies and cytotypes on a high-resolution-scale in space and time. The resulting evolutionary-systematic framework will lay the ground to study in particular hypotheses on parallel evolution and adaptation to cold environments with its respective characteristics and types of habitats (e.g. bedrock types, elevation, etc.). The *Cochlearia* study system provides the great opportunity to study closely linked traits and characters, because of various naturally occurring species pairs which are obviously, at least geographically, separated from each other. This will allow to study and test explicitly parallel evolution and adaptation. The data used herein are mostly based on next-generation-sequencing data utilizing information from all three plant genomes (nuclear, plastid, mitochondrial). These data will not only allow high-resolution analysis, but will also provide first access to thousands of genes and loci. The data will be compared with metabolomic footprints to cold treatment (experimental data) and climatic niche analysis (environmental footprints). The genus *Cochlearia* should be also developed towards a system to study in future molecular (genomic)-evolutionary signatures of cold adaptation.

Invited talks by Next Generation Scientists (in alphabetical order)

Mechanistic models in macroecology

Juliano Sarmento Cabral[1,2], Luis Valente[3], Florian Hartig[4],
Kerstin Wiegand[5], Holger Kreft[6]
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Macroecology and biogeography are concerned with the description and explanation of biodiversity patterns across space and time. In the past, this question has been mainly addressed via correlative approaches, although calls for more mechanistic explanations have often been voiced. In recent years, computational power as well as theoretical and statistical tools have advanced sufficiently to allow the development of process-based or mechanistic simulation models that investigate biodiversity patterns across scales. I will review this development, comparing different models, their theoretical framework and their findings, while placing my own research in perspective. Various ecological processes have been modelled, mainly physiological, demographic and dispersal constraints as well as biotic interactions. Environmental and human-induced drivers are increasingly modelled explicitly, with climate change being one major motivation for building predictive models. Less studied are, however, evolutionary processes. Models still tend to include only a few of these processes and drivers at a time. For example, models that treat physiology explicit tend to treat space implicit, whereas models focused at larger scales ignore local processes. Almost all models include some degree of stochasticity. These trends imply that particular combinations of processes may still be understudied and the integration of processes acting at different ecological levels still poses challenges. Therefore, many ecological and methodological questions remain open, such as relevant processes interactions, scaling, validation, and the appropriate level of mechanistic complexity. Finally, I exemplify how models can tackle such issues by models developed in the recent years integrating eco-evolutionary processes across spatial and temporal scales.

Earth observation in biogeography and macroecology: mapping patterns and monitoring changes

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A key question that biogeographers and macroecologists have strived to understand is the spatial patterns and temporal dynamics of the biota. In this age of climatic and land use changes and rapid rates of species extinctions, such knowledge has become an essential component for management and conservation. The synoptic view provided by earth-imaging sensors constitutes an important source of information on the distribution of habitats and biodiversity patterns, but also provides vital information about broad-scale environmental drivers of these patterns. Remote sensing therefore has become one of the most powerful techniques to provide observations of biogeographic patterns in reduced time and costs. Novel analytical techniques, increasing computational capacity and free access to satellite data have greatly promoted the use of Earth observation data in biogeography and macroecology at different spatio-temporal scales. However, there are some conceptual and methodological issues that impede interdisciplinary approaches in this field of research. In several cases, there is a lack of interoperability between remotely sensed information and ecological databases which may lead to unfounded hopes. The aim of the presentation is therefore to elaborate upon opportunities and illusions regarding the potential of Earth observation data in biogeography and macroecology.

Macroecology in space and time: how recent advances allow adding the temporal dimension

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Spatial patterns of diversity and species' traits are well-known today, but temporal dynamics are rarely studied. If biogeographic history, macroevolutionary processes or past environmental dynamics are considered in macroecological studies, they are usually reduced to a "footprint measure" that sums up accumulated change prior to today, e.g. the amount of evolutionary history represented by a phylogenetic lineage, or the velocity of climate change since the Last Glacial Maximum. I argue that next-generation macroecology should go beyond such first approximations, because recent advances would allow explicit consideration of both space and time in combined analyses. I draw on two examples to illustrate these ideas. Firstly, paleontological databases are rapidly growing and nowadays reflect the deep-time history of taxa and environments well. I use the mammalian fossil record over the last 23 million years to illustrate deep-time dynamics of macroecological patterns. Secondly, citizen science can provide enormous temporally explicit datasets of species' occurrences today. These offer huge opportunities in measuring seasonal or short-term temporal dynamics of species' ranges and diversity patterns, as I will show for bird assemblages in Australia.

Understanding responses of biodiversity to global change: integration at the macro-scale

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To understand whether and how species and ecosystems are able to respond to global change is still one of the major challenges in ecological and biogeographical research. Over the recent decades, macroecology has developed powerful tools to study species' responses to anthropogenic impacts. Here, I will discuss several avenues of how our analytical and predictive abilities of biotic responses to global change may be improved by integrating data and approaches from different areas of ecological research. As examples, I will present recent studies on (1) how thermal trait data from physiological experiments may help to better understand relationships between species distributions and ambient climatic conditions, (2) the relationships between species' thermal tolerances and empirical dispersal abilities (i.e. two key response pathways of species to react to climate change), and (3) how data from correlative species distribution models can be combined with information on species interaction networks in order to assess species' vulnerability to climate change. Overall, I will highlight the need for and the opportunities of more and better integration among (sub)disciplines of ecology and biogeography in order to improve our understanding of macroecological patterns as well as the potential effects of global change threats on species and biodiversity.

Environmental signals in evolutionary patterns

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Ecological and evolutionary processes form a continuum. But how short-term ecological interactions are translated in long-term evolutionary dynamics remains one of the key lacks in our understanding. This challenge is reflected in the unresolved debate on one of the most prominent but also controversial examples of convergent evolution – the above average development of secondary woody structure among herbaceous species on islands. The evolutionary phenomenon is particularly emergent on oceanic islands were almost 50% of all plants that evolved to new species are herbs that developed secondary woodiness, independent of phylogenetic history. Despite various prominent studies, all of the five major ecological hypotheses put forward to explain this global evolutionary

phenomenon since Darwin first discussed insular woodiness in 1859 are still valid. I will show that the current distribution of species that develop insular woodiness has a clear environmental signal that can help to enhance our understanding on the drivers behind this evolutionary phenomenon. Secondary woodiness is, however, not the only phenomenon were the simultaneous study of current ecological characteristics and long term evolutionary dynamics yields promising insights.

Island Biogeography meets Macroecology

Patrick Weigelt[1,*], Holger Kreft[1]
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Islands are key model systems in biogeography and ecology. Thanks to recent methodological advances and increased accessibility to large data sources, studying island biodiversity at the global scale has become feasible. This opens up new avenues to better understand general patterns and their drivers in a changing world. In this talk, I present the first comprehensive environmental characterization of the world's islands, covering past and present bioclimatic and physical island characteristics. To investigate how these island characteristics influence the diversity and assembly of island floras, my colleagues and I assembled a global database of vascular plant species composition currently including 180,000 species and covering 1,350 islands and 500 mainland regions. We show how different aspects of island environments affect various facets of insular diversity (including species richness, turnover, phylogenetic diversity) across spatial scales and major plant groups, in accordance with their predominant dispersal- and speciation-related traits and adaptations to climate. We furthermore show how Late Quaternary environmental change, e.g. climate-induced sea-level change, is essential to understand patterns of island endemism and its underlying immigration, speciation and extinction dynamics on islands. As such, our research contributes to a better understanding of the environmental and evolutionary drivers of plant assemblage composition.

Regular talks (in alphabetical order by first author)

Adding a genotypic perspective in niche modeling and theory

Jan O. Engler[1,2,*], Niko Balkenhol[2], Catherine H. Graham[3]
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Environmental niche models (ENM) are a central tool to quantify species-environment relationships and understand species distributions. These models are based on Hutchinson's niche concept which assumes that species niches are constrained by a combination of environmental tolerances and biotic interactions. Use of this concept as a basis for ENMs has been criticized and should be refined to include more biological detail. To this end, researchers have called for an integration of genetic information into ENMs. However, a conceptual framework that integrates contemporary genetic information into niche theory is currently lacking, but necessary to realize the full potential of amalgamating genetics and ENMs. Here, we build on existing ENM theory to show how genetic data can be used to evaluate functional connectivity, spatial genetic structure, hybridization, density-dependent priority effects, and source-sink dynamics – all of which can influence species niches and hence ENMs. Linking genetic and distribution data offers the opportunity for making better predictions of current and future distributions, and expands our understanding of inter- and intraspecific niche dynamics. We provide recommendations for the design of integrated studies using genetic information that will enhance our understanding of species distributions in the era of the Anthropocene.

Spatial patterns of Leaf Mass per Area in a wetland under water stress

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Leaf Mass per Area (LMA) is related to the leaf investment of plants. Differences in LMA between species as well as among individuals of a single species indicate plant responses to environmental processes. LMA is further linked to the spectral signal and can be recovered from optical remote sensing data. In the present study we test the indicator potential of remotely sensed LMA in a wetland under water stress. The study took place in Las Tablas de Daimiel, Spain. Human induced activities led to decreasing water levels in this wetland. We sampled the vegetation and soil and acquired imaging spectroscopy data of the study area. To quantify the relation between the spectra and LMA, an inverted radiative transfer model was used. This model had a fit of R^2=0.93 and a RMSE=0.0013 gcm^{-2}. The model was applied onto the image data for a pixel-wise prediction of LMA. For plants in good vigor, the prediction met the LMA values published in trait data bases. The resulting map allowed for spatial analyses of the LMA distribution across different vegetation types and of effects of plant stress. We conclude that imaging spectroscopy is a powerful tool for spatial analyses of functional traits.

Body-mass evolution in Neogene large mammals and the status of Cope's rule

Shan Huang[1,*], Jussi T. Eronen[2], Christine M. Janis[3], Juha J. Saarinen[2,4],
Daniele Silvestro[5], Susanne A. Fritz[1]
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Body mass increased towards Recent in many taxa, and several different processes can generate this trend. A bounded diffusive process can generate a significant increase of median and maximum body mass through time, without raising the minimum. An active evolutionary trend of increasing body mass might be generated by strong associations of body mass with taxon origination and/or extinction. To identify the macroevolutionary scenarios for body mass in Neogene large mammals (e.g. terrestrial ungulates), we analysed an extensive body mass data set of fossil and extant species in a Bayesian framework. To reconstruct the temporal patterns of body mass evolution, we estimated species origination and extinction times based on fossil occurrences. We then assessed whether changes in body mass are linked to species diversification dynamics by comparing different trait-correlated birth-death models. We found that not all of our focal groups show significant increases of body mass through time. More interestingly, for groups that apparently evolved to larger size since Miocene, body mass might covariate with speciation or extinction depending on the taxa and regions. Our results convey contrasting processes that lead to apparently similar evolutionary trends, and suggest an important role of regional effects in shaping mammal body mass evolution.

Ecological implications of flower color change in fertilized and unfertilized grassland over the past 150 years

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Scientists and nature conservation agencies claim a change in the colour composition of mesic grasslands over the past decades. However, flower colour diversity has mainly been addressed via indirect processes like the loss of species richness through shifts in land-use intensity or management practices. Quantitative studies, directly investigating flower colour change over time are still lacking. We analysed data from the Park Grass Experiment, the oldest, still maintained long-term experiment worldwide, to evaluate

changes in the herb species community coloration under varying management scenarios. Community coloration was assessed over the last 150 years for fertilized and unfertilized sites. Flower colour diversity was quantified by assessing community coloration in the colour perceptional space for the common honey bee. Our results show a continuous decrease in flower colour diversity over time and an increase with species richness in the unfertilized sites. In fertilized grassland sites, community coloration is less diverse than in unfertilized sites and decreases with intensification of nutrient application. A decline in flower colour diversity along with a reduction in herb species richness likely has a strong impact on prevailing plant pollinator interactions with high flower colour diversity promoting a more diverse set of pollinating species with different foraging strategies.

Latitudinal and altitudinal plant diversity patterns in the tropical Andes

Jens Mutke[1,*], Tim Böhnert[1], Constantin Poretschkin[1], Corinna Treydte[1],
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The tropical Andes are a hotspot of biodiversity, housing at least four times more plant species than the entire European flora. Today, especially the highly diverse mountain forests are under severe threat from the expanding agricultural frontier and mining activities. Additional impact by future climate change is predicted. Unfortunately, the detailed spatial patterns of biodiversity in many parts of the tropical Andes are still very poorly known and only limited data are available for prioritizing conservation action in this region. We investigate distribution and diversity patterns of plants along altitudinal and latitudinal gradients with two main datasets. Over 1.3 million GBIF records were used to investigate genus level patterns of floristic turnover. Additionally, a dataset of selected mid elevation to upper montane plant genera (12 genera, > 600 species, c. 12,000 records) was used for a more detailed study, based exclusively in critically revised records. Both datasets confirm extremely small distribution ranges for many taxa, resulting in high floristic turnover and a high irreplaceability of the respective forests in a species conservation context. The Amotape-Huancabamba Zone in northern Peru and southern Ecuador shows a clear diversity peak of overall species richness as well as for narrowly endemic species.

Ensemble Forecasting of Raccoon Distribution in West Asia

Aidin Niamir[1,*], Sam Khosravifard[2]
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Raccoon (*Procyon lotor*) is a native species in the Western Hemisphere and has been introduced to the Eastern Hemisphere less than 100 years ago. Raccoon has been extending its range in Northern Europe and Caucasia. In Iran, raccoon was reported for the first time in 1991. Since then, scattered observation records implied that the

distribution of raccoon is rapidly advancing in Caspian forests. In this study we employed an ensemble of species distribution models, to forecast the potential invasive distribution of raccoon in mainland Iran and West Asia. We used 12 environmental explanatory variables prone to affect the distribution of raccoon. We trained our models using species occurrence records from their native distribution obtained from GBIF, and then transferred the models to the study area. The forecasted potential distributions were evaluated using observation records from Iran. Our results revealed that the potential invasive distribution of raccoon in West Asia is quite widespread. Distance to anthropogenic activities increased the habitat favorability, while long freezing period and severe drought were limiting factors. Furthermore, we projected the models using global climate data from IPPC Fifth Assessment to explore the potential dispersal extent of raccoon in response to climate change.

Seasonality of habitat selection shown to buffer alpine reindeer pastoralism against climate variability

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Climate-driven variability of habitat selection of large herbivores has not yet been explicitly analyzed. To this end, we aimed to better understand the climate-ecological mechanisms behind geographic patterns of reindeer (*Rangifer tarandus tarandus*) habitat utilization. We analyzed habitat selection of GPS-collared reindeer over a period of five years by applying a novel stepwise factor analysis approach based on the niche concept. Our results reveal complex spatiotemporal patterns of habitat selection that are driven by seasonality, year-to-year climate variability, and the choice of individual animals. Contrasting expected similarities between conspecifics, our analyses revealed varying degrees of intra-species variability and therefore suggest that responses of individual reindeer to climate variability are inconsistent. Moreover, we found annually reoccurring patterns of habitat selection strength during different seasons that help explain coping capacities of reindeer against climate variability. In contrast with our expectations, we detected a very high inter-annual variability in habitat preferences to be related to governing climatic conditions. Here, we present new evidence for the variability of response mechanisms of reindeer's habitat selection to buffer alpine pastoralism against climate variability. Our work contributes to a better understanding of alpine ecological response mechanisms as a key for projections of future responses to climate change.

The macroecology of alien species – challenges, patterns and predictions

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Thousands of species were introduced into regions outside their native range by human assistance. After initial introduction many of these species establish populations and spread further within the alien range. The highly dynamic nature of alien species distributions represents a major challenge for the analysis of the marcoecology of alien species. The macroecology of alien species can therefore only be understood if the global spreading dynamics of alien species are taken into account. A major driver of alien species spread is global trade, but the global flows of commodities have never been compared to the global flows of alien species. Using global databases of native and alien ranges, we show that the distance between native and alien ranges is a hump-shaped function of distance, while trading activities decline with distance. Thus, trade alone is a poor predictor for the spread of alien species particularly at short distances, which is in contrast to common knowledge. This discrepancy can be solved in a simple model thereby combining trading activities with biogeographical dissimilarity, a measure for the probability of introducing an alien species. Model predictions agree well with field observations. This study represents an example of how socio-economic and biogeographical processes can be combined to describe global patterns of alien species spread.

Examining macroecological patterns of animal movement

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Understanding the causes and consequences of animal movements is important because any changes in movement can have both direct and indirect effects on ecosystem structure and function. There are large variations in movement patterns among animal species and this variation has been attributed to life history traits, environmental characteristics and phylogenetic relationships. Despite the abundance of movement ecology research, the effects of life history, environment and phylogeny have often been studied in isolation and the majority of movement ecology studies have focused on single species, limiting our understanding of how individual movements form global movement patterns. In collaboration with more than 100 co-authors and data contributors, we compiled a data base of more than 50 mammal and 70 bird species to characterise global movement patterns and examine their underlying drivers. We calculated various movement measures, extracted life history traits and phylogenetic information from the literature, and annotated relocations using environmental data on vegetation and climate.

We compare movements across taxonomic groups, diet guilds, and also examine environmental influence on movement patters. Our findings contribute to the broad-scale understanding of animal movements and are important for understanding a range of ecological patterns including species interactions and animal responses to changing environments.

Degradation and Greening in an arid mountain ecosystem – the case of the Western Pamirs of Tajikistan

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The Western Pamir of Tajikistan is an arid mountain region that is strongly affected by climate and land-use change. In particular, after the breakdown of the Soviet Union in 1991 pressure on natural resources and human induced land cover degradation strongly increased. This is primarily associated with a demand for fuel and agricultural products leading to deforestation and overgrazing, in particular of lower elevation vegetation types. In contrast to degradation, an increase in vegetation cover could be detected on highly elevated screes and moraines, landscape units where no or very scattered vegetation was mapped by Soviet scientist in 1960. This development might be linked to a consistent temperature increase over the last decades. As temperature is one of the major limits on plant growth, global warming reduces this constraint. The consequence is an increment of species richness and vegetation cover in alpine areas, triggered by an upward shift of species from lower elevations. In the talk I will evaluate, where, why and when degradation and greening occurred in the Western Pamir's Rushan Range, based on historical vegetation maps and remote sensing time series.

Short talks (in alphabetical order by first author)

Erosion of natural darkness in the geographic ranges of cacti

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Naturally dark nighttime environments are being widely eroded by the introduction of artificial light at night (ALAN). The biological impacts vary with the intensity and spectrum of ALAN, but have been documented from molecules to ecosystems. How globally severe these impacts are likely to be depends in large part on the relationship between the spatio-temporal distribution of ALAN and that of the geographic ranges of species. Here, we determine this relationship for the Cactaceae family. Using maps of the geographic ranges of cacti and nighttime stable light composites images for the period 1992 to 2012, we found that a high percentage of cactus species were experiencing ALAN within their ranges in 1992, and that this percentage had increased by 2012. For almost all cactus species (89.7%) the percentage of their geographic range that was lit increased from 1992-1996 to 2008-2012, often markedly. There was a significant negative relationship between both the species richness of an area, and that of threatened species, with the level of ALAN. Cacti could be particularly sensitive to this widespread and ongoing intrusion of ALAN into their geographic ranges, especially when considering the potential for additive and synergistic interactions with the impacts of other anthropogenic pressures.

Abandoned foreigners: is the stage set for pet reptiles to invade Central Europe?

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Several reptiles are commonly traded on pet markets and the question arises at what extend they might succeed to establish and pose a threat to native reptile species, when intentionally or accidentally released into the wild. We performed an integrative risk assessment for 20 frequently traded reptile taxa. Species distribution models were conducted to determine the climate match between native and non-native geographic ranges. Niche assessments were employed to characterise traits and niche axes that are shared by native and non-native species. We tested for discrepancies in niche breadth between native and non-native ranges and additionally estimated the ability of the target species to coexist with humans. For the majority of species potentially suitable climates were found throughout the study region. Already being characterised by broad climate niches in their native ranges, niche breadth of the target species considerably increased with regard to their introduced ranges. Nevertheless, climate match scores between native and non-native ranges were consistently low. High percentages of presence localities found in human-dominated areas suggest high capabilities to cope with anthropogenic impacts. In non-native ranges, human foot print indices considerably decreased in all studied taxa. Climate niche overlap between native and non-native species was low to moderate in terms of Schoener's D values. However, high similarity was found in reproductive niche space, with squamates showing larger overlap than testudines with native species. Despite high propagule pressure and the presence of climatically suitable habitats with moderate human impacts, none of the study species showed a distinct invasion risk. Hence, competitive displacement of native reptiles due to overlap in climatic and reproductive niche space may be neglected.

Estimation of taxonomic richness variation through geological times: a simulation approach

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Estimating taxonomic richness and its variations through geological time is a notoriously difficult task, due to several taphonomical and methodological reasons making the reconstructed signal potentially distinct from the real (but unknown!) one. Through a simulation approach, we examine the effect of a major, while surprisingly still understudied source of potential disturbance: the effect of time discretization through biochronological construction, generating spurious coexistences of taxa within biozones, and thus ultimately making continuous- and discrete-time taxonomic richness curves very different. Our approach relies on continuous-time simulated biodiversity curves, then time-discretized to estimate the actual loss of information generated by this manipulation. A broad spectrum of dataset parameters (e.g., average biozone duration, total number of taxa, average taxonomic longevity) are tested through sensitivity analysis, showing that the worsening effect of time-discretization on the biodiversity signal highly depends on such parameters. Based on these simulation results, we propose a simple algorithm allowing the back-transformation of a discrete-time taxonomic richness dataset as customarily constructed by palaeontologists into a continuous-time dataset. We show that the biodiversity curve obtained this way fits the original signal much more closely, even when the initial dataset conditions are particularly hostile to an efficient time-discretized reconstruction.

Do biogeographic drivers modify global treeline elevations?

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Today's treeline research generally focuses on physiological limitations of tree growth whereas biogeographic drivers such as isolation, continentality and mass elevation effect (MEE) often neglected or reduced as local or regional peculiarities. Even tough trees cannot avoid fundamental environmental limitations, biogeographic drivers modify treeline elevations also at the global scale. MEE, which affects regional climate conditions, and continentality have been described quite often, but these quantifications have often been unconvincing and a clear separation of both concepts is often missing. We sampled the largest global treeline data sets up to date (n=672) to investigate these biogeographic drivers using a systematic sampling design with GoogleEarth. We found a subtropical double hump of treeline elevations along the latitudinal gradient, negative isolation effects on both, island and continental mountains, a strong increase of treeline elevation with MEE and independent effects of continentality. Interestingly, besides latitude, MEE was thereby the most important of global treeline elevations. Our study shows a globally consistent effect of MEE on treeline elevations, contributing to our basic understanding of large-scale biogeographic processes governing treeline formation. Isolation may be a result of immigration; cloudiness seems to modulate the solar radiation regime thus MEE and continentality increase treeline elevations.

Where are the most unique forested area to preserve?
– A cross-scale study –

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The importance and role of forest on earth in crucial for the global climate, atmosphere composition, biodiversity and therefore, human well-being. Abiotic factors such as the temperature or topography of an area are known to impact its biodiversity. For this purpose, we identified the worldwide unique forests through two different scales according to their biophysical conditions with the assumption that the disappearing of these unique sites would lead to abiotic local changes and impact the local biodiversity. We used a bird's range size indicator to identify the diversity value of these sites and prioritize the conservation effort. To identify forested areas having the most singular biophysical features, we used a systematic screening method analysing the ecological features through multivariate statistics. Once we identified such areas at the global and

biome scales, our results revealed the importance of the link between the forest land cover type and the biophysical uniqueness.

Cross-scale similarity of species temperature niches

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Scale-dependence is still one of the major topics in ecology. Ecosystem responses to environmental stressors are believed to be scale-dependent. However, projections about future climate change effects on biodiversity are still restricted to certain scales with lacking knowledge about scale-dependence of ecological patterns and processes. Here we propose that strong cross-scale links between micro- and macro-environmental drivers and low environmental noise on small spatial scale will go along with high cross-scale similarity (low scale-dependence) of ecological patterns. We therefore combined information of species spatial occurrence with information about the corresponding temperature regime of vascular plant species occurring in environmentally stable, wetland ecosystems characterized by tight cross-scale links micro- and macroclimatic conditions. We observed high cross-scale similarity of species temperature niche characteristics across the seven orders of magnitude of investigated spatial scale ranging from local to continental scale. However, the importance of temperature as abiotic driver decreased non-linearly with decreasing scale, suggesting a higher importance of additional (biotic) drivers of species occurrence on small spatial scales. By increasing general understanding about scale-dependence of species temperature niches our results will help to improve niche-based species distribution modelling, one of the major assessment-tools for ecological climate change effects.

Scales have a major impact on the cross-relationships among phylogeny, spatial distribution and species duration in fossil cephalopods

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Using a high-resolution dataset on Early Jurassic (~190.8 Ma to 187.6 Ma) ammonites of the western Tethys and adjacent areas (*i.e.,* the present-day Europe and North Africa), we investigate their deep-time macroecological properties in a context of marked provincialism. We focus our study on the potential correlation among phylogenetic

relatedness, range size, and species duration. We find that the relationship among these three parameters depends on both the range-size estimate (area, latitudinal/longitudinal range, or the number of occurrences) and the area considered (a province or the whole western Tethys). We also analyze Similarity Distance Decay (SDD) relationships - the decrease in compositional similarity with geographical distance - at various spatial, sampling and phylogenetic scales. We show that the spatial scale may influence SDD patterns in an unpredictable way and that the phylogenetic level has a major impact on these patterns. Our results also indicate that SDD cannot be used as a straightforward mean to characterize the existence of a biogeographical structuring; and that the long-distance dispersal of ammonites is not related to shell size and morphology, but rather to the environmental characteristics of the province to which they belong. Overall, we call for a multi-scale approach when studying biogeographical patterns with SDD analyses in order to distinguish genuine signals from scale effects.

Ignites (in alphabetical order by first author)

A model-based approach to calculating the community temperature index

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Monitoring species response to climate change is an important challenge for ecologists. Generalized and relatively simple approaches that can be applied to population census data regardless of taxonomic group and habitat are particularly useful as climate change indicators. Temperature niche is a key species attribute expected to strongly influence how species respond to climate change. The community temperature index (CTI) - a community weighted mean of temperature niche - has been used as an indicator of climate change impacts on communities. However, species temperature niche covaries with other species attributes, such as habitat preference, and thus the CTI might also capture the effects of other environmental drivers. We propose a model-based approach to separate temperature niche effects from other potential species attribute effects. We apply our approach to long-term population data of breeding birds in Denmark and demersal marine fish in the North Sea and compare the CTI trends with and without accounting for covariation among species attributes.

Testing for body size divergence in Neotropical bats

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Closely related species are usually similar in morphology and ecological preferences. When close relatives live in the same area, they must differ in at least one ecologically-relevant trait to avoid competition. Body size can be such trait, because it relates to reproduction, physiology, and ecology. Divergence in body size might allow closely related species to partition space or resources. Two species of yellow-shouldered bats (*Sturnira hondurensis* and *S. parvidens*) occur in Mexico, with geographic ranges and diagnostic physical measurements that almost completely overlap. At a finer geographic scale *S. parvidens* is a predominantly lowland species, while *S. hondurensis* occupies higher elevations. On average, the highland species *S. hondurensis* is slightly larger-bodied. Anecdotal field data suggests that the interspecific difference in body size is greater when both species occur in the same area than the overall size difference between both species. To test this, representative body size measurements and elevation data for both species across their range have been collected from museum specimens. This presentation aims to generate discussion on the best ways to test for body size divergence.